Cellular Responses of *Candida albicans* to Phagocytosis and the Extracellular Activities of Neutrophils Are Critical to Counteract Carbohydrate Starvation, Oxidative and Nitrosative Stress

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Cellular Responses of *Candida albicans* to Phagocytosis and the Extracellular Activities of Neutrophils Are Critical to Counteract Carbohydrate Starvation, Oxidative and Nitrosative Stress

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Abstract

Neutrophils are key players during *Candida albicans* infection. However, the relative contributions of neutrophil activities to fungal clearance and the relative importance of the fungal responses that counteract these activities remain unclear. We studied the contributions of the intra- and extracellular antifungal activities of human neutrophils using diagnostic Green Fluorescent Protein (GFP)-marked *C. albicans* strains. We found that a carbohydrate starvation response, as indicated by up-regulation of glyoxylate cycle genes, was only induced upon phagocytosis of the fungus. Similarly, the nitrosative stress response was only observed in internalised fungal cells. In contrast, the response to oxidative stress was observed in both phagocytosed and non-phagocytosed fungal cells, indicating that oxidative stress is imposed both intra- and extracellularly. We assessed the contributions of carbohydrate starvation, oxidative and nitrosative stress as antifungal activities by analysing the resistance to neutrophil killing of *C. albicans* mutants lacking key glyoxylate cycle, oxidative and nitrosative stress genes. We found that the glyoxylate cycle plays a crucial role in fungal resistance against neutrophils. The inability to respond to oxidative stress (in cells lacking superoxide dismutase 5 or glutathione reductase 2) renders *C. albicans* susceptible to neutrophil killing, due to the accumulation of reactive oxygen species (ROS). We also show that neutrophil-derived nitric oxide is crucial for the killing of *C. albicans*: a yhb1ΔΔ mutant, unable to detoxify NO, was more susceptible to neutrophils, and this phenotype was rescued by the nitric oxide scavenger carboxy-PTIO. The stress responses of *C. albicans* to neutrophils are partially regulated via the stress regulator Hog1 since a hog1ΔΔ mutant was clearly less resistant to neutrophils and unable to respond properly to neutrophil-derived attack. Our data indicate that an appropriate fungal response to all three antifungal activities, carbohydrate starvation, nitrosative stress and oxidative stress, is essential for full wild type resistance to neutrophils.

Introduction

*Candida albicans* is a polymorphic opportunistic fungus, commonly found as a commensal in healthy subjects [1]. It colonises distinct niches in the human body such as the oral and vaginal cavities and gut. *C. albicans* causes superficial infections, including oral and vaginal thrush, and deep-seated life-threatening infections such as disseminated candidiasis. One of the best investigated virulence attributes of *C. albicans* is the ability to switch between yeast and hyphal growth forms. Both morphologies seem to be important for virulence and have distinct functions during the different stages of disease progression, including adhesion, invasion, damage, dissemination, immune evasion and host response [2]. The balance between host factors and virulence attributes of *C. albicans* determines the outcome of the interaction leading to commensalism or infection [3]. However, certain predisposing factor increase the risk of candidiasis, for instance, long-term antibiotic therapy, immunity-suppression or disruption of anatomical barriers. Not surprisingly, the host is able to sense and respond to *C. albicans*. In the commensal state, *C. albicans* is tolerated, for example by the oral or vaginal epithelium, to prevent an inflammatory reaction against a relatively harmless component of the microbiota. However, epithelial cells are able to sense when this fungus represents a danger, because of increased proliferation or hyphal production, thereby inducing a proinflammatory response [4–6].
The response of the host towards the potentially dangerous C. albicans includes the recruitment of phagocytes from blood and tissues, considered as the first line of defence. Monocytes and granulocytes are immune cells with phagocytic activity that circulate in the bloodstream, priming the endothelium and responding to inflammatory signals coming from infected tissues. Neutrophilic granulocytes are unique in the response towards pathogens, since they respond rapidly and aggressively to potentially dangerous microorganisms. Neutrophils employ diverse antimicrobial killing mechanisms that include intra- and extracellular activities, as well as oxidative and non-oxidative mechanisms [7]. Neutrophils express receptors on their surface, including TLR2, TLR4 and dectin-1, that mediate the recognition of fungal cells, while other receptors, such as FCyR and CR3, aid in the opsonin-dependent phagocytosis of microorganisms [8].

Upon phagocytosis, the phagosome fuses with preformed granules containing several enzymes (e.g. cathepsin G, neutrophil elastase) and antimicrobial cationic peptides (z-defensins). A notable characteristic of the neutrophils is the production of copious amounts of oxidants in a process known as the respiratory burst [9]. It involves the assembly of the enzyme complex NADPH oxidase, on the plasma and phagosomal membranes of the phagocyte. This enzyme complex produces the highly reactive superoxide anion \( \text{O}_2^– \), which is further metabolised to form hydrogen peroxide \( \text{H}_2\text{O}_2 \). Other reactive species are produced inside the neutrophil. For instance, peroxynitrite (\( \text{ONOO}^– \)) is formed upon production of nitric oxide (\( \text{NO}^– \)) by the inducible nitric oxide synthase \( \text{iNOS} \) [10]. These two compounds are collectively known as reactive nitrogen species, and are extremely toxic for cells, reacting with thiol groups in proteins, thereby inactivating them. Additional compounds with oxidative properties (for example, hypochlorous acid, \( \text{HClO} \)), are produced by myeloperoxidase, an enzyme that is highly abundant in the neutrophil granules [7]. Degranulation is the hallmark of all neutrophil activities. It involves the secretion of peptides and enzymes stored in the neutrophil granules. Amongst the granule components, myeloperoxidase, lactoferrin and azurocidin are known to have candidacidal properties [11–13]. The production of neutrophil extracellular traps (NETs) provides another mechanism by which neutrophils contain infection. This involves the extrusion of chromatin scaffolding net-like structures decorated with antimicrobial proteins [14].

During adaptation to the host, C. albicans has evolved the ability to respond to host-generated stresses. We have shown that of all the cellular types present in blood, neutrophilic granulocytes exert the strongest effect on C. albicans, by inhibiting growth and evoking a response at the transcriptional level to overcome stresses such as carbohydrate and nitrogen starvation and oxidative stress, which contributes to the relatively high resistance of C. albicans to neutrophils in vitro [15]. It has long been known that the glyoxylate cycle contributes to the virulence of C. albicans [16], and that genes encoding the enzymes of this cycle, e. g. ICL1 and MLS1, are induced upon phagocytosis by murine macrophages [17] and human neutrophils [15]. This metabolic pathway enables the fungus to utilise two-carbon molecules as a carbon source, and the induction of this pathway probably reflects the nutrient-deprived environment inside the phagocytes. Additionally, C. albicans faces amino acid deprivation upon neutrophil phagocytosis, and upregulates pathways for the synthesis of methionine and arginine [18]. We have observed an up-regulation of ammonium permease coding genes (\( \text{MEPI} \) and \( \text{MEP2} \)), as well as genes encoding vacuolar proteases (\( \text{APR}1, \text{PRB}1, \text{PRB}2, \text{PRC}1 \)), which might be involved in protein turnover under starvation conditions, supporting the idea of nutrient limitation, and in particular nitrogen starvation [19]. Furthermore, it has been shown that C. albicans cell surface-associated superoxide dismutases are expressed in response to murine derived phagocytes, and are necessary for resistance to macrophages since in the absence of these enzymes there is accumulation of toxic oxygen radicals that eventually increases the susceptibility of C. albicans to killing by these cells [20]. We have demonstrated that SOD3 gene expression, which is normally activated during hyphal growth, is induced during interactions with neutrophils [15], despite of the repression of filamentation by these phagocytes. Although it has long been known that neutrophils are able to produce nitric oxide during bacterial infections [21], the contribution of this compound to fungal killing by neutrophils has not being studied. C. albicans is able to respond to nitric oxide by up-regulating genes such as \( \text{HBB}1 \), a nitric oxide dioxygenase, and \( \text{SSU}1 \), a sulphite transporter protein [22]. Although these authors suggest that NO’ production is not a major determinant of virulence, we and others [23] argue that nitric oxide is relevant as a killing mechanism during the interaction of C. albicans with neutrophils.

The response of C. albicans cells to nutrient deprivation and oxidative stress within blood is primarily caused by exposure to neutrophils [15]. However, it is not clear whether phagocytosis is essential for these transcriptional responses, because this type of study averages the molecular behaviour of the fungal cell population as a whole, only a portion of which is phagocytosed when the transcriptional profiles are monitored [15]. The starvation and stress responses could have arisen from a subpopulation of phagocytosed cells. Alternatively, non-phagocytosed cells that have made contact with neutrophils may also face nutrient deprivation. Therefore, in this study we assess the contributions of intra- and extracellular neutrophil activities towards the induction of the C. albicans responses associated with neutrophil exposure and investigate the importance of the up-regulated genes and key stress regulators for survival during the interaction of C. albicans with neutrophils.

**Results**

**Validation of GFP reporters as markers of stress specific response**

We used diagnostic GFP reporter strains to monitor C. albicans gene expression at a cellular level (“single cell profiling”). First, we characterised the in vitro expression pattern of each reporter used in this study to define their specificity for given stresses. The stressors were based on previous studies [24–26]. To induce carbohydrate starvation and the expression of glyoxylate cycle genes, the non-fermentable carbon source acetate (\( 2\% \) potassium acetate) was chosen. To impose oxidative stress, we used a moderate concentration of hydrogen peroxide (\( 2\, \text{mM} \) \( \text{H}_2\text{O}_2 \)), and to expose the fungal cells to nitrosative stress, we used the nitric oxide-releasing compound S-nitrosoglutathione (GSNO, 0.6 mM).

C. albicans cells carrying GFP, a promotorless GFP gene [27], were used as negative control. As shown in Fig. 1A, this strain exhibited no significant GFP fluorescence in all the conditions examined. In contrast, the positive control was the C. albicans strain carrying \text{ACT1p-GFP}, in which the GFP under the control of the actin gene (\text{ACT1}) promoter. \text{ACT1p-GFP} cells generally showed high fluorescence levels.

\( \text{ICL1p-} \) and \( \text{MLS1p-GFP} \) reporters expressed GFP under the control of the promoters from the isocitrate lyase (\text{ICL1}) and malate synthase genes (\text{MLS1}) respectively. C. albicans cells with these reporters showed increased GFP fluorescence when grown on acetate as sole carbon source, a condition known to induce the glyoxylate cycle [16]. Both of these reporters displayed similar
expression patterns, showing a 3.3–fold and 3.8–fold increase in fluorescent, respectively, during growth on acetate compared to glucose. Carbohydrate starvation was the only condition in which these reporter strains showed an increase in fluorescence relative to the control condition. However, they did display a decrease in fluorescence the presence of H2O2. No significant changes were observed under nitric oxide stress (Fig. 1A).

The oxidative stress reporters responded specifically to the presence of hydrogen peroxide (Fig. 1B). The CTAlp- GFP strain, expressing GFP under control of the catalase CTAl promoter, exhibited a 5-fold higher fluorescence intensity after hydrogen peroxide treatment compared to the unstressed control. Both, the TRX1p-GFP and GRX2p-GFP strains, in which GFP is under control of the thioredoxin TRX1 and glutathione reductase GRX2 promoters, respectively, displayed a >6-fold increase in fluorescence intensity when compared to the unstressed control (Fig. 1B).

As expected, these oxidative stress-specific reporters showed no major changes in GFP fluorescence after carbohydrate starvation or in the presence of GSNO. Interestingly, the SOD5p-GFP, cells, expressing GFP under control of the superoxide dismutase SOD5 promoter, did not show any significant increase in fluorescence under any of the conditions tested at 30°C, regardless of the presence of H2O2. Therefore, we tested the expression of this GFP reporter under further conditions including increased temperature. At 37°C, the SOD5p-GFP strain responded to the presence of H2O2 (Fig. 1D). Under all other stress conditions, the GFP signal remained as low as in the unstressed control, thus indicating that SOD5 is specifically up-regulated in response to oxidative stress at 37°C. No morphological changes were observed during the course of these experiments.

Finally, GFP expression levels were examined in the SSU1p- and YHB1p-GFP strains, which express GFP under the control of the sulphite transporter SSU1 and nitric oxide dioxygenase YHB1 promoters, respectively. As shown in Fig. 1C, the greatest GFP expression was observed when these strains were exposed to GSNO. Fluorescence intensities from these strains were not significantly changed in the unstressed control, under oxidative stress or under carbohydrate starvation. This indicates that the nitrosative stress reporters respond specifically to the presence of the nitric oxide-releasing compound GSNO.

Taken together, these results demonstrate that the GFP reporter strains respond to the relevant stress (Fig. 1D).

Single cell profiling of the GFP reporters during cocubation with neutrophils

Having established that the GFP reporter strains respond specifically to the relevant stress conditions, we then investigated the responses of these reporters in the presence of neutrophils. Two subsets of C. albicans cells were analysed in a series of experiments: phagocytosed and non-phagocytosed cells. The latter set represented those cells that are attached to neutrophils without
being internalised as well as cells that are not in direct contact with the phagocytes. To discriminate between internalised and non-
internalised fungal cells, samples were counterstained using ConA-
AF647, which binds strongly to non-phagocytosed C. albicans cells, while those within the neutrophils are faintly stained or not stained at all. As a control, each reporter strain was incubated under the
same conditions in the absence of neutrophils.

As shown in Fig. 2A and B, a low fluorescent signal was detected
whenever the pGFP strain was used. In contrast, the ACT1p-GFP
strain showed high fluorescence levels under all three conditions.
The moderately higher fluorescence in phagocytosed cells was not statistically
significant.

To determine whether carbohydrate starvation is imposed intra-
, extracellularly or under both conditions, the ICL1p-GFP and
MLS1p-GFP strains were used. These strains exhibited a higher
fluorescence intensity only in the phagocytosed population (Fig. 2A
and C), suggesting that carbohydrate starvation is imposed only in
the intracellular environment.

For the oxidative stress reporters (CTA1p-, SOD5p-, TRX1p-
and GRX2p-GFP), the highest fluorescent signal was also observed in
the phagocytosed fungal cells (Fig. 2D). However, some of these
reporters also showed relatively high GFP expression levels before internalisation by the phagocytes (Fig. 2D). CTA1p-GFP exhibited the
highest fluorescence when C. albicans cells were inside the
neutrophils. SOD5p- and TRX1p-GFP reporter strains displayed similar expression patterns in that phagocytosed cells responded to
the greatest extent. However, SOD5p- and TRX1p-GFP cells that
remained outside of phagocytes also displayed significantly
elevated GFP expression levels, indicating that they sensed and
responded to extracellular neutrophil-derived reactive oxygen
species. However, the full response occurred only following
phagocytosis. Consistent with our previous results and despite
the fact that SOD5 expression is associated with the morphogenetic
program [28], the fungal cells expressed the SOD5p-GFP construct
even though they remained in the yeast morphology (data not shown). The GRX2p-GFP reporter also exhibited a slight increase in
fluorescence in the phagocytosed population, but this increase
was not statistically significant when compared to the control
without neutrophils. Taken together, these results indicate that the
full exposure and response to oxidants occurs in the intracellular
environment, but some oxidative stress genes are induced by extracellular neutrophil-derived activities.

Next, we tested whether C. albicans readily responds to nitrosative
stress. For this, we made use of the nitrosative stress reporter strains
carrying YHB1p- and SSU1p-GFP. Both genes have been shown to be
upregulated in response to nitric oxide [22]. As shown in Fig. 2A
and E, these GFP reporters responded to neutrophils by increasing the
fluorescence levels upon phagocytosis. YHB1p-GFP showed the
strongest GFP induction, while up-regulation of SSU1p-GFP was
evident, but not significant. We concluded that nitrosative stress is
imposed only in the intracellular environment as YHB1p-GFP
responded only following phagocytosis.

The glyoxylate cycle but not gluconeogenesis is needed to
resist neutrophil-mediated killing

Having characterised reporter gene activation during C. albicans-
neutrophil interactions, the contribution of the corresponding gene
products to fungal fitness and survival was evaluated. To achieve
this we determined the susceptibility of the mutants in a
neutrophil-mediated killing assay (Fig. 3–5). In this assay, fungal
cells lacking the specific factors were confronted with freshly
isolated human neutrophils. The susceptibility of each mutant
strain was then normalised against the susceptibility of an isogenic
wild type strain.

Based on previously performed transcriptional analyses, it was
known that C. albicans up-regulates the glyoxylate cycle when
confronted to neutrophils, most likely to enable the fungus to use
alternative carbon sources in a glucose-deprived environment. We
hypothesised that the inability to metabolise via the glyoxylate cycle
would render C. albicans more susceptible to neutrophil-mediated
killing. As predicted, an sod1ΔΔ mutant lacking the iso-citrate lyase
gene showed a significant increase in susceptibility to neutrophil
killing (Fig. 3A). We also predicted that gluconeogenesis, a metabolic
pathway required for the generation of hexoses in a sugar-scarce
environment, might also contribute to fitness. However, when we
examined a pkd1ΔΔ mutant, which lacks phosphoenolpyruvate
carboxykinase and is unable to perform gluconeogenesis, this strain
showed no significant increase in the susceptibility to neutrophil
killing (Fig. 3A). This suggested that this pathway is not essential for
survival under these conditions. This is in accordance to the
transcriptional data, where the genes coding for the key enzymes of
this pathway, FBP1 and PKC1, were not up-regulated in the presence
of neutrophils [15].

Superoxide dismutase 5 (Sod5) is pivotal for normal
resistance to neutrophil-derived ROS

Next, we investigated whether superoxide dismutases are crucial
to counteract the oxidative stress imposed by neutrophils. C. albicans possesses an isoenzyme family of six superoxide dismutases
localised in different cellular compartments. Superoxide dismu-
tases 1, 2 and 3 (Sod1-3) are intracellular enzymes, whereas Sod4,
5 and 6 are GPI-anchored cell wall-associated enzymes that face
the extracellular environment. SOD5 expression is induced in
response to neutrophils and a mutant defective in SOD5 is unable
to resist neutrophil killing at wild type levels [15]. Moreover, Sod5
has been linked to the detoxification of ROS derived from myeloid
dendritic cells and bone marrow-derived macrophages [20]. As
shown in the expression analysis, SOD5 was upregulated during C.
albicans-neutrophil interactions. The expression of this gene is
normally associated with filamentation, but expression was
increased in fungal cells that did not undergo the morphogenetic
transition once internalised by neutrophils [15]. The sod5ΔΔ mutant
was clearly more susceptible to neutrophil killing than the respective wild type (P value = 0.0474, Fig. 4A). To assess the
contribution of the additional surface-associated Sod5s, we tested
single sod4ΔΔ and sod6ΔΔ mutants, a double sod4ΔΔ sod5ΔΔ mutant
and a triple sod4ΔΔ sod5ΔΔ sod6ΔΔ mutant in the neutrophil killing
assay, as well as the sod1ΔΔ mutant, which lacks the cytoplasmic Sod1. As shown in Fig. 4A, the sod1ΔΔ mutant was as sensitive to neutrophil killing as the wild type strain, suggesting that Sod1 does not play a major role in the
detoxification of ROS generated by neutrophils. Neither the single
sod4ΔΔ mutant nor the sod6ΔΔ mutant displayed significant changes in sensitivity to neutrophils, compared to the
wild type control. In contrast, the double sod4ΔΔ sod5ΔΔ (P value
= 0.0326) and the triple sod4ΔΔ sod5ΔΔ sod6ΔΔ (P value
= 0.0024) mutants were only slightly more sensitive than the
sod2ΔΔ single mutant, suggesting that, despite the presence of
apparently redundant Sods, Sod5 plays the pivotal role in the
detoxification of neutrophil-derived oxidative stress.

Next, we tested whether inhibition of the neutrophil NADPH
oxidase complex rescues the hypersensitive phenotype of sod3ΔΔ
cells, since superoxide production in neutrophils relies almost
exclusively on this enzymatic complex. The inhibition of NADPH
oxidase with apocynin completely abolished superoxide produc-
tion (data not shown). After challenging apocynin-treated neutro-
phils with C. albicans, the sod5ΔΔ mutant displayed similar
survival rates to wild type cells (Fig. 4B). Furthermore, the survival
Figure 2. Expression analysis using GFP reporter strains during interaction with neutrophils. Exponential GFP reporter cells were co-incubated with neutrophils for 1 h. The GFP signal was quantified as described in the experimental procedures. (A) Representative microphotographs of selected GFP strains incubated in RPMI +5% FBS in the absence of neutrophils or coincubated with the phagocytes. Boxes in the right lower corner belong to different fields of the same microphotograph. White bars represent 10 μm. (B) pGFP strains was used as negative control, and ACT1p-GFP as positive control. (C) The carbohydrate starvation reporters ICL1p- and MLS1p-GFP showed an increase in the GFP expression in those cells that were phagocytosed by the neutrophils, while the GFP expression in the non-phagocytosed cells remain as low as in the control without neutrophils. (D) Cells from the CTA1p- and GRX2p-GFP strains showed increased GFP expression in the phagocytosed population. The SOD5p- and TRX1p-GFP cells inside the neutrophils showed the highest fluorescent signal, however, cells that were not phagocytosed also had a significant increase in the GFP expression. (E) Reporter strains for the nitrosative stress response YHB1p- and SSU1p-GFP showed increased GFP expression only in those cells that were phagocytosed. The average of at three biological replicates is shown. *P<0.05, **P<0.01, compared to the control. doi:10.1371/journal.pone.0052850.g002
of the double and triple sod mutants increased to the wild type levels when challenged with apocynin-treated neutrophils. Interestingly, almost no effect could be observed in the survival of the wild type strain upon NADPH oxidase inhibition.

To determine whether there is a correlation between the generation and accumulation of ROS and increased susceptibility to neutrophil killing, we measured the production and accumulation of neutrophil-derived ROS. As shown in Fig. 4C-D, neutrophils exposed to sod1ΔΔ, sod4ΔΔ and sod6ΔΔ mutants produced ROS at comparable levels to those produced upon challenge with the wild type strain. In stark contrast, sod5ΔΔ, sod4ΔΔ sod5ΔΔΔ and sod4ΔΔ sod6ΔΔΔ caused more ROS accumulation. To determine whether superoxide is accumulated upon stimulation with the sod5ΔΔΔ mutants, a luminescent determination using lucigenin as the chemiluminescent substrate, which specifically detects the superoxide anion, was performed. As shown in Fig. 4E-F, more than 3-fold more superoxide accumulated upon neutrophil challenge with sod5ΔΔΔ, sod4ΔΔΔ sod5ΔΔΔ or sod4ΔΔΔ sod5ΔΔΔ sod6ΔΔΔ cells compared with wild type cells. In contrast, exposure to sod4ΔΔΔ or sod6ΔΔΔ cells did not cause increased superoxide accumulation. This suggests that, following exposure to neutrophils, Sod5 is the major enzyme required for ROS detoxification and in particular for superoxide detoxification. No significant differences in superoxide accumulation were detected between the single sod5ΔΔΔ mutant and the double sod4ΔΔΔ sod5ΔΔΔ and triple sod4ΔΔΔ sod5ΔΔΔΔ sod6ΔΔΔΔ mutants, although a trend of increased accumulation was observed.

We next investigated whether the elevated ROS accumulation was due to increased activation of the neutrophils by these mutants. We quantified the expression of the activation markers CD11b (also known as integrin αIIb) and CD66b (also known as CEACAM8) on the surface of the phagocytes. Neutrophils stimulated with any of the sodΔΔΔ mutants were activated to the same extent as the wild type strain, as indicated by the expression of these two activation markers on the surface of the neutrophils (Fig. S1 A-B). This suggested that the increased ROS accumulation was mediated by the reduced ability of the C. albicans cells to eliminate the oxidants rather than by increased neutrophil activation.

Mutants defective in the catalase activity do not exhibit significantly increased sensitivity towards neutrophil-mediated killing

Next, we tested mutants lacking further key effectors of the oxidative stress response. It has been previously shown that several genes encoding enzymes or signalling pathway components involved in the oxidative stress response in C. albicans are up-regulated during the interaction with neutrophils [15]. Moreover, we demonstrated the expression of some of these genes (CTA1, TRX1, GRX2) in phagocytosed and non-phagocytosed fungal cells by using GFP reporter strains (Fig. 2). We hypothesised that mutants lacking the corresponding genes might display increased susceptibility to neutrophils and that the ROS levels in neutrophils exposed to these mutants would be increased due to inefficient detoxification. First, we investigated ROS levels in neutrophils exposed to a cta1ΔΔΔ mutant, lacking detectable catalase activity (Alistair J. P. Brown, unpublished data). Interestingly, despite the lack of catalase activity, this mutant induced ROS almost to the same extent as the wild type (Fig. 5A a-b). Moreover, when we determined the residual metabolic activity of the cta1ΔΔΔ mutant after confrontation with neutrophils, we found that although this mutant showed a trend towards decreased survival, the susceptibility in the killing assay was not significantly increased (Fig. 5A). This suggested that, even though CTA1 is upregulated and may be involved in the detoxification of neutrophil-derived oxidants, specifically H2O2, the catalase activity might be dispensable for normal susceptibility to neutrophils.

Glutathione reductase activity is crucial for ROS detoxification and resistance to neutrophils

We also investigated a mutant lacking the gene coding for the glutathione reductase GRX2, involved in the reduction of oxidised glutathione, a tripeptide associated with the oxidative stress response. As shown in Fig. 5A a, ROS accumulated when the grx2ΔΔΔ mutant was coincubated with neutrophils in the oxidative burst assay, and this accumulation was significantly greater than for neutrophils coincubated with wild type C. albicans cells (Fig. 5A-C).
Figure 4. *C. albicans* mutants lacking SOD5 are hypersensitive to neutrophil killing and induce ROS accumulation. (A) *C. albicans* mutants sod5Δ/Δ, sod4/5 Δ/Δ and sod4/5/6 Δ/Δ were more susceptible to neutrophil-mediated killing. Fungal cells were exposed to neutrophils for 3 h. Results from three independent replicates are shown, lines represent the mean value from the replicates. Survival of wild type strain was set to 100%. (B) Neutrophils were incubated with 1 mM apocynin for 30 min at 37°C with 5% CO2, before infection with opsonised fungal cells. Lines represent the mean values of each strain in the presence of neutrophils (filled red circles) and apocynin-treated neutrophils (open blue squares). Results from four replicates are shown. Statistical significance was tested by two-way ANOVA with Bonferroni post-tests. (C) Luminol-enhanced chemiluminescence assay was performed to determine the accumulation of neutrophil-derived ROS upon stimulation with *C. albicans* mutants (MOI 1) lacking genes coding for superoxide dismutases. Neutrophils were left unstimulated or stimulated with 20 nM PMA (not shown) as negative and positive controls, respectively. A representative result of one replicate is shown. (D) The area under the curve was calculated to determine the total ROS accumulation during the course of the experiment (150 min). The average of four independent replicates is presented. *P<0.05; **P<0.01; compared to the control.
b). The total amount of ROS accumulated with grx2Δ/Δ cells was not as striking for the sod5Δ/Δ and related mutants, and this might be related to the inability of these C. albicans cells to fully detoxify the oxidants generated upon neutrophil activation. Consistent with the increased accumulation of ROS, the grx2Δ/Δ mutant exhibited a decreased survival after it was confronted with neutrophils for 3 h (Fig. 5A c).

Since we showed that grx2Δ/Δ also induces accumulation of ROS at significant levels, we investigated whether superoxide was one of the accumulated ROS. In contrast to the sod5Δ/Δ mutants, the grx2Δ/Δ did not induce accumulation of superoxide (Fig. S2 B–C), suggesting that this mutant is not defective in the ability to eliminate this radical, but probably unable to keep the redox balance necessary for the maintenance of reduced glutathione in the cell after oxidative stress exposure. Strikingly though, other ROS-independent mechanisms may be rendering this mutant more susceptible, since inhibition of the NADPH oxidase, did not have an effect on the survival outcome (Fig. S2 A).

We then investigated the role of thioredoxin, which is involved in oxidative stress sensing and detoxification [29]. In the presence of neutrophils, TRX1-GFP levels were markedly up-regulated (Fig. 2C). The behaviour of the trx1Δ/Δ mutant in the oxidative burst assay was different to the other mutants, since it consistently induced slightly less ROS production than its isogenic wild type control (Fig. 5B a–b). Moreover, we did not observe a clear effect upon the survival of this mutant upon exposure to neutrophils in the killing assay (Fig. 5B c).

Inability to detoxify neutrophil-derived RNS renders C. albicans more susceptible to killing

The next aspect we focused on was the ability of C. albicans to overcome neutrophil-derived nitrosative stress. In our expression analyses, we showed that C. albicans up-regulates the HHB1 gene. Furthermore, SSU1, a gene which expression is induced in the presence of nitric oxide, was also up-regulated in response to neutrophil phagocytosis. We then tested a mutant lacking the HHB1 gene. Consistent with our observation, the mutant yhb1Δ/Δ showed a clear increase in sensitivity to neutrophil killing (Fig. 3B a), suggesting that nitric oxide detoxification contributes to the survival of C. albicans following neutrophil-derived nitrosative stress. To test whether the neutrophil sensitivity of yhb1Δ/Δ cells is related to their defect in nitric oxide detoxification, we tested whether the neutrophil sensitivity of
The stress regulator Hog1 is required for normal survival of C. albicans upon neutrophil attack

Stress responses in C. albicans are largely coordinated by the stress regulator Hog1, a stress activated protein kinase that mediates the expression of genes in response to oxidative, osmotic and heavy metal stress [30]. In addition to an increased sensitivity to oxidative stress, the hog1Δ/Δ mutant displays morphological defects, forming filaments under non-inducing conditions [31,32]. We hypothesised that the inability to mount a robust stress response, in addition to the morphogenetic defects, will render the hog1Δ/Δ mutant hypersensitive to killing by neutrophils. When confronted to neutrophils, hog1Δ/Δ was clearly impaired in its ability to resist phagocytic attack (Fig. 6A). This decreased resistance to neutrophils was even more dramatic in the double mutant hog1Δ/Δ cap1Δ/Δ, which also lacks the gene encoding Cap1, a regulator that mediates the transcriptional response to oxidative stress.

To provide some mechanistic explanation for this increased sensitivity to neutrophils, we investigated the behaviour of these mutants in the oxidative burst assay. When neutrophils were exposed to hog1Δ/Δ cells, the kinetics of ROS production differed significantly compared to the parental wild type strain, showing a clear delay (Fig. 6B). When the total ROS accumulation was determined, hog1Δ/Δ showed only slightly and not significantly increased ROS levels as compared to the wild type C. albicans control, despite the altered dynamics. Similarly, the double mutant hog1Δ/Δ cap1Δ/Δ also induced a delayed ROS production response. In addition, the total ROS induced by this double mutant was significantly higher in comparison to the single hog1Δ/Δ mutant (Fig. 6C).

To test whether the increased ROS production was due to increased neutrophil activation by these mutants, we assayed the expression of the activation markers CD11b and CD66b on the neutrophil surface. CD11b expression was not significantly altered in response to the single mutant hog1Δ/Δ or the double mutant hog1Δ/Δ cap1Δ/Δ compared to their respective wild type strains (Fig. S1 C–D). However, we detected a moderate but significantly lower expression of CD66b upon stimulation of neutrophils with hog1Δ/Δ cells after 1 h co-incubation (Fig. S1 D).

Taken together, these results suggest that the inability of these mutants to properly respond to the neutrophil-generated oxidative stress renders them significantly more sensitive to the attack by these phagocytes, and highlights the relevance of Hog1 signalling during the interactions between fungal and innate immune cells.

Discussion

Neutrophils are one of the most important types of phagocytes during Candida infections, acting as a first line of defence. We have previously shown that, amongst blood cell types, neutrophils exert the greatest effects upon C. albicans and govern the transcriptional response in blood infections [15]. Upon attack by neutrophils, C. albicans activates specific responses that include the up-regulation of metabolic pathways necessary for the assimilation of alternative carbon sources, and the induction of proteins involved in the detoxification of oxidants. Moreover, the up-regulation of genes that normally respond to the presence of nitric oxide led us to
hypothesis that nitrosative stress is a relevant stress that *C. albicans* encounters during interaction with neutrophils.

Neutrophils can kill microorganisms either by phagocytosis (a process involving the sensing, recognition and ingestion of microorganisms) or by extracellular mechanisms involving the release of antimicrobial compounds, such as oxidants, enzymes or peptides. Using a single cell profiling approach, we show that carbohydrate starvation is imposed only upon fungal cells that have undergone phagocytosis. The genes coding for the glyoxylate cycle enzymes isocitrate lyase (*ICL1*) and malate synthase (*MLS1*) were up-regulated upon phagocytosis. These findings are in accordance to Bareille et al. [24] and suggest that phagocytosed fungal cells are exposed to an intracellular environment that is relatively poor in carbohydrates. Therefore, in order to survive, *C. albicans* is forced to use alternative carbon sources that might be available within the phagocyte (such as organic acids). Alternatively, *C. albicans* might refocus its metabolism such that it can recycle its own carbon-containing molecules. The relevance of the glyoxylate cycle in the survival of *C. albicans* upon exposure to neutrophils is supported by the finding that an *icl1ΔΔ* mutant showed decreased resistance to neutrophil-mediated damage, similar to observations made with macrophages [16]. Under the same conditions one would expect an additional up-regulation of genes involved in gluconeogenesis, since this pathway drives the synthesis of hexoses under starvation conditions. However, our previous study suggested that this pathway is not up-regulated during the interaction with neutrophils [15]. In addition, it has been shown that *PCK1*, encoding a central enzyme of gluconeogenesis, is not up-regulated upon phagocytosis by neutrophils [24], and we provide evidence in this study that the inability to perform gluconeogenesis has no effect in the overall survival of *C. albicans* after exposure to these phagocytes (Fig. 3A). The data suggest that the glyoxylate cycle, but not gluconeogenesis, plays a key role in the adaptive responses of phagocytosed *C. albicans* cells.

*C. albicans* responds robustly to oxidative insults. The fungus possesses a number of signalling pathways that regulate several mechanisms to cope with the oxidative stress [33]. In agreement with the “commensal school” concept [34], it is not surprising that this otherwise commensal organism has evolved the ability to cope with oxidative stress. The fungus probably encounters phagocytes, at least transiently, during its normal commensal life style, which utilises oxidants to damage and kill microorganisms. *C. albicans* is able to detoxify the superoxide anion, which is produced by the enzyme complex NADPH oxidase, present in all types of phagocytes. To accomplish this, *C. albicans* has a family of superoxide dismutases that transform superoxide into hydrogen peroxide. The main focus of research regarding *C. albicans* Sods has been the surface-associated Sods, namely *Sod4* and *Sod5*, because they are responsible for the immediate ROS detoxification upon exposure to superoxide. It has been shown that these enzymes display morphotype-specific expression patterns: yeast cells readily express *Sod4*, while expression of *Sod5* is detected only under hypha-inducing conditions [28,35]. We have demonstrated that *C. albicans* up-regulates the *SOD5* gene, not only in response to phagocytosis by neutrophils, but also to extracellular oxidants produced by the phagocytes, since fungal cells that remain outside of neutrophils display significantly elevated *SOD5* expression levels. Moreover, *C. albicans* relies on *Sod3* to resist the neutrophil attack, since *sod5ΔΔ* mutants are more sensitive to neutrophil killing. We provide evidence supporting the idea that superoxide detoxification contributes significantly to the normal outcome in the survival of this pathogen after confrontation with neutrophils. In the absence of *Sod3*, neutrophil-derived ROS accumulated upon stimulation. This is in accordance with previous work where it was shown that ROS accumulated upon stimulation of bone-marrow derived macrophages (BMDMs) and myeloid dendritic cells (mDCs) from mice with mutants lacking *Sod5* [20]. Our results demonstrate that superoxide is accumulated as part of the total ROS. The lack of *SOD5* significantly contributes to the ROS accumulation. This was further supported by the observation that specific inhibition of the NADPH oxidase by apocynin greatly enhanced the survival of *sod5ΔΔ* mutants. Similarly, other fungal pathogens also rely on the ability to detoxify host-derived ROS via superoxide dismutases. For example, it has recently been shown that *Histoplasma capsulatum* requires *Sod3*, a surface-associated superoxide dismutase, to successfully overcome the killing by murine cytokine-stimulated macrophages and human neutrophils, and that *Sod3* is directly involved in the elimination of host-derived ROS [36].

Neutrophil-derived superoxide anion is further transformed into hydrogen peroxide. Amongst the enzymes capable of catalysing hydrogen peroxide are catalase and peroxidases. *C. albicans* possesses one gene encoding catalase, *CTA1*. We and others [25] have shown that this gene is induced upon phagocytosis, whereas extracellular neutrophil activities did not seem to influence the expression of this gene. When confronted with neutrophils, the *cta1ΔΔ* mutant did not show a significant reduction in its ability to survive the phagocyte attack although we observed a trend towards decreased survival. This finding is in contrast to earlier work [37] where a *cta1ΔΔ* mutant was tested and shown to be significantly reduced in survival when exposed to neutrophils at different MOIs, including the MOI used in this study. However, in that previous work, the authors tested the susceptibility of 3 h-induced hyphae in RPMI at 37°C, while in our study the infection was done with cells of the yeast morphotype, which eventually formed germ tubes during the course of the experiment. This may explain the difference in the two studies and may suggest a different role of Cta1 in yeast and hyphal cells. Surprisingly, the *cta1ΔΔ* mutant did not significantly induce the accumulation of total ROS. Since this mutant is unable to metabolise H$_2$O$_2$ via catalase, this oxidant was expected to accumulate, and therefore be detected in the ROS assay. This finding indicates that the catalase activity is dispensable for normal resistance to neutrophils, despite the fact that *CTA1p-GFP* expression was strongly induced upon neutrophil phagocytosis. It is therefore possible that *C. albicans* relies on other activities to further metabolise and detoxify critical and detrimental H$_2$O$_2$ levels. For example, *C. albicans* up-regulates genes coding for peroxidases when co-incubated with neutrophils [15]. Whether peroxidase activity is responsible for the detoxification of H$_2$O$_2$ in the absence of catalase activity remains unclear. Another hydrogen peroxide detoxification mechanism potentially used by *C. albicans* when confronted with neutrophils or other phagocytes could be the induction of glutathione as an oxidant scavenger. Glutathione is a small molecule that possesses two thiol groups that are sensitive to oxidation by H$_2$O$_2$. Once oxidised, glutathione can be reduced and thus recycled by the action of glutathione reductase, using NADPH as electron donor. *C. albicans* has at least two genes coding for putative glutathione reductases, *GRA2* and *GLR1*. Both genes were shown to be up-regulated in the presence of neutrophils [15]. This finding is in accordance with another previous study, which showed that this gene was up-regulated in the presence of neutrophils, but not by macrophages [25]. In our study, we showed that *GRA2* (also known as *TTR1*) was moderately up-regulated upon phagocytosis by neutrophils. In agreement with Chaves et al. [38] we found that a *gra2ΔΔ* mutant was hypersensitive to neutrophils, which is likely to contribute to the observed attenuated virulence of the mutant in a murine model of disseminated candidiasis. One explanation for
the increased sensitivity of this mutant to neutrophil killing might be its inability to readily detoxify neutrophil-derived oxidants other than superoxide (Fig. 5A a), possibly H$_2$O$_2$, since this mutant did not accumulate the superoxide radical (Fig. S2). However, since we observed no increase in the survival of this mutant upon inhibition of the NADPH oxidase, the most relevant source of oxidants in the neutrophil, it is also possible that other non-oxidative mechanisms are responsible for the increased susceptibility of this mutant.

In addition to detoxification mechanisms, C. albicans possesses proteins involved in sensing the presence of oxidants. Thioredoxin, encoded by TRX1, has recently been shown to be involved in sensing of oxidative stress [29]. Supporting this observation, our data show that, TRX1 is up-regulated during co-incubation with neutrophils. This up-regulation occurs after phagocytosis, but also in cells that have not been ingested. However, the sensitivity of a trx1A/Δ mutant to neutrophils was not increased. Consistently, accumulation of ROS was not increased, but significantly decreased in this mutant when challenged with neutrophils. We conclude that, despite the involvement of Trx1 in the oxidative stress sensing mechanisms, Trx1 is dispensable for survival after neutrophil exposure. The fact that this mutant was not more sensitive to neutrophil killing, but still displayed attenuated virulence in mice [29] shows that Trx1 may have additional roles in vivo or simply that the role of Trx1 during the interaction with neutrophils in vivo cannot be mimicked in the in vitro setting. Since the trx1A/Δ mutant has morphological defects [29], it may also be possible that these defects contribute to reduced recognition, reduced stimulation of neutrophils and/or reduced virulence of this mutant. Phagocytes are well known for their ability to generate ROS, but they are also capable of producing nitric oxide and related metabolites, altogether referred as reactive nitrogen species (RNS). The production of nitric oxide by phagocytes largely depends on the inducible nitric oxide synthase, or iNOS. We provide evidence that C. albicans responds to neutrophil-derived nitric oxide, and that this neutrophil activity contributes to the killing of C. albicans, demonstrating that nitric oxide detoxification has a significant impact on the survival of this fungus in presence of neutrophils. We confirmed an observation of a previous study from our group that the gene YHB1, coding for a nitric oxide dioxygenase, is induced during co-incubation with neutrophils [15], using a YHB1p-GFP reporter strain, which responded to the presence of the nitric oxide-releasing compound GSNO. We further showed that the YHB1 expression occurred only upon phagocytosis, indicating that its expression contributes to fungal extracellular defence mechanisms against neutrophils. This is in accordance with the dynamics of the generation of nitric oxide by the phagocytes. Whereas superoxide is produced by the active NADPH oxidase complex assembled in cytoplasmic and phagosomal membranes, the nitric oxide synthase is localised in the cytoplasm or associated with vesicles that fuse with the phagosome, delivering the nitric oxide directly into this organelle [10]. Thus, the nitric oxide is only encountered in the intracellular environment. Moreover, lack of YHB1 rendered C. albicans clearly more susceptible to neutrophil-mediated killing, highlighting the importance of nitric oxide detoxification. The ability to cope with nitric oxide is advantageous for pathogens to successfully colonise the host. Several examples are found in bacteria, noteworthy Escherichia coli [39], Salmonella serovar Typhimurium [40] and Mycobacterium tuberculosis [41]. These bacterial pathogens possess flavohaemoglobinins that detoxify host-generated nitric oxide, providing protection against macrophage-derived nitric oxide and thus improving their survival when confronted with phagocytes. In the case of fungal pathogens, the contribution of host-derived nitrosative stress is less well studied. However, an earlier report showed that Cryptococcus neoformans relies on two nitric oxide detoxification systems, the flavohaemoglobinin Fhb1, that consumes nitric oxide, and a GSNO reductase Gno1, that metabolises GSNO [42]. Mutants lacking these enzymes showed attenuated virulence in a mouse model. Similarly, as a consequence of the inability to detoxify nitric oxide, C. albicans yhb1A/Δ mutants showed reduced virulence in models of disseminated candidiasis [22,23,43]. The fact that C. albicans yhb1A/Δ cells were protected against neutrophils in the presence of carboxy-PTIO, a nitric oxide scavenger, suggests that the underlying reason for the increased sensitivity of this mutant to neutrophil killing is linked to the nitric oxide exposure upon attack by the phagocytes. It seems unlikely that neutrophil-derived nitric oxide is sufficient to directly kill C. albicans, but it is possible that nitric oxide exerts its effect by halting the fungal growth [44], and acts synergistically with other fungicidal mechanisms, like oxidants, antimicrobial peptides or lytic enzymes. In addition, nitric oxide by-products (peroxynitrite, peroxynitrous acid and others) may participate in the damage and eventual killing of the fungus.

The ability of C. albicans to sense and respond to stress largely depends on the Hog1 signalling pathway. It has been shown that mutants lacking Hog1 have an increased susceptibility to host immune cells [26] and an overall decreased virulence in a model of disseminated candidiasis [45]. We included the hog1A/Δ mutant in our study in order to evaluate the role of stress response signalling. Consistent with previous works, lack of HOG1 renders C. albicans more sensitive to the killing by neutrophils. Interestingly, the hog1A/Δ mutant exhibited a clear delay in the induction of neutrophil-derived ROS. Despite this delayed induction, it accumulated slightly more ROS than the respective wild type. This was also observed in the double mutant hog1A/Δ cap1A/Δ, lacking an additional key regulator of stress response signalling, in a more pronounced manner, and the accumulation of ROS by this double mutant was actually significantly higher. The reasons underlying the delayed ROS induction, and therefore neutrophil stimulation, may rely on the morphological defects of the hog1A/Δ mutants [31,32], which exhibits hyphal formation even under non-inducing conditions. In fact, the morphology of C. albicans plays a crucial role in neutrophil activation and mutants with morphological defects are unable to activate the neutrophil ERK1-kinase, involved in motility and killing of C. albicans [46]. We initially hypothesised that, if the hog1A/Δ mutant exhibits a hyperfilamentous phenotype, it may greatly induced the production of ROS. However, as shown by Wozniok et al. [46], the filamentous morphotype exhibited by some mutants is not sufficient to properly activate the neutrophils. This is also supported by the observation that the expression of the activation markers CD11b and CD66b on neutrophils upon stimulation with either the hog1A/Δ or the hog1A/Δ cap1A/Δ mutants was not increased as compared to the wild type. In addition, it has been documented that deletion of HOG1 has a profound effect on the cell wall architecture, which is associated with a constitutive activation of the Cek1 cell wall-stress pathway [45], which in turn may also account for the differences we observed in the dynamics of the ROS induction. The overall outcome of the lack of Hog1 either in the hog1A/Δ or the hog1A/Δ cap1A/Δ mutants is a decreased survival. We have previously shown that the cap1A/Δ mutant is more sensitive to neutrophil killing [15]. The fact that the double mutant is more prone to killing evidences that both stress signalling pathways are necessary for full wild type resistance of C. albicans to neutrophils.

Taken together, our results show that C. albicans responds to a combination of insults upon neutrophil attack, including nutri-
tional, oxidative and nitrosative stresses. It shows that some of these stresses are imposed exclusively in the intracellular milieu, like carbohydrate starvation or exposure to nitric oxide, while others occur in both the intra- and extracellular environments, such as insults of oxidative nature. In addition to starvation and oxidative stress, nitrosative stress is relevant for neutrophil-mediated killing of this fungus, and C. albicans responds readily to this kind of insult. Moreover, the integrity of signalling pathways such as Hog1 and Cap1 are pivotal for the normal resistance of this pathogen when confronted with neutrophils. We have dissected the responses at the transcriptional level using GFP reporter strains, and we have assessed the actual contribution of the gene products for the survival of C. albicans by using mutant strains. Although this works emphasises the relevance of certain stresses imposed by the neutrophil, it is expected that other mechanisms contribute to the killing of C. albicans; for instance, the production of non-oxidative molecules such as lytic enzymes (e.g. cathepsin G, neutrophil elastase), cationic peptides (α-defensins, LL-37, histones) or metal chelator proteins (lactoferrin, calprotectin).

**Experimental Procedures**

**Ethics statement**

Blood was obtained from healthy human donors with written informed consent. The blood donation protocol and use of blood for this study were approved by the institutional ethics committee (Ethik-Kommission des Universitätsklinikum Jena, Permission No 2207-01/08).

**Strains and culture conditions**

Strains used in this work are listed in table S1. Strains were routinely grown in liquid YPD (1% yeast extract, 2% bactopeptone, 2% D-glucose, 2% agar if needed), or SD minimal medium (2% D-glucose, 0.17% yeast nitrogen base, 0.5% ammonium sulphate, 2% agar if needed). For liquid overnight cultures, strains were grown in YPD in a shaking incubator at 30°C, 180 rpm. Exponential cultures were obtained by diluting an overnight culture in fresh YPD to an OD_{600} of 0.2 and incubated at 30°C and 180 rpm until the culture reached an OD_{600} of 0.5.

**Strain construction**

*C. albicans* CAI-4 was used for the construction of the MLS1p-, SSU1p- and YHB1p-GFP reporter strains, in order to use the same genetic background as the previously described GFP strains [24,25,27]. Primers sequences are listed in table S2. To generate the plasmid pMLS1-GFP, the *C. albicans* MLS1 promoter (−1000 to −1, relative to the start codon) was PCR amplified with the primers MLS1 Xho1 5’ and MLS1 HindIII 3’ and cloned between the Xho1 and HindIII sites of pGFP [27]. To construct pSSU1-GFP, the SSU1 promoter (−1000 to −1) was PCR amplified with the primers SSU1 Xho1 5’ and SSU1 PstI 3’, and cloned between the respective sites in pGFP. Likewise, to generate pYHB1-GFP, the YHB1 promoter (−3077 to −1) was amplified with the primers YHB1 Xho1 5’ and YHB1 Mlu1 3’ and cloned between the Xho1 and Mlu1 sites in pGFP. Plasmids were linearised with Stul, integrated in the *RPS10* locus in CAI-4 and correct chromosomal integration was PCR confirmed as described elsewhere [27].

**GFP reporter stress – specific response**

The GFP reporter strains were grown overnight in YPD, diluted in fresh YPD to an OD_{600} of 0.2 and regrown to an OD_{600} of 0.5. Carbohydrate starvation was imposed by diluting the cultures to an OD_{600} of 0.1 in 2% potassium acetate – YP medium. Oxidative stress was imposed by diluting the cultures in 2 mM H_{2}O_{2} – YPD. Similarly, nitrosative stress was imposed by diluting the cultures in 0.6 mM S-nitrosoglutathione (GSNO, Sigma Aldrich) – YPD. As controls, strains were grown in YPD medium without stress. After 2 h of exposure at 30°C, samples were fixed with 4% paraformaldehyde, washed with 1x Dulbecco’s Phosphate-Buffered Saline (DPBS, PAA) and analysed by fluorescence activated cell analysis (FACS, BD Biosciences, UK). The median GFP fluorescence from 10 000 events was recorded. Three independent experiments were performed.

**Isolation of polymorphonuclear cells from human peripheral blood**

Neutrophils were isolated using a gradient centrifugation method. Briefly, 1 part of 1x DPBS-diluted blood was layered on top of 1 part of Polymorphrep (Axis-Shield) and centrifuged for 45 min at 500 g, at 20°C. After centrifugation, plasma and monocyte layer were discarded. The polymorphonuclear cell (PMN) fraction was collected in a fresh tube containing 1 volume of 0.5x DPBS and centrifuged for 10 min at 400 g. Residual erythrocytes were removed with ACK lysing buffer (Life Technologies). Neutrophils were washed with 1x DPBS and resuspended in RPMI1640+5% heat inactivated (10 min at 56°C) foetal bovine serum (FBS), if not stated otherwise.

**Single cell profiling using GFP reporters in an ex vivo neutrophil infection model**

The response of GFP reporter strains to neutrophil phagocytosis or extracellular activities was examined using an ex vivo infection model and a counterstrain to differentiate between phagocytosed and non-phagocytosed fungal cells. Freshly isolated neutrophils were seeded in wells with a 12 mm diameter gelatine – coated coverslip at the bottom, at a concentration of 2.5×10^6 cells ml^{-1} in a volume of 400 μl. Neutrophils were incubated for 1 h at 37°C with 5% CO₂ to let them attach to the glass surface. An aliquot of exponentially growing cultures of the GFP strains was washed twice with 1x DPBS. The cells were diluted to a concentration of 4×10^6 fungal cells ml^{-1} in RPMI1640+5% FBS and 100 μl of this suspension were used to infect the neutrophils (MOI 5). Infection was allowed to proceed for 1 h, at 37°C with 5% CO₂. Cells were fixed with 4% paraformaldehyde and carefully washed with 1x DPBS. Counterstaining was performed using 5 μg concanavalin A – Alexa Fluor 647 (ConA – AF647, Life Technologies) ml^{-1}, which readily binds to non-phagocytosed cells and poorly, or not at all, to intracellular fungal cells. After washing with 1x DPBS, coverslips were mounted upside down on slides with ProLong Gold Antifade Reagent with DAPI (Life Technologies). Fluorescence microscopy was performed in a Leica DM5500B microscope, using appropriate filters for the detection of GFP, Alexa Fluor 647 and DAPI fluorescence. Micrographs were taken in the Leica Application Suite (Leica Microsystems, Mannheim). Fluorescence measurement was done using the quantification tool for regions of interest. For each reporter strain, the GFP fluorescence was measured in at least 30 phagocytosed and 30 non-phagocytosed fungal cells. As controls, the GFP reporters were incubated in wells without neutrophils. All strains were tested in three independent biological replicates.

**Susceptibility to neutrophil killing – XTT assay**

To determine the susceptibility of different *C. albicans* deletion mutants, cells from exponential cultures were washed twice with 1x DPBS, and opsonised with 50% human serum (diluted in 1x DPBS, and opsonised with 50% heat inactivated (10 min at 56°C) foetal bovine serum (FBS), if not stated otherwise.
Neutrophil activation

The activation of neutrophils upon stimulation with C. albicans deletion strains was determined by means of reactive oxygen species (ROS) production in an oxidative burst assay, and changes in the expression of receptors on the neutrophil surface.

The oxidative burst assay was performed using the luminol-enhanced chemiluminescence method for the quantification of total reactive oxygen species. For the specific detection of the superoxide anion, lucigenin was used as the chemiluminescent probe. To prevent unspecific activation of the neutrophils, wells from a 96-well white plate (Corning) were coated with 0.05% albumin (in 1x DPBS) for 1 h at 4°C, and washed twice with 1x DPBS afterwards. Freshly isolated neutrophils were resuspended in RPMI1640 w/o phenol red with 5% FBS at a concentration of 5×10⁶ cells ml⁻¹ and 100 µl of this suspension was seeded. Neutrophils were incubated for 30 min to 1 h at 37°C and 5% CO₂ to let them attach. Fungal cells from exponential cultures were pre-incubated with 1 mM apocynin (Sigma) for at least 30 min before infection with fungal cells. The nitric oxide scavenger carboxy-PTIO (Sigma) was used at a final concentration of 10 mM, when required. Cells were incubated for 3 h at 37°C and 5% CO₂. Control samples with only fungal cells were incubated and further processed under the same conditions.

Neutrophils were lysed by addition of 1 ml cold water. Fungal cells were centrifuged for 5 min at 16 000 g, at 4°C and 1 ml of the supernatant was carefully removed to avoid aspiration of the pellet. 400 µl of 0.5 mg ml⁻¹ XTT (Sigma) and 50 µg ml⁻¹ coenzyme Q₁₀ (Sigma) diluted in 1x DPBS were added. Samples were incubated for 1 h at 37°C and centrifuged for 5 min at 16 000 g, at 4°C. Supernatants were used to measure the absorbance at 450 nm in a Tecan Infinite M200 microplate reader. Background absorbance (neutrophils only and medium only) was subtracted from the samples. The residual metabolic activity was measured every 2.5 min for 2.5 h in a Tecan Infinite M200 microplate reader. Experiments were done in at least three independent occasions using neutrophils from different donors. GraphPad Prism 5.03. Experiments were done in at least three times, using neutrophils from different donors.

**Statistical analysis**

Data are presented as the mean of at least three independent biological replicates, error bars represent standard deviation. Statistical tests were performed using GraphPad Prism 5.03. Two-tailed Student’s t-test was used for two groups comparison. When more than two groups were compared, one-way analysis of variance (ANOVA) with Tukey post-tests was used. Two-way ANOVA with Bonferroni post-tests was used to analyse the results from the survival assays upon NADPH inhibition, or nitric oxide scavenging.

Supporting Information

Figure S1 Neutrophil expression of CD11b and CD66b upon stimulation with sodΔ/Δ, hog1Δ/Δ and cap1Δ/Δ mutants. Surface expression of the activation markers CD11b (A and C) and CD66b (B and D) on neutrophils stimulated with FITC-stained C. albicans (MOI 1), analysed by FACS. A and B show results after 1 h exposure to the sodΔ/Δ mutants. C and D show results of 1 h and 1.5 h exposure to hog1Δ/Δ and hog1Δ/Δ cap1Δ/Δ mutants. The average of the median fluorescence intensities of at least three biological replicates is shown. Data represent the fluorescence values from neutrophils associated with C. albicans cells (phagocytosed or attached). Unstimulated and PMA-stimulated neutrophils were used as negative and positive controls, respectively. **P<0.01, compared to the control. (TIF)

Figure S2 Neutrophil-derived superoxide does not contribute to the hypersensitive phenotype of the mutant gpx2Δ/Δ. (A) Apocynin-treated neutrophils were infected with opsonised fungal cells. Infection was allowed to proceed for three hours and residual metabolic activity was determined at the end. Lines represent the mean values of each strain in the presence of neutrophils (filled red circles) and apocynin-treated neutrophils (open blue squares). Results from four replicates are shown. Statistical significance was tested by two-way ANOVA with Bonferroni post-tests. (B) Detection of superoxide radicals using lucigenin as chemiluminescent probe. One representative replicate is shown. Neutrophils were left unstimulated as negative control. (C) Quantification of area under the curve. Superoxide production...
from PMA-stimulated neutrophils was included as the positive control. Results from four independent replicates are shown. (TH)

**Table S1** C. albicans strains used in this work.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Details</th>
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<td>Wild-type strain</td>
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<tr>
<td>hOGFW</td>
<td>ΔOGF: galactose induced hypomycolate production</td>
</tr>
<tr>
<td>ΔOGFW:ΔSqi</td>
<td>ΔOGF:ΔSqi: galactose induced hypomycolate production</td>
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**Table S2** Primers used in this work.

<table>
<thead>
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<td>YHB1</td>
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</tr>
<tr>
<td>YHB1 reverse</td>
<td>Reverse primer, 5'-GACCGAAATCTGACATTCTGA-3'</td>
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**Author Contributions**

Conceived and designed the experiments: PM HW IMB AJPB OK BH. Performed the experiments: PM CD HW. Analyzed the data: PM HW IMB AJPB OK BH. Wrote the paper: PM HW IM KBJ BH.

**References**