The Mkk2 MAPKK Regulates Cell Wall Biogenesis in Cooperation with the Cek1-Pathway in Candida albicans

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Abstract

The cell wall integrity pathway (CWI) plays an important role in the biogenesis of the cell wall in Candida albicans and other fungi. In the present work, the C. albicans MKK2 gene that encodes the putative MAPKK of this pathway was deleted in different backgrounds and the phenotypes of the resultant mutants were characterised. We show here that Mkk2 mediates the phosphorylation of the Mkc1 MAPK in response to cell wall assembly interfering agents such as zymolyase or tunicamycin and also to oxidative stress. Remarkably, mkk2 and mkc1 mutants display related but distinguishable cell wall associated phenotypes and differ in the pattern of MAPK phosphorylation under different stress conditions. mkk2 and mkc1 mutants display an altered expression of GSC1, CEK1 and CRH11 genes at different temperatures. Combined deletion of MKK2 with HST7 supports a cooperative role for the Cek1-mediated and CWI pathways in regulating cell wall architecture under vegetative growth. However, and in contrast to Mk1, Mkk2 does not seem to play a role in the virulence of C. albicans in the mouse systemic model or the Galleria mellonella model of infection.

Introduction

Maintenance of fungal integrity relies on proper signalling mechanisms within the cell. Potentially harmful environmental conditions trigger signalling pathways that lead to appropriate transcriptional responses. While these responses are important to every living organism, they are crucial in pathogens, where continuous challenge to host defences may lead to efficient eradication of the pathogen or lead to the development of disease. Candida albicans is an opportunistic pathogen that inhabits the gastrointestinal and vaginal tract of humans, being able to cause different diseases upon alteration of host defences. Within these niches, C. albicans may be exposed to changes in pH, oxidative stress, detergents or interactions with other components of the host microbiota and host immune defences that trigger in the fungus a coordinated response. In C. albicans, as in almost every eukaryotic cell, different MAPK pathways have been described to play an essential role in these processes [1]. The Cek1 MAPK was isolated as a dominant negative gene that interfered with pheromone-mediated cell cycle arrest...
in *Saccharomyces cerevisiae* [2]. In *C. albicans*, Cek1 was later shown to be involved in invasive growth [3] and participate in cell wall construction [4]. Cek1 receives the input via the Sho1 [4], Msb2 [5] and Opy2 [6] membrane proteins which connect the triggering stimulus through Cst20 to the Ste11-Hst7-Cek1 MAPK cascade core. Cek1 also participates in the white-cell pheromone response (involved in biofilm formation) and the opaque-cell pheromone response (involved in mating). Transcription factors mediating these responses are Tec1 and Cph1 respectively [7–9]. Cek1 is a member of the formerly called SVG pathway (Sterile_Vegetative Growth) [10] that in *S. cerevisiae* mediates cell wall growth under vegetative conditions. The HOG (High Osmolarity Glycerol response) pathway is important for adaptation to osmotic and oxidative stress [11–14] but is also involved in morphogenesis and virulence [15, 16]. This pathway also participates in cell wall biogenesis as shown by the decreased susceptibility of hog1 mutants to certain antifungals such as Congo Red and Calcofluor White [15], which suggests a connection of this pathway with chitin synthesis [17]. The situation is complex, as deletion of *HOG1* results in an enhanced basal activation of Cek1 while diminishes the activation of the cell integrity MAPK (Mkc1) upon different stresses, indicating the existence of cross-talk mechanisms among these routes [4, 18–20].

The cell wall integrity (CWI) pathway is mediated by the *MKC1* gene, originally cloned by its ability to complement *S. cerevisiae* slt2 mutants thermosensitivity [21]. In *S. cerevisiae*, activation of Slt2 (the homologue of Mk1) is dependent on the presence of different membrane sensors (Wsc1, Wsc2, Mid2 and Mtl1) which connect to the conserved MAPK core: Bck1-Mkk1/Mkk2–Slt2 (see [22] for a review). In this yeast, two redundant MAPKKs have been described, ScMKK1 and ScMKK2 [23], both being able to interact not only with Slt2 [24] but also Mkc1 [25] in a *S. cerevisiae* two hybrid system. Interestingly, ScMkk2 and ScMkk1 are able to be phosphorylated by Slt2 in a complex feedback mechanism which modulates the activity of Slt2 [26]. The relevance of this route in *C. albicans* is revealed by the fact that *mkc1* mutants are sensitive to different antifungals such as azoles, echinocandins and cell wall degrading enzymes [25]. Mk1 is also involved in biofilm formation being activated by surface contact that presumably facilitates invasion of solid surfaces [27]. Mk1 is activated in response to a wide variety of stresses [20] and plays a role in virulence in the mouse systemic model [28]. Its role in promoting cell integrity seems especially relevant under temperature stress [21, 29]. Mk1 is a client protein to the Hsp90 chaperone [30], which controls antifungal resistance in close connection with the calcineurin pathway [31]. While phenotypic analyses indicate close similarities between *S. cerevisiae* and *C. albicans* CWI routes, there also seem to exist important differences. A relevant feature is the presence in *C. albicans* of a single MAPKK, named Mkk2. Given the potential role of this pathway in antifungal discovery, we were interested in knowing the role of this gene in the biology and pathogenesis of this fungus. We demonstrate here that it participates in fungal cell wall construction showing similar, but also distinct, phenotypes with those displayed by *mkc1* mutants.

**Materials and Methods**

**Ethics statement**

All the animal experiments performed in this work were carried out in strict accordance with the regulations in the “Real Decreto1201/2005, BOE 252” for the Care and Use of Laboratory Animals of the “Ministerio de la Presidencia”, Spain. The protocol was approved by the Animal Experimentation Committee of the University Complutense of Madrid (Permit Number: BIO2012-31839–1). Animals were monitored every 12 hours (approx., first 5 days) or daily (days 5 to 15) and all efforts were made to minimise suffering. When visible signs of disease where observed (reluctance to move, disorientation and/or lack of mobility), mice were
immediately euthanised. The procedure used was by CO₂ inhalation following standard protocols (AVMA Guidelines for the Euthanasia of Animals: 2013 Edition). Mice were also euthanised at the end of the experiment (15 days). The number of animals used in the experimentation was minimised for ethical reasons.

**Strains and growth conditions**

Yeast strains used in this work are summarised in Table 1. Unless otherwise stated, the mutant strains used here are all homozygous null mutants (deletion of both alleles) in a heterozygous (URA3/ura3) background. Yeast strains were routinely grown in YPD medium (1% yeast extract, 2% peptone, 2% glucose) at 30°C. Drop susceptibility tests were performed by adjusting cell suspension to 10⁸ cells/mL; then 1/10 serial dilutions of cells were spotted on plates supplemented with the compound under analysis at the indicated concentration. Plates were incubated at 37°C (unless otherwise stated) until they were scanned. The colony morphology was tested using Spider medium (1% mannitol, 1% nutrient broth, 0.2% K₂HPO₄, and 1.35% agar) and incubated for seven days at 37°C as previously described [32]. We have avoided using the prefix Ca to refer to *C. albicans* genes, but used instead the prefix Sc to refer to the corresponding *S. cerevisiae* gene only where confusion could occur.

**Molecular biology procedures and plasmid constructions**

For the disruption of the MKK2 gene, the primers o-1MKK2 (GGTACCAGGAAGGAATGTA TAATGACAA) and o-2MKK2 (CTCGAGATCTCTTTTGGGAGGTCTTCTTC) were used to amplify a 712 bp fragment flanking the 5’ region of the MKK2 ORF; similarly, o-3MKK2 (GCGGCCGCTGATGAATGGTGCTTGATCC) and o-4MKK2 (GAGCTCGCACAAATAAACAGAT ACACAAAGC) were used to amplify a 832 bp fragment flanking the 3’ region of the MKK2 ORF. Both fragments were subcloned in the cloning vector pGEM-T (Promega) and excised as a KpnI-XhoI and NotI-SacI fragments respectively. These fragments were then cloned into the *C. albicans* disruption plasmid pSFS2a [33] which carries the nourseothricin resistance marker (SAT1) and the 2 μ flipase gene (FLP) under the control of the MAL2 promoter flanked by FRT sequences. The plasmid generated, pDMKK2, was digested with KpnI and SacI for integration in the *C. albicans* genome. Two rounds of integration/excision were necessary to generate a homozygous deletion mutant in the CAF2 background following the method described previously [33]; nourseothricin concentration for transformant selection was 200 μg/mL. Correct integration and excision were tested by Southern blot. A similar procedure was followed to delete the gene in the other strains (mkc1, hst7 and pbs2). For MKK2 reintegration, a fragment of 2794 bp that includes both the MKK2 ORF and 938 bp upstream was amplified by PCR with the primers o-MKK2-R-up (TTGAACTCGAGTGTTGGTGGTAAAAGAGCTGCAGC) and o-MMK2-R-low (GTTAATCGATAACACAGATGGAATAG). This fragment was subcloned in the cloning vector pGEM-T (Promega), excised with Hind III-XhoI and inserted in the pDARD1 vector [16] digested with the same pair of enzymes. The resulting plasmid, pDMKK2-R, was digested with PvuI SacI for reintegration in the ARD1 locus.

**Growth inhibition assays**

To measure growth inhibition caused by either zymolyase or tunicamycin, cell cultures were inoculated from an overnight culture to an O.D.₆₂₀nm = 0.025 in YPD medium supplemented with different amounts of either zymolyase100T (ICN Biomedicals, Inc., dissolved in Tris-HCl [pH 7.5]–5% glucose) or tunicamycin (Sigma-Aldrich, dissolved in DMSO). The assay was performed using duplicate rows of a 96-well plate and incubated overnight at 37°C. Graphs
| Strain   | Genotype                                                                 | Nomenclature in Manuscript and Figures | Source |
|---------|---------------------------------------------------------------------------|---------------------------------------|--------|
| CAF2    | URA3::ura3Δ::imm434                                                       | wt                                    | [65]   |
| RM100   | ura3Δ::imm434/ura3Δ::imm434 his1Δ::hisG/URA3-hisG                          |                                       |        |
| CNC13   | ura3Δ::imm434/ura3Δ::imm434 his1Δ::hisG/URA3-hisG                          | hog1                                  | [11]   |
| BRD3    | ura3Δ::imm434/ura3Δ::imm434 his1Δ::hisG/URA3-hisG                          | pbs2                                  | [18]   |
| CDH10   | ura3Δ::imm434/ura3Δ::imm434 hst7Δ::hisG/URA3-hisG                          | hst7                                  | [66]   |
| CM-1613 | ura3Δ::imm434/ura3Δ::imm434 mkk1Δ::hisG/URA3-hisG                          | mkk1                                  | [21]   |
| AMB1    | URA3/ura3Δ::imm434 MKK2/ mkk2Δ::SAT1-FLIPP                                  | This work                             |        |
| AMB2    | URA3/ura3Δ::imm434 MKK2/ mkk2Δ::FRT                                        | This work                             |        |
| AMB3    | URA3/ura3Δ::imm434 mkk2Δ::FRT/mkk2Δ:: SAT1-FLIPP                            | This work                             |        |
| AMB4    | URA3/ura3Δ::imm434 mkk2Δ::FRT/mkk2Δ:: FRT                                  | mkk2                                  | This work |
| AMB5    | ura3Δ::imm434/ura3Δ::imm434 mkk1Δ::hisG/URA3-hisG MKK2/ mkk2Δ:: SAT1-FLIPP  | This work                             |        |
| AMB6    | ura3Δ::imm434/ura3Δ::imm434 mkk1Δ::hisG/URA3-hisG MKK2/ mkk2Δ:: FRT         | This work                             |        |
| AMB7    | ura3Δ::imm434/ura3Δ::imm434 mkk1Δ::hisG/URA3-hisG mkk2Δ:: FRT/ mkk2Δ:: SAT1-FLIPP | This work                             |        |
| AMB8    | ura3Δ::imm434/ura3Δ::imm434 mkk1Δ::hisG/URA3-hisG mkk2Δ:: FRT/ mkk2Δ:: FRT  | mkk1 mkk2                             | This work |
| AMB9    | ura3Δ::imm434/ura3Δ::imm434 hst7Δ::hisG/URA3-hisG MKK2/ mkk2Δ:: SAT1-FLIPP  | This work                             |        |
| AMB10   | ura3Δ::imm434/ura3Δ::imm434 hst7Δ::hisG/URA3-hisG MKK2/ mkk2Δ:: FRT         | This work                             |        |
| AMB11   | ura3Δ::imm434/ura3Δ::imm434 hst7Δ::hisG/URA3-hisG mkk2Δ:: FRT/ mkk2Δ:: SAT1-FLIPP | This work                             |        |
| AMB12   | ura3Δ::imm434/ura3Δ::imm434 hst7Δ::hisG/URA3-hisG mkk2Δ:: FRT/ mkk2Δ:: FRT  | hst7 mkk2                             | This work |
| AMB13   | ura3Δ::imm434/ura3Δ::imm434 pbs2Δ::cat/URA3- cat MKK2/ mkk2Δ:: SAT1-FLIPP  | This work                             |        |
| AMB14   | ura3Δ::imm434/ura3Δ::imm434 pbs2Δ::cat/URA3- cat MKK2/ mkk2Δ:: FRT         | This work                             |        |
| AMB15   | ura3Δ::imm434/ura3Δ::imm434 pbs2Δ::cat/URA3- cat mkk2Δ:: FRT/ mkk2Δ:: SAT1-FLIPP | This work                             |        |
| AMB16   | ura3Δ::imm434/ura3Δ::imm434 pbs2Δ::cat/URA3- cat mkk2Δ:: FRT/ mkk2Δ:: FRT  | pbs2 mkk2                             | This work |
| AMB17   | URA3/ura3Δ::imm434 mkk2Δ:: FRT/mkk2Δ:: FRT ARD1/ard1Δ:: MKK2-SAT1          | MKK2                                 | This work |

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represented the percentage of growth estimated by O.D. 620 nm measures for each strain in YPD plus both compounds compared to similar untreated cells.

### Protein extracts and immunoblot analysis

Yeast strains were exposed to different compounds for different times, indicated in each case. Samples were then collected on ice and processed for immunoblot following the protocol previously described [34]. To equalise the amount of protein loaded, samples were analysed by
measuring the $A_{280}$ nm and then by Coomassie staining and 50 μg of protein was used for western blot. Blots were probed with anti-phospho-p38 MAP kinase (Thr180/Tyr182) 28B10 monoclonal antibody for Hog1-P detection (Cell Signaling Technology); ScHog1 (γ-215) polyclonal antibody for detection of Hog1 (Santa Cruz Biotechnology), anti-phospho-p44/p42 MAPK (Thr202/Tyr204) antibody (Cell Signaling Technology, Inc.) was used for Cek1-P and Mk1-P detection. Cek1 and Mk1 protein levels were determined using previously described polyclonal sera [4, 20].

Virulence assays

Female BALB/c mice obtained from Harlan Laboratories Inc. (Italy) were used within an age of 7 to 10 weeks-old and around 18 g weight. Mice housing and other non-invasive procedures were performed in the animal facility from the Medical School of the Universidad Complutense de Madrid. Virulence of C. albicans strains was tested using a murine systemic infection model described previously [28]. Briefly, mice were randomly separated into groups of 10 mice. This number was chosen using a Power and Sample Size Software (http://biostat.mc.vanderbilt.edu/PowerSampleSize) using an independent t-test assay, with the parameters $\alpha = 0.05$, Power = 0.90, difference in population means = 3, within group deviation = 2, and ratio of groups = 1. Cells of strains to be tested were collected from fresh YPD plates, washed twice with PBS and recovered by low speed centrifugation; then, $10^6$ yeast cells (in 250 μL) were inoculated into the lateral tail vein of BALB/c mice and the mortality was followed during 15 days. For the infection of Galleria mellonella we used a standard protocol [6]. Briefly, $10^6$ cells from overnight cultures grown in YPD at 30°C and washed in PBS were inoculated (10 μL) in the hemocoel at the last pro-leg with a Hamilton syringe. Groups of 20 larvae were used for each strain with an approximate weight of 300 mg and survival was monitored during the next 4 days. This number provides a Power = 0.95 using the above mentioned Power and Sample Size Calculation software using an independent t-test assay, with the parameters $\alpha = 0.05$, difference in population means = 1.2, within group deviation = 1 and ratio of groups = 1. Kaplan–Meier survival curves are shown.

Quantitative reverse transcription-PCR assay

Overnight C. albicans cultures incubated at 24°C were diluted to an O.D. $620$ nm = 0.1 in pre-warmed YPD at 24°C, 30°C, 37°C and 42°C and incubated for 1 h before being collected. Total RNA was isolated from cells using the RNeasy MINI kit (Qiagen, Hilden, Germany) and following the mechanical disruption protocol provided by the manufacturer. RNA concentrations were determined by measuring absorbance at 260 nm in a nanodrop spectrophotometer (ThermoScientific NanoDrop 2000C). First-strand cDNAs were synthesised from 2 μg of total RNA, using the Reverse Transcription System (Promega) following the recommendations of the manufacturer. Quantitative reverse transcription-PCR assay was performed following the protocol described previously [35] using SYBR Green Universal Master Mix (Applied Biosystems). Real-time PCR conditions were selected according to the Universal conditions (default conditions) recommended by the manufacturer of the instrument. Each cDNA was assayed in triplicate PCR reactions. The quantification of the abundance of each transcript was determined relative to the amount of the standard transcript of $ACT1$ at 24°C, and the final data on relative gene expression between the two conditions tested were calculated following the $2^{-\Delta\Delta Ct}$ method [36]. The primers were designed using the Primer Express Software 2.0 (Applied Biosystems). Primers Tm was close to 60°C and amplicons between 74 and 121 bp. The specificity of the primers was tested previously performing a melting curve analysis. The following forward and reverse primers were used as internal control o-ACTQTup (TGGTGTTCTATCTTGGCTTCA);
o-ACTQTw (ATCCACATTTGTTGGAAAGTAGA). To quantify the expression of CEK1 the primers used were: o-CEK1QTup (TTAGAAATTGTTGGAGAAGGAGCAT) and o-CEK1QTlw (GCAACTTTTTGTTGTGATGGTTTATG). GST1 and CRH11 expression was quantified using o-GST1QTup (TCAACAACAACCATATGACATGGA), o-GST1QTlw (ACCGCCATAACTAAAGTCAGAAAAG), o-CRH11QTup (ATCAAGAAATTGGAAAGTGGACAAT) and o-CRH11QTlw (AAGAGGCGGATGGACTGGGAT), respectively. Two independent experiments were done and the interexperiment Mean ± standard deviation (SD) is shown.

Flow Cytometry and fluorescence microscopy

To quantify glucan exposure yeast cells were grown overnight in YPD at 37°C. Cells were fixed with 3.7% paraformaldehyde (for 15 min at 4°C). Then, cells were collected and washed twice with PBS, incubated with 1% BSA in PBS 30 min and then incubated with anti-β(1,3)-glucan mAb (Biosupplies) for 30 min at 4°C. Then, cells were washed three times and incubated with the secondary antibody anti-IgG Alexa 488 for 30 min at 4°C. Cells were washed three times before being analysed by flow cytometry. The analyses were performed with a FACS guava easyCyte (Millipore). The relative mean fluorescence intensity is represented for each strain compared to wt strain values. The graph represents the mean of three independent experiments ± SD.

Chitin staining was performed on stationary phase cells grown at 30°C of the indicated strains. Cells were obtained by low speed centrifugation, washed twice with distilled water, fixed with 1% paraformaldehyde for 30 min. and stained at room temperature for 30 minutes with Calcofluor White (Sigma) at 50 μg/mL. Mean fluorescence intensity was determined from 50 single cell images taken in a Nikon Eclipse TE2000-U fluorescence microscope using a Hamamatsu camera and ImageJ Fiji software; the ratio to wild type is given ± SD.

Statistical analysis

One-way or two-way ANOVA followed by Dunnett’s correction for multiple comparisons was applied to evaluate differences among mutants as indicated in the figures. Data are expressed as the mean of at least three experiments ± SD. Statistics were performed using the GraphPad software. In all cases “ indicates p ≤ 0.05, “” p ≤ 0.01, and “”” p < 0.001. Survival data was analysed by Kaplan-Meier Log-Rank statistics. The Holm-Sidak post hoc test in an ANOVA test was used to evaluate significant differences in gene expression in qPCR experiments.

Results

Mkk2 controls the activation of Mkc1 in response to oxidative stress

To analyse the role of the MAPKK Mkk2 in C. albicans, the gene encoding Mkk2 was disrupted using the SAT1 flipper strategy; this system uses the dominant nourseothricin SAT1 marker flanked by the flipase recognition site FRT [37]. MKK2 5’ and 3’ regions were accommodated flanking this construction and used to sequentially delete both alleles of MKK2 (see Materials and Methods). We also deleted this gene in an mkc1 background to carry out epistasis studies. Given the relevance of responding appropriately to oxidative stress for pathogens and the implication of Mkc1 in this kind of stress [20], we first analysed the role of Mkk2 in response to hydrogen peroxide (H2O2). Exponentially growing cultures were challenged with 10 mM H2O2 and samples were collected 10 minutes later for western blot analysis. Wild type (wt) strain displayed a basal Mkc1 phosphorylation level that increased significantly when H2O2 was added to the cultures (Fig 1A). No Mkc1 phosphorylation was detected in mutants lacking Mkc1 and/or Mkk2 neither in basal nor upon H2O2 challenge. No major changes in Mkc1
Fig 1. Role of CWI pathway mutants in oxidative stress. A), B) and C) Exponentially growing cells (O.D. 620 nm = 1) of the indicated strains were exposed (+) or not (-) to 10 mM H₂O₂ for 10 min and samples were processed. The phosphorylated form of the MAPKs is expressed as Mkc1-P, Cek1-P and Hog1-P. Hog1 indicates the total amount of Hog1 protein which is used as an additional loading control; Mkc1 levels were determined using a polyclonal anti-Mkc1 serum. D) Susceptibility to H₂O₂ was analysed by standard drop susceptibility assays. Cultures growing exponentially were plated (10 fold serial dilutions) on YPD plates supplemented or not with 5 mM hydrogen peroxide and incubated at 37°C for 24 h.

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protein levels were observed in the mkk2 background. Therefore, Mkk2 is required for Mk1 phosphorylation upon basal and H2O2 addition. We have previously reported that the absence of Hog1 reduces the phosphorylation of Mk1 upon H2O2 [20] or arsenate challenge [38], reflecting the crosstalk between both MAPK pathways involved in oxidative stress response. We therefore also analysed the activation of Hog1 phosphorylation in mkk2 and mkc1 mutants. As observed in Fig 1B, the absence of Mkk2 did not reduce the activation of Hog1 in response to H2O2. Contrary, mkc1 cells showed reduced Hog1-P after a 10 min challenge with the oxidant. The double mkc1 mkk2 mutant behaved closer to a single mkc1 mutant, suggesting that this is an Mk1-dependent phenotype.

The MKK2 ORF under the control of its own promoter was integrated in the genome of the mkk2 mutant in order to verify that the lack of Mk1 activation was due to the presence of Mkk2. The generated strains were named M KK2 reint-1 and M KK2 reint-2 and included in the analysis. As expected, the reintegration of the MKK2 gene fully allowed Mk1 phosphorylation in response to oxidative challenge (10 mM H2O2 for 10 min) (Fig 1C) demonstrating that Mkk2 is the only MAPKK involved in Mk1 phosphorylation upon oxidative stress response.

The susceptibility of the mutant strains was determined on YPD plates supplemented with 5 mM H2O2. As showed in Fig 1D, no significant differences were observed between wt and mkc1, mkk2 and mkc1 mkk2 mutants. Since the HOG pathway is also involved in the response to oxidative stress we wondered if the deletion of MKK2 could influence the susceptibility of mutants in this pathway to oxidants. M KK2 was deleted in a pbs2 background (Pbs2 is the HOG pathway MAPKK) and susceptibility to H2O2 tested. As shown in Fig 1D, a double pbs2 mkk2 mutant did not show an increased susceptibility to this oxidant compared to a pbs2 strain. Collectively, these results indicate that Mkk2 plays an important role in sensing peroxide stress but it does not significantly alter the overall susceptibility to this compound in C. albicans.

**Mkk2 mediates Mk1 phosphorylation upon treatment with cell wall disturbing compounds**

Given the role of Mk1 in cell wall biogenesis, the phosphorylation pattern of MAPKs was analysed upon the addition of specific drugs previously known to activate this pathway [20]. Exponentially growing cultures were challenged either with tunicamycin, an inhibitor of N-glycosylation, or with the enzymatic complex zymolyase 100-T for 2 h. Both Mk1 and Cek1 become phosphorylated upon drug addition (Fig 2A). Mk1 phosphorylation was completely impaired in an mkk2 background, both under basal conditions as well as upon tunicamycin or zymolyase treatment. Also, Cek1 phosphorylation in response to tunicamycin was reduced in mkk2, mkc1 and mkc1 mkk2 backgrounds. However, the intensity of Cek1 phosphorylation was not diminished in response to zymolyase in the strains analysed. Zymolyase treatment resulted in the appearance of an additional band (named X-P in Fig 2A) which has been previously reported to be derived from Cek1-P [20]. This band was not detected in an mkc1 mkk2 background and was less intense in the mkk2 and mkk1 mutant compared to the wt strain. These data indicates that the CWI pathway plays a role in Cek1 activation.

We wondered if this effect would be also detected under other activating signals. Cek1 becomes activated upon growth resumption from stationary phase cultures [4] in a process that is dependent on quorum sensing [39]. We therefore tried to determine if signals leading to this activation were dependent on MKK2. This was not the case and activation of Cek1 was completely independent of the presence of a functional cell integrity pathway (Fig 2B). Summarising, MAPK activation studies revealed that 1) Mkk2 is the only MAPKK responsible for Mk1 activation under our tested experimental conditions and 2) there exists a crosstalk
between both the Cek1 and Mkc1-mediated pathways upon cell wall disturbing compounds as evidenced by the altered Cek1 phosphorylation in CWI pathway mutants.

**mkk2 and mck1 mutants displays different cell wall-related phenotypes**

In order to assess the role of Mkk2 in the biogenesis of the cell wall we analysed the susceptibility of *mck1* and *mkk2* mutants to cell wall disturbing agents. We used Calcofluor White and

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**Fig 2. Mkk2 controls the activation of the Mkc1 MAPK upon cell wall stress.**

A) Effect of tunicamycin (T) and zymolyase (Z) on the pattern of Mkc1 and Cek1 phosphorylation (Mkc1-P and Cek1-P in the figure). Exponentially growing cells (O.D. 620 nm = 1) were challenged with 5 μg/L tunicamycin or 2 U/mL zymolyase 100-T and samples were taken after 2 hours of incubation at 37°C. X-P specifies a Cek1-P derived band. B) Cek1 activation (Cek1-P in the figure) during the resumption of growth from stationary phase. Cells were diluted in fresh YPD at O.D. 620 nm = 0.2 and grown at 37°C for 1 hour before collected and processed for western blot analysis.

![Image](image-url)
Congo Red (that interfere with chitin assembly) as both are useful indicators of cell wall associated defects in yeasts. Mutants defective in both the SVG [39, 40] and CWI pathways [21] are sensitive to these drugs. These compounds were added to YPD solid plates and 10-fold dilution cell suspensions of the indicated strains growing in exponential phase were spotted. Plates were incubated at different temperatures since cell wall related phenotypes have been associated to the growth temperature. As shown in Fig 3A, mkk2 mutants were found to be more sensitive to both compounds than the wt strain. CFW susceptibility was diminished when temperature was increased (37 and 42°C). We observed that mkk2 and mkc1 mutants displayed a different pattern of susceptibility to these drugs, with mkk2 mutants being more susceptible than mkc1. This effect was highly dependent on the temperature (Fig 3A). The susceptibility displayed by the double mkc1 mkk2 mutant depended on the temperature and the compounds but this double mutant was unable to grow at 42°C, even in YPD. The re-integration of MKK2 gene improved the growth on Calcofluor White plates close to the growth of the wt strain, although they showed partial complementation, especially on Congo Red plates.

We also tested the susceptibility of mkk2 mutants to tunicamycin in a liquid culture assay. Stationary growing cells were subjected to increasing concentrations of tunicamycin in a 96-well assay, and final growth was tested by measuring the O.D.620 nm after 18 hours at 37°C. All mutant strains analysed (mkk2, mkc1 and mkc1 mkk2) showed an increased susceptibility to tunicamycin as determined by a reduced growth compared to the wt (Fig 3B). These effects were statistically significant (shown as ***, p<0.001, two way ANOVA plus Dunnett’s multiple comparisons test) for concentrations higher than 0.2 mg/L for all strains (mkk2, mkc1 and mkc1 mkk2) compared to wt cells. The effect of the tunicamycin depended on the temperature of growth. At 24°C mkc1 was significantly more susceptible to tunicamycin than mkk2, double mkc1 mkk2 and wild type strain. At 37°C CWI pathway mutants displayed increased sensitivity to this compound while at 42°C all the analysed strains (even the wild type) become sensitive to tunicamycin (S1 Fig). We also performed an enzymatic assay to reveal structural cell wall alterations. Cells of the indicated strains were incubated with the enzymatic complex zymolyase 100-T (an enriched β(1,3)-glucanase preparation from Arthrobacter luteus). Under these conditions, only mkc1 cells were found to be sensitive to this enzymatic complex, with significant reduced growth at all activity units of zymolyase tested (Fig 3C) (shown as ***, p<0.001, two way ANOVA plus Dunnett’s multiple comparisons test). This effect was largely independent of the temperature with mkc1 the only mutant that displayed significant susceptibility at 24, 30, 37 and 42°C (S2 Fig). Interestingly, mkk2 mutants resisted better the presence of zymolyase compared to the wt strain (**, p<0.05, two way ANOVA plus Dunnett’s multiple comparisons test) while mkc1 mkk2 cells showed almost a wt phenotype. Finally, the mean intensity values of Calcofluor White stained cells compared to wt cells were 1±0.26 (wt), 1.25±0.14 (mkk2), 1.18±0.24 (mkc1) and 0.980±0.26 (mkc1 mkk2), with no statistical significant differences, suggesting no major changes in chitin amounts. These data suggest that although both Mkk2 and Mkc1 kinases are relevant in cell wall integrity and influence cell wall architecture, they play distinct roles in cell wall biogenesis that consequently renders different phenotypes.

Mkk2 and Mkc1 control the expression of cell wall related genes

Given the phenotypic differences observed among wt, mkc1, mkk2 and mkc1 mkk2 mutants at different temperatures, we analysed the expression of different genes involved in cell wall biogenesis by qRT-PCR at 24, 30, 37 and 42°C. For this purpose, cells grown overnight at 24°C were diluted at O.D.620 nm = 0.1 and allowed to grow at 24, 30, 37 or 42°C for 1 hour. The transcript of actin, encoded by ACT1, was used as internal control and all the values were expressed relative to ACT1 values and 24°C values (see Materials and Methods). The selected genes for
Fig 3. Mkc1 and Mkk2 play crucial but different roles in cell wall maintenance. A) Serial ten-fold dilutions of exponentially growing cells (O.D. 620 nm = 1) were spotted on YPD agar plates supplemented or not with Congo Red (CR) or Calcofluor White (CFW) and incubated at 24, 30, 37 or 42°C for 24 hours before being scanned; B and C) wt, mkc1, mkk2 and mkc1 mkk2 stationary phase cells were grown overnight at 37°C in the presence of different amounts of tunicamycin (B) or zymolyase (C) starting at O.D. 620 nm 0.025. Growth is depicted as the percentage of growth in YPD supplemented with cell wall interfering compounds compared to growth in YPD alone. Mean values of 3 independent experiments (two samples per experiment) are represented with bars indicating the SD (standard deviation). Two way ANOVA was used to analyse the significance of the data compared to the wild type strain (*, p<0.05; **, p<0.01, ***, p<0.001, ****, p<0.0001).

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this assay were CRH11, GSC1 and CEK1. As shown in Fig 4 (see also S1 Table), CEK1 expression increased with temperature in wt strains (≈4x at 30°C, ≈14x at 37°C and ≈ 20x at 42°C). However, this induction was completely absent in mkc1, mkk2 and double mkc1 mkk2 mutants up to 37°C. At 42°C an increase in CEK1 expression was detected in mkc1 (≈12x) and to a
minor extent in \( \text{mkk2} \) (=6x) and \( \text{mkc1 mkk2} \) (=3x) mutants. These changes are in accordance with protein levels detected by western blot (S3 Fig). This indicates that the CWI pathway positively regulates \( \text{CEK1} \) expression.

Another gene analysed was \( \text{GSC1} \) which encodes the essential \( (1,3) \)-glucan synthase subunit \[41\] in \( \text{C. albicans} \). Similarly to \( \text{CEK1} \), induction of the expression of \( \text{GSC1} \) in the wt strain increased with the temperature, with a maximum (≈22x) at 37 but decreased at 42°C (≈10x). This induction was not observed in mutants lacking \( \text{MKC1} \) and/or \( \text{MKK2} \) at any temperature (Fig 4) indicating a complete dependence of glucan synthase on CWI pathway. The expression of \( \text{GSC1} \) was also dependent on the Cek1 pathway as revealed by the absence of significant increases at the different temperatures tested in a \( \text{cek1} \) mutant, in accordance with the already indicated dependence of \( \text{CEK1} \) with the CWI pathway. The third cell wall related gene tested was \( \text{CRH11} \), homolog of ScCRH1 in \( \text{S. cerevisiae} \) [42]. In a wt strain, the expression of \( \text{CRH11} \) increased at 30 (≈18x) and 37°C (≈15x) and at 42°C returned to values closer to 24°C. CWI pathway mutants were able to increase \( \text{CRH11} \) expression at 37°C although the expression levels were slightly lower than in the wt strain (≈11x). At 42°C, the \( \text{mkc1} \) mutant showed a \( \text{CRH11} \) expression decrease while \( \text{mkk2} \) and \( \text{mkc1 mkk2} \) mutants increased drastically \( \text{CRH11} \) expression (≈40x). In a \( \text{cek1} \) mutant, these values were 6x at 37°C and 19x at 42°C. These results indicate that both CWI and SVG pathways mediate the expression of \( \text{CEK1}, \text{GSC1} \) and \( \text{CRH11} \) and that this role is dependent on temperature of growth. The different expression pattern displayed by the different CWI pathway mutants may explain the diverse cell wall related phenotypes described above.

**Deletion of \( \text{MKK2} \) in a \( \text{hst7} \) mutant increases the susceptibility to cell wall disturbing compounds and prevents MAPKs phosphorylation**

Since our results suggest a crosstalk between CWI and SVG pathways, the \( \text{MKK2} \) gene was deleted in an \( \text{hst7} \) background, defective in the MAPKK of the Cek1-mediated pathway. \( \text{hst7} \) mutants show increased susceptibility to Congo Red [19]. Deletion of \( \text{MKK2} \) in an \( \text{hst7} \) background clearly aggravated the susceptibility to Calcofluor White of \( \text{hst7} \) cells on solid media (Fig 5A) and this effect was more evident in Calcofluor White plates supplemented with as low as 12 mg/L drug concentration. We also observed an increased sensitivity to zymolyase in liquid medium (Fig 5B) in \( \text{hst7} \) cells (**\( p < 0.01 \)) at 40 U/mL and ***\( p < 0.001 \)) at 80 U/mL). The \( \text{hst7 mkk2} \) double mutant was more susceptible to zymolyase compared to single \( \text{mkk2} \) and \( \text{hst7} \) mutants and to the wt (Fig 4B), being statistically significant (**\( p < 0.001 \)) for all the concentrations higher than 5 U/mL. \( \text{hst7} \) mutants also displayed an enhanced susceptibility to tunicamycin (Fig 4C). This sensitivity was detected at lower concentration compared to \( \text{mkk2} \) mutants. Double \( \text{hst7 mkk2} \) mutants showed an aggravated phenotype at lower tunicamycin concentrations (Fig 4C).

Given the implication of \( (1,3) \)-glucan synthase as a target of the CWI pathway, we also checked the exposure of \( (1,3) \)-glucan in different mutants. This polymer is normally hidden within the mannoprotein layer but is easily detected upon environmental and morphological changes [43]. In \( \text{S. cerevisiae} \) and \( \text{C. albicans} \), specific mutations have been shown to affect recognition of \( (1,3) \)-glucan via an altered cell wall [44, 45]. As shown in Fig 5D, neither \( \text{mkc1}, \text{mkk2} \) nor \( \text{mkc1 mkk2} \) cells showed an altered \( (1,3) \)-glucan exposure compared to the wt. In contrast, \( \text{hst7} \) cells were found to have increased (≈4x) levels and pattern of localization similar to \( \text{cek1} \) cells [46]. Consistent with the above results, \( \text{hst7 mkk2} \) mutant displayed \( (1,3) \)-glucan exposure levels similar to \( \text{hst7} \) single mutant (≈3.9x). These results indicate that although \( \text{MKK2} \) regulates \( (1,3) \)-glucan synthase expression, neither \( \text{MKK2} \) nor \( \text{MKC1} \) significantly alters \( (1,3) \)-glucan exposure in the fungal surface which is mainly dependent on the Cek1-mediated pathway.
Fig 5. SVG and CWI pathways cooperate in cell wall biogenesis. A) 10-fold dilutions from exponentially growing cells (O.D.620 nm = 1) of the indicated strains were spotted onto YPD agar plates supplemented with Congo Red (CR) or Calcofluor White (CFW) and incubated at 37°C before scanned. B) Stationary growing cells of the indicated strains were analysed for growth inhibition in the presence of zymolyase as indicated in Fig 2C (**, p<0.01; ****, p<0.0001 according to a two-way ANOVA test). C) Cultures in stationary phase of growth were refreshed in YPD medium supplemented with tunicamycin to different concentrations and incubated at 37°C overnight. Statistical differences compared to the wild type strain are indicated (**, p<0.01; ****, p<0.0001 according to a two-way ANOVA test). D) Representative flow cytometry analysis of β(1,3)-glucan exposure on live stationary C. albicans strains at 37°C.
We also analysed the MAPK phosphorylation pattern by immunoblot under activating stimuli such as zymolyase and tunicamycin. First, as shown in Fig 5E, hst7 mutants displayed an elevated Mkc1 phosphorylation under basal conditions (exponentially growing cells) and addition of cell wall impairing compounds (zymolyase or tunicamycin) led to a less pronounced increase in Mkc1 phosphorylation. No activation of Cek1 was observed in hst7 mutants indicating that Hst7 is the only MAPK leading to Cek1 phosphorylation. As expected, hst7 mkk2 mutants showed a complete absence of Mkc1 and Cek1 phosphorylation that correlates with the increased susceptibility to compounds that impair the cell wall architecture. In addition, the MAPK phosphorylation pattern upon H₂O₂ was also analysed to detect a potential cross talk among these pathways. Addition of H₂O₂ still enabled activation of Mkc1 in hst7 mutants (Fig 5F), indicating that both pathways work independently under these conditions.

Role of Mkk2 in morphogenesis and virulence

The role of mkk2 mutants in morphogenesis was analysed on special solid media. mkk2 cells is able to invade on Spider agar plates similarly to wt cells although invasive borders were thicker. (Fig 6A). However, mkc1 did not display invasive borders on this solid medium and mkk2 double mutants behaved as mkc1, showing smooth colony borders (Fig 6A). Regarding filamentation in response to serum in liquid medium, CWI pathway mutants were able to form true filaments under a range of serum proportions in YPD medium similarly to wt cells (not shown). These observations indicate that Mkk2 and Mkc1 play different roles in morphogenesis.

We also analysed the relevance of a mkk2 mutant in virulence in the standard systemic murine infection model. For this purpose, 10⁶ C. albicans cells were inoculated in the lateral tail vein of BALB/c mice. Survival of the mice was followed for 15 days and represented in a Kaplan-Meier curve (Fig 6B). mkk2 mutants displayed a virulence similar to the wt strain RM100 (p = 0.88 using a Log-rank (Mantel-Cox) test). Median survival times were 6 days (SC5314) and 7 (mkk2 and RM100). Differences were found between SC5314 and mkk2 (p = 0.0030 using a Log-rank (Mantel-Cox) test) and between SC5314 and RM100 ((p = 0.008 using a Log-rank (Mantel-Cox)), reflecting most probably URA3 genetic effects and not MKK2 related defects, as URA3 profoundly influences virulence in C. albicans [47, 48]. In order to confirm this result (that is, no role of MKK2 in virulence) and compare all strains, we additionally used the Galleria mellonella model [49] which has been shown to correlate, to a certain extent, with the mouse systemic model [50, 51]. Under our conditions, no significant differences in the median survival time were observed in mkk2 mutants and MKK2²⁺⁺⁺ compared to wt cells (2 days for both strains; p = 0.8). In contrast, mkc1 cells showed a median survival time of 3.5 days (p<0.001), in close agreement with previous observations in the mouse systemic model which indicates reduced virulence for this mutant [28]. The double mkc1 mkk2 showed in this model an intermediate behaviour (median survival time 2.5 days) (p = 0.012). Therefore, in contrast to Mkc1, Mkk2 does not play a significant role in C. albicans virulence in two different experimental models.

![Statistical analysis of these data is shown and represents the relative mean fluorescence intensity (MFI) compared to the wt strain ± SD. Ten thousand cells were analysed in each flow cytometry run, and MFI mean values were obtained from three different experiments. One way ANOVA was used to analyse the significance of the data (**, p<0.01; ***, p<0.001). E) The effect of 5 mg/L tunicamycin or 2 U/mL zymolyase 100-T on Cek1 and Mkc1 (Cek1-P and Mkc1-P respectively) activation was tested on exponentially growing cells of the indicated strains after 2 hours of treatment at 37°C. X-P indicates a Cek1-P derived band observed upon zymolyase addition. F) Hydrogen peroxide effect on MAPK phosphorylation was analysed 10 minutes after the addition (+) or not (−) of 10 mM H₂O₂ (Hog1-P means phosphorylated form of Hog1).](10.1371/journal.pone.0133476.g005)

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Discussion

The current work reports the role that the Mkk2 MAPKK plays in the opportunistic pathogen *C. albicans*. Unlike *S. cerevisiae* that has two MAPKK proteins in the CWI pathway, ScMkk1 and ScMkk2, only one gene named *MKK2* is present in *C. albicans*. Mkk2 shares an overall 50% identity (66% similarity) to both ScMkk1 and ScMkk2; this similarity extends from amino acid 147 to the C-terminus of the protein, while there is substantial divergence in the first (1–146) N-terminal portion of the protein. Curiously, ScMkk1 and ScMkk2 N-terminal domains were reported to play an important role in the interaction with the Slt2 MAPK [24] and Mkc1 [25]. Although we have not tested the physical interaction between Mkk2 and Mkc1, the genetic relationship was evident since no Mkc1 phosphorylation was detected in the absence of Mkk2 (Fig 1A). This data supports the epistatic relationship between Mkk2 and Mkc1 and the
existence of a unique MAPKK in the *C. albicans* CWI pathway responsible for the transmission of both cell wall and oxidative stress signals (Fig 7). Oxidative stress (through Reactive Oxygen Species (ROS)) also activates Hog1 [14] via the Ssk1 [52] and Ssk2 [53] proteins. *hog1* mutants fail to efficiently activate Mkc1 [18] and, conversely, *mkc1* mutants show defects in Hog1 activation [20], suggesting the existence of a mechanism of control that prevents activation of only one of these MAPK pathways under oxidative stress. However, while Hog1 activation results in glycerol accumulation [11] and resistance to stress [12, 14], the physiological role of Mkc1 activation via ROS is currently unknown. In addition, the precise point where the signal generated by ROS feeds into the CWI MAPK pathway is not known, although this work indicates that it occurs upstream Mkk2. We show here that the MAPKK Mkk2 performs an important function in the construction of the cell wall. *mkk2* mutants were found to be sensitive to cell wall interfering drugs such as tunicamycin, Congo Red and Calcofluor White compared to wt cells. Although *mkc1* and *mkk2* mutants displayed cell wall related phenotypes, clear differences were observed between them and these differences depend on the drug used and the growth temperature. The lack of Mkk2 rendered cells more susceptible to Calcofluor White and Congo Red than the lack of Mkc1; interestingly, at higher temperatures (37 and 42°C) susceptibility to CFW was suppressed in both mutants. Such differences have been also reported in *S. cerevisiae* [54]. A possible explanation for this phenotype may reside in the role of Mkc1 as client protein to the CaHsp90 chaperone, which influences thermal adaptation in *C. albicans* by its concerted action with MAPK signalling pathways [30]. Depletion of Hsp90 has been shown to influence drug sensitivity and cell wall composition [55]. The existence of differences between *mkc1* and *mkk2* cells in cell wall related phenotypes is striking as Mkk2 is the only MAPKK activating Mkc1 under all conditions tested. While we do not have an definite explanation for this, it must be considered that MAPK deletion mutant phenotypes are not necessarily similar to those with inactive alleles [56], being possible that the Mkc1 protein still present in *mkk2* cells exerts a type of control in the CWI pathway, maybe preventing crosstalk with other pathways or occupying regulatory regions in the kinase complex. We also found differences with other cell wall stressors such as zymolyase, an enzymatic cocktail with a predominant β(1,3)-glucanase activity. *mkc1* mutants were sensitive while *mkk2* mutants behaved as a wt and deletion of MKK2 restored wt phenotype in *mkc1* mutants. In *S. cerevisiae*, zymolyase-mediated cell wall damage activates both the HOG and PKC pathways, although it seems that the transcriptional response depends mainly on Slt2 [35]. We show here that CRH11 induction does not take place in *mkc1* mutants at high temperatures but does in *mkk2*, confirming that the transcriptional response to environmental conditions in both mutants is different, which may contribute to explain this different behaviour. In fact, CRH11 is an homologue of a glycosylphosphatidylinositol [GPI]-cell wall protein [42] that is involved in what has been called the “compensatory mechanism” [57] induced upon zymolyase treatment that regulates cell wall architecture. This different response may also be involved in a different behaviour in the interaction with host cells. Mkk2 does not seem to play a major role in invasion on solid surfaces in different media, a trait that has been shown to contribute to virulence [27, 28] (see [58] and [59] for recent reviews) and does not affect filamentation in the presence of serum. Survival of mice systemically infected is not altered in *mkk2* cells, and analyses post mortem do not reveal altered fungal burden of organs infected with *mkk2* cells. Similar results are observed in the *Galleria mellonella* insect model. Therefore, Mkk2, unlike Mkc1 [28], does not seem to contribute to virulence [28].

We have paid attention to the role of β(1,3)-glucan, the major component of the cell wall. This polymer is important for the maintenance of the cell wall, being normally hidden under a mannoprotein layer and only visible during division [43]. In *S. cerevisiae* it has been proposed that Slt2 plays a central role in a glucan masking network that occludes β(1,3)-glucan from


immune cells [45]. Neither mkc1 or mkk2 had more exposed β(1,3)-glucan on their surfaces than wt, and the amount of exposed β(1,3)-glucan on the surface of an hst7 mkk2 double mutant was not significantly different to that of an hst7 single mutant Therefore, our data support the idea that in C. albicans this process seems to be mainly controlled by the Cek1-mediated pathway [46] and not by the CWI pathway (Fig 7). However, we also show that both Mkk2 and Mkc1 control the expression of the inducible essential β(1,3)-glucan synthase encoded by CaGSC1 under defined conditions. Glucan synthesis is essential for fungal cells which, in S. cerevisiae, are accomplished via different genes: ScFKS1, ScFKS2 (GSC2) and ScFKS3. ScGSC2 is the orthologue of CaGSC1, whose expression is induced under starvation, during sporulation and in response to mating pheromones [60, 61]. In this organism, ScFKS2 is a cell cycle regulated gene, controlled by the CWI pathway, and is activated in response to increases in temperature [62]. We show here that expression of CaGSC1 is also induced upon a temperature increase in C. albicans and this is prevented in both mkc1 and mkk2 mutants, indicating similarities between both models. However, β(1,3)-glucan content does not seem to explain the differences in zymolyase sensitivity between both mkk2 and mkc1 mutants. It is possible that this may result from altered permeability in the cell wall arising from altered Cek1 expression as it has been shown that upstream elements of the Cek1 pathway severely influence the mannanprotein layer [63]. We show here that major differences between mkc1 and mkk2 mutants reside in Congo Red and Calcofluor White susceptibility, dyes that interfere with chitin assembly [64] that is partially regulated by the CWI pathway [17], coherent with this observation. However, in a semiquantitative analysis, we do not observe altered amounts of chitin in mkk2 cell walls, as also occurs with mkc1 mutants [25] suggesting that the defect may be either

![Diagram showing the main crosstalk mechanisms among the three MAPK pathways under study.](Fig 7)
more related to specific linkages and/or organisation of the cell wall than alteration of absolute amounts.

Our results demonstrate that the impairment of both the CWI and CEK1 pathways aggravate susceptibility to certain stresses. Double hst7 mkk2 mutants are more susceptible to Calcofluor White and Congo Red as well as zymolyase (see Fig 5). Tunicamycin, an inhibitor of the first steps of N-glycosylation, triggered both Mkc1 and Cek1 phosphorylation. This phosphorylation was prevented in mkc1 mutants, suggesting that Cek1 phosphorylation is partially dependent on Mkc1. Therefore, cell wall glycosylation defects in response to tunicamycin may trigger Mkc1 phosphorylation that, indirectly, may lead to Cek1 activation. Tunicamycin also induced Cek1 expression and this was independent of upstream elements of the pathway such as Msb2 and Sho1 [5]. Cek1 is not only regulated by phosphorylation but also at the transcriptional level and even via proteolytic degradation [39]. Cek1 becomes phosphorylated and its expression is induced when stationary growing cells at 24°C were refreshed in fresh pre-warmed medium and allowed to grow at 37°C. This induction is independent of elements of the Cek1-mediated pathway (R. Alonso-Monge, personal communication) but we show here that it depends on the CWI pathway. This reinforces the idea of the CWI pathway promoting Cek1 production as a cooperative mechanism that may be needed during certain conditions (growth resumption from stationary phase and temperature increase) where substantial cell wall remodelling may be needed (Fig 7). Both mkc1 and mkk2 mutants display similar sensitivity to tunicamycin, in agreement with the effect exerted on CEK1 expression by both mutants. Therefore, Cek1 phosphorylation/expression may be relevant for tunicamycin resistance, as Msb2 and Sho1 (which mediate Cek1 phosphorylation) are sensitive to this inhibitor [4, 5]. While both the Cek1 and Mkc1-mediated pathways cooperate in cell wall biogenesis, share some triggering stimuli (zymolyase and tunicamycin) and phenotypes (susceptibility to Congo Red or tunicamycin), they still respond to separate stimuli and display separate phenotypes. Cek1 is activated in response to growth signals coming from release of quorum sensing molecules from stationary phase cells; this signalling mechanism is independent of Mkc1 and Mkk2. In parallel, Mkc1 is activated in response to oxidative stress [20], while this does not occur with Cek1. Therefore, the interaction between both pathways is dependent on the triggering stimulus which is closely linked to cell wall biogenesis (Fig 7). In conclusion, collectively our data support that both the CWI and Cek1-mediated pathways function during vegetative growth to promote a proper cell wall assembly and remodelling.

Supporting Information

S1 Fig. Cell cultures were diluted in YPD supplemented with tunicamycin at different concentrations at 24, 30, 37 and 42°C. Cultures were incubated overnight and growth was expressed as the percentage of growth in YPD supplemented with the cell wall interfering compound compared to growth in YPD alone. Mean values of 3 independent experiments (two samples per experiment) are represented with bars indicating the SD (standard deviation). Two-way ANOVA test was performed to assess differences (*, p<0.05; ****, p<0.0001). (TIF)

S2 Fig. Overnight cells from cultures grown at 37°C were diluted and grown 18 hours at 24, 30, 37 and 42°C in the presence of different amounts of zymolyase starting at O.D.₆₀₀ = 0.025. Growth is depicted as the percentage of growth in YPD supplemented with the cell wall interfering compound compared to growth in YPD alone. Mean values are represented with bars indicating the SD (standard deviation) and two-way ANOVA test compare to the parental wild type strain was performed to evidence significant differences (**, p<0.01; ***, p<0.001).
S3 Fig. Detection of Cek1 in CWI mutants. Overnight cultures at 24°C of the indicated strains were shift to pre-warmed YPD medium at 24, 30, 37 and 42°C and incubated for 1 h. Extracts were obtained and Cek1 protein levels were detected using a polyclonal anti-Cek1 antibody.

S1 Table. Relative expression of cell wall related genes. The levels of expression of each gene (CEK1, GSC1 and CRH11) (compared to ACT1) at each temperature normalised to the value at 24°C for the wild type background are indicated for each of the mutant backgrounds analysed (wt, mkc1, mkk2 and mkc1 mkk2). The relative abundance of CEK1, GSC1 and CRH11 mRNA at 24°C in wt cells was 1/14 ± 1.22, 1/35.7 ± 5.2 and 1/66.7± 6.21 compared to ACT1 mRNA levels at the same temperature. n.d. Not determined. The statistical significance (p < 0.05) using the Holm-Sidak post hoc test after ANOVA is shown for each value for the comparison of wt with mkc1 (a), wt with mkk2 (b), wt with mkc1 mkk2 (c) and wt with cek1 (d).

Author Contributions
Conceived and designed the experiments: ER RA AM JP. Performed the experiments: ER RA AM JP. Analyzed the data: ER RA AM JP. Contributed reagents/materials/analysis tools: ER RA JP. Wrote the paper: ER RA JP.

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