

# **Antifungal properties of cathelicidin LL-37: current knowledge and future research directions**

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## **Abstract**

The threat of fungal diseases is substantially underestimated worldwide, but they have serious consequences for humans, animals, and plants. Given the limited number of existing antifungal drugs together with the emergence of drug-resistant strains, many researchers have actively sought alternatives or adjuvants to antimycotics. The best way to tackle these issues is to unearth potential antifungal agents with new modes of action. Antimicrobial peptides are being hailed as a promising source of novel antimicrobials since they exhibit rapid and broad-spectrum microbicidal activities with a reduced likelihood of developing drug resistance. Recent years have witnessed an explosion in knowledge on microbicidal activity of LL-37, the sole human cathelicidin. Herein, we provide a summary of the current understanding about antifungal properties of LL-37, with particular emphasis on its molecular mechanisms. We further illustrate fruitful areas for future research. LL-37 is able to inhibit the growth of clinically and agronomically relevant fungi including *Aspergillus*, *Candida*, *Colletotrichum*, *Fusarium*, *Malassezia*, *Pythium*, and *Trichophyton*. Destruction of the cell wall integrity, membrane permeabilization, induction of oxidative stress, disruption of endoplasmic reticulum homeostasis, formation of autophagy-like structures, alterations in expression of numerous fungal genes, and inhibition of cell cycle progression are the key mechanisms underlying antifungal efects of LL-37. Burgeoning evidence also suggests that LL-37 may act as a potential anti-virulence peptide. It is hoped that this review will not only motivate researchers to conduct more detailed studies in this feld, but also inspire further innovations in the design of LL-37-based drugs for the treatment of fungal infections.

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#### **Graphical abstract**



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# **Introduction**

Fungal infections are responsible for almost 1.6 million deaths, a number equal to that of tuberculosis and three times that of malaria (Bongomin et al. [2017;](#page-23-0) Alves et al. [2023\)](#page-23-1). The global burden of fungal diseases is expected to rise substantially in the forthcoming years, secondarily owing to the expanding number of individuals living with human immunodeficiency virus (HIV), transplant receivers, immunosuppressive drugs users, patients with advanced cancer, and the elderly (Brackin et al. [2021](#page-23-2)). Even though the epidemiology of fungal diseases has undergone many changes over the past decades, certain pathogens such as *Aspergillus*, *Candida*, *Cryptococcus*, *Pneumocystis*, and *Histoplasma* are still the principal culprits implicated in the invasive forms of mycoses (Bongomin et al. [2017](#page-23-0)). Indubitably, the impact of fungi upon living beings goes far beyond causing infectious diseases. The presence of mycotoxins in agricultural products poses either visible, acute efects or chronic, long-term hidden damages to humans and animals (Adedara and Owumi [2023\)](#page-23-3).

As opposed to antibiotics that target specifc bacterial structures, the development of antifungal drugs confronts a fundamental problem: similarities between mammalian and fungal cells (Mosallam et al. [2022\)](#page-25-0). In fact, the biochemical pathways and cytoplasmic organelles of fungal cells are analogous to those of human cells because of their eukaryotic heritage. As a result, only a handful of clinically useful classes of antifungal agents have hitherto been developed, such as azoles, allylamines, echinocandins, polyenes, and pyrimidine analogs (Vanreppelen et al. [2023\)](#page-26-0). The longterm therapeutic efficacy of antifungal drugs may be counterbalanced by their limited tolerability and serious adverse efects. To add insult to injury, resistance to antifungals is growing at an unprecedented rate, primarily on account of the unbridled and indiscriminate use of such agents outside of medical care facilities (Memariani et al. [2022](#page-25-1)). The best way to tackle these issues is to unearth any potential novel antimicrobial agents with new modes of action.

Ubiquitous throughout all biological kingdoms, antimicrobial peptides (AMPs) have transcended million years of evolution and are amongst the most ancient constituents of the immune system (Yarbrough et al. [2015](#page-26-1)). These peptides serve as endogenous antibiotics of the host to stave of pathogenic invaders. Aside from variations in their amino acid sequences, AMPs are typically less than 50 residues in length, hydrophobic, and cationic at physiological pH, all of which contribute to their antimicrobial activities (Memariani et al. [2020\)](#page-25-2). Mechanistically, AMPs directly attack microbial membranes and/or counteract intracellular machinery in order to kill or to stymie the proliferation of pathogens (de Souza et al. [2023\)](#page-23-4). In addition, anticancer potential of various AMPs is now beginning to be appreciated (Tornesello et al. [2020\)](#page-26-2). The last two decades have witnessed an explosion of research efforts aiming at developing novel AMP-based drugs since they exhibit rapid and broadspectrum microbicidal activities with a low probability of drug-resistance evolution in infectious diseases (Datta and Roy [2021;](#page-23-5) Memariani et al. [2018](#page-25-3)). Although these endeavors have yielded some success, the full therapeutic potential of AMPs remains untapped.

Cathelicidins are cationic peptides with amphipathic properties that form an integral part of the immune system of many vertebrates, including humans and farm animals (Holani et al. [2023](#page-24-0)). The cathelicidin family possesses two functional domains, one at the N-terminus which is conserved (the cathelin pro-domain) and another at the C-terminus which is highly variable and exhibits antimicrobial properties. Proteases remove the pro-domain from cathelicidins once they are secreted, forming mature bioactive peptides (Aghazadeh et al. [2019](#page-23-6)). At the time of writing, there are over 140 amino acid sequences of cathelicidins available in the Antimicrobial Peptide Database (<https://aps.unmc.edu>).

LL-37 is the only member of the cathelicidin family found in humans to date. An 18 kDa precursor of cationic AMP, hCAP18, is encoded by a gene called *CAMP*. By cleaving hCAP-18 with proteinase-3, LL-37 is released as an active helical peptide of ∼ 4.5 kDa (Gwyer Findlay et al. [2013\)](#page-24-1). As the name suggests, LL-37 (LLGDFFRKSKEKIG-KEFKRIVQRIKDFLRNLVPRTES) consists of a total of 37 amino acids; the two leading residues are leucine. Its structure consists of a curved amphipathic helix-bend-helix motif spanning residues 2–31, followed by a disordered C-terminal tail (Wang [2008](#page-26-3)). The primary source of LL-37 is neutrophils, but it was later shown to be expressed by various cells and tissues such as keratinocytes in infamed skin, surface epithelial cells of the conducting airways, and mucous cells of the submucosal glands (Wang et al. [2019](#page-26-4)). LL-37 has well-documented antimicrobial activities toward bacteria, fungi, viruses, and even parasites. It can also exert a multitude of immunomodulatory efects by augmenting cellular killing capacity, diferentiating of immune cells, recruiting leukocytes, inducing or mitigating the production of pro-infammatory cytokines, triggering apoptosis, and promoting angiogenesis (Memariani and Memariani [2023](#page-25-4)). Although these immunomodulatory efects play a pivotal role in killing microbial cells, their discussion does not ft into the scope of the present review.

LL-37 has so far been extensively investigated for its antimicrobial properties against a gamut of fungal pathogens. Despite the wealth of data that has been amassed on the antifungal efects of LL-37, no attempt has been made to provide a comprehensive review of the literature on this subject. Hence, this review is intended to summarize the current knowledge on the antifungal properties of the human cathelicidin LL-37 and to discuss potential directions for future studies. Particular attention is devoted to the molecular mechanisms underlying antifungal activities of LL-37. For the sake of readers' convenience, each section commences with a brief explanation concerning the signifcance of the relevant fungal pathogens.

# **Antifungal efects of LL‑37 on planktonic fungal cells**

#### **Efects on** *Aspergillus* **species**

*Aspergillus* species are filamentous fungi that exist as saprobes in soil and vegetative material. The exposure to conidia can lead to a number of clinically signifcant outcomes, from asymptomatic colonization to invasive infections. Those with structural lung diseases are more likely to develop a fungus ball (aspergilloma) or chronic pulmonary aspergillosis, whereas hypersensitivity to fungal antigens after repeated inhalations of airborne conidia in susceptible hosts may give rise to allergic bronchopulmonary aspergillosis (Russo et al. [2020\)](#page-25-5). Invasive forms of the disease also occur more frequently in patients with severe respiratory viral infections such as infuenza, respiratory syncytial virus infection, and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Physiologically, invasive pulmonary forms begin with alveolar damage, and then the fungal pathogen binds to surfactant proteins, leading to epithelial damage and vascular invasion. This is the main reason why invasive pulmonary forms of aspergillosis are deadly and difficult-to-treat diseases. Influenza viruses are responsible for a suppression of NADPH oxidase, causing dysfunction of neutrophils. In SARS-CoV-2, there is a direct damage to the airway epithelium that are thought to enable the invasion by *Aspergillus*. Several risk factors for COVID-associated invasive aspergillosis include age over 62, use of dexamethasone and anti-interleukin-6 (IL-6), and duration of mechanical ventilation exceeding two weeks (Ledoux and Herbrecht [2023](#page-24-2)). Besides this, glucocorticoids and other immunomodulating drugs may predispose a patient to pulmonary mold infections during treatment for severe SARS-CoV-2 disease (Thompson and Young [2021\)](#page-26-5).

Among the pathogenic aspergilli, *A. fumigatus* is most prevalent in the environment and is responsible for the majority of diseases, followed by *A. favus*, *A. niger*, *A. terreus*, and *A. nidulans* (Sugui et al. [2015\)](#page-26-6). There exist indications that *A. fumigatus* could upregulate the LL-37 expression levels in human corneal epithelial cells (Zhang et al. [2014\)](#page-26-7) and nasal tissue of chronic rhinosinusitis patients (Ooi et al. [2007\)](#page-25-6), suggesting a conceivable role of LL-37 in the battle against *Aspergillus* infections. These fndings have propelled several investigators to address the question of how, and to what extent, the growth and virulence of *A. fumigatus* are afected by LL-37.

In one study (Ballard et al. [2020\)](#page-23-7), a 2-h incubation with LL-37 ( $5-50 \mu$ M) did not lower metabolic activities of clinical and environmental *A. fumigatus* strains (Table [1](#page-4-0)). In another work (van Eijk et al. [2020\)](#page-26-8), metabolic activity of two azole-resistant *A. fumigatus* strains was not inhibited in the presence of 1 or 5 µM of LL-37. Nevertheless, conspicuous increments in conidial growth of either *A. fumigatus* or *A. favus* in response to LL-37 treatment were observed by Sheehan et al. [\(2018](#page-25-7)). Flow cytometric studies revealed, however, that the average percentage of *A. fumigatus* in the hyphae gate of LL-37-treated cells (12.5 µM) did not differ signifcantly from that of the control after 10 h, indicating that LL-37 had no inhibitory activity upon *A. fumigatus* hyphal growth (Ballard et al. [2020\)](#page-23-7). Moreover, there were no morphological alterations in hyphae of either *A. fumigatus* or *A. favus* when challenged with LL-37 (31.25 µg/mL) for 24 h (Sheehan et al. [2018](#page-25-7)).

Species assigned to the *Aspergillus* genus produce a wide range of mycotoxins, such as afatoxins, ochratoxins, gliotoxin, fumonisins, sterigmatocystin, and patulin (Abo Nouh et al. [2020](#page-23-8)). Evidence suggests that LL-37 is capable of enhancing both hyphal mass and gliotoxin secretion (Sheehan et al. [2018](#page-25-7)). Gliotoxin may play a part in regulation of the redox status of *A. fumigatus* and is believed to protect *A*. *fumigatus* toward oxidative stress (Gallagher et al. [2012\)](#page-24-3). It would thus seem that cell stress due to the peptide treatment may alter fungal cell redox status, resulting in enhanced production of gliotoxin to restore cell redox homeostasis. Shotgun proteomics of LL-37-treated hyphae also revealed an increase in the abundance of proteins related to growth, tissue degradation, allergic reactions, cellular stress, and virulence (see Table [2](#page-8-0)). The reader is encouraged to consult the original paper for a more detailed information (Sheehan et al. [2018\)](#page-25-7). These results need further verifcation in terms of whether or not LL-37 augments expression levels of various mycotoxins and virulence factors in *A*. *fumigatus*.

Contrary to what was implied above, Luo et al. [\(2019\)](#page-24-4) demonstrated that LL-37 (1–20  $\mu$ M) could prevent hyphal growth of *A. fumigatus* in a dose-dependent fashion after 12 h of incubation. The diference in strains may explain these contradictory results. Other factors including the initial inoculum size, the peptide purity, media composition, and the duration of exposure ought to be taken into consideration (Memariani and Memariani [2020](#page-25-8)). Given that low concentrations of LL-37 may activate compensatory growth pathways in *A. fumigatus*, as discussed by Luo et al. ([2019\)](#page-24-4) when comparing their own results to those reported by Shee-han et al. [\(2018\)](#page-25-7), threshold concentration of LL-37 below which fungal growth occurs should be determined in future research.

So far, only one study has investigated in vitro antifungal activity of LL-37 on *A. nig*er. In this context, Kamysz et al. [\(2012\)](#page-24-5) found that both LL-37 and its cyclic counterpart exerted an inhibitory activity on *A. nig*er at 128 µg/ mL. Complete suppression of the fungal growth was also observed when the concentration of each peptide increased to 512 µg/mL. Additionally, LL-37 and its cyclic analog showed comparable hemolytic activity against the human red blood cells (Kamysz et al. [2012\)](#page-24-5). Antifungal and hemolytic activities of the cyclic LL-37 were identical to those of LL-37. Final judgment on this matter should be withheld until the subject can be followed up by further research.

LL-37 can bind directly to the fungal surface and disrupt the cell wall architecture, leading to inhibition of fungal adhesion in vitro (Table [2](#page-8-0)). *A. fumigatus* invasion and cytotoxicity on alveolar epithelial cells were weakened in the presence of  $LL-37$  (4  $\mu$ M), indicating host cell protective activity of LL-37 (Luo et al. [2019](#page-24-4)). The peptide also reduced the levels of pro-inflammatory cytokines, such as tumor necrosis factor-alpha (TNF-α) and IL-6, by *A. fumigatus*-stimulated macrophages. Furthermore, LL-37 downregulated transcriptional levels of M1 type markers, such as iNOS, CXCL9, and CXCL10. Neither phagocytosis nor killing capacity of macrophages toward *A. fumigatus* were attenuated by LL-37 (Luo et al. [2019](#page-24-4)). Based on these results, the conclusion was drawn that the production of *A. fumigatus*-induced pro-infammatory cytokines by macrophages and expression of M1-type markers could be reduced in response to LL-37 without negatively afecting macrophage phagocytosis or killing activity.

In a preclinical study, wherein mice were intratracheally infected with *A. fumigatus* conidia and then treated with LL-37, lung tissues of the peptide-treated animals had remarkably lower fungal burdens, moderate pathological damage, and reduced levels of pro-infammatory cytokines (TNF- $\alpha$  and IL-6) as compared to the control (PBS-treated) groups (Luo et al. [2019](#page-24-4)). A similar trend was observed in transgenic mice expressing hCAP18/LL37. Accordingly, LL-37 may be efective in treating *A. fumigatus* pulmonary infections since it seems to exhibit both anti-infammatory and antifungal properties. In spite of these promising results, further animal studies are warranted to explore the antimycotic potential of LL-37 against an expanded set of *Aspergillus* strains.

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Low-electroendosmosis type; MEC Minimum effective concentration; MFC Minimum fungicidal concentrations; MIC Minimum inhibitory concentration; MMB Minimal medium broth (con-*N*-morpholino)propanesulfonic acid; *MTT* 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; *NM* Not mentioned;  $OD_{570nm}$  Optical density at 570 mm; PBS Phosphate-buffered saline; PDB Potato dextrose broth; PPB Potassium phosphate buffer; R Resistant; RDA Radial diffusion assay; RPMI Roswell Park<br>Memorial Institute; SDB Sabouraud's *R* Resistant; *RDA* Radial difusion assay; *RPMI* Roswell Park taining 2% glucose and 0.5% yeast nitrogen base); MOPS 3-(N-morpholino)propanesulfonic acid; MTT 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; NM Not mentioned; Low-electroendosmosis type; *MEC* Minimum efective concentration; *MFC* Minimum fungicidal concentrations; *MIC* Minimum inhibitory concentration; *MMB* Minimal medium broth (con-Memorial Institute; *SDB* Sabouraud's dextrose broth; *SDD* Susceptible-dose dependent; *TSB* Trypticase soy broth; *XTT* 2,3-bis-(2-methoxy-4-nitro-5-sulfophenyl)-2H-tetrazolium-5-carboxanil-*OD*570nm Optical density at 570 nm; *PBS* Phosphate‐bufered saline; *PDB* Potato dextrose broth; *PPB* Potassium phosphate bufer; taining 2% glucose and 0.5% yeast nitrogen base); *MOPS* 3-(

<span id="page-8-0"></span>

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*CGD* Chronic granulomatous disease; *CPA* Chronic pulmonary aspergillosis; *CWPs* Cell wall proteins; eIF-5A Eukaryotic translation initiation factor 5A; *ELISA* Enzyme-linked immunosorbent assay; ER Endoplasmic reticulum; FFEM Freeze-fracture electron microscopy; FITC Fluorescein isothiocyanate; FIZ Fluconazole; GIR Glutathione reductase; GPx Glutathione peroxidase; assay; *ER* Endoplasmic reticulum; *FFEM* Freeze-fracture electron microscopy; *FITC* Fluorescein isothiocyanate; *FLZ* Fluconazole; *GLR* Glutathione reductase; *GPx* Glutathione peroxidase; dehyde; MDR Multi-drug resistant; MFC Minimum fungicidal concentrations; PI Propidium iodide; p-Mkc1 Phosphorylated Mkc1; ROS Reactive oxygen species; RP-HPLC Reversed-phase dehyde; *MDR* Multi-drug resistant; *MFC* Minimum fungicidal concentrations; *PI* Propidium iodide; *p-Mkc*1 Phosphorylated Mkc1; *ROS* Reactive oxygen species; *RP*-*HPLC* Reversed-phase high-performance liquid chromatography; SDS-PAGE Sodium dodecyl sulphate polyacrylamide gel electrophoresis; SEM Scanning electron microscopy; SG SYTOX Green; SOD Superoxide high-performance liquid chromatography; *SDS*-*PAGE* Sodium dodecyl sulphate polyacrylamide gel electrophoresis; *SEM* Scanning electron microscopy; *SG* SYTOX Green; *SOD* Superoxide CGD Chronic granulomatous disease; CPA Chronic pulmonary aspergillosis; CWPs Cell wall proteins; eIF-5A Eukaryotic translation initiation factor 5A; ELI3A Enzyme-linked immunosorbent GST Glutathione transferase; IEM Immunoelectron microscopy; IL-6 Interleukin-6; iNOS Inducible nitric oxide synthase; LDH Lactate dehydrogenase; NM Not mentioned; MDA Malondialdismutase; TEM Transmission electron microscopy; TNF-a Tumor necrosis factor-alpha; UPR Unfolded protein response; XTT 2,3-bis-(2-methoxy4-nitro-5-sulfophenyl)-2 H-tetrazolium-5-car-<br>dismutase; TEM Transmission electron mi GST Glutathione transferase; IEM Immunoelectron microscopy; IL-6 Interleukin-6; iNOS Inducible nitric oxide synthase; LDH Lactate dehydrogenase; NM Not mentioned; MDA Malondialdismutase; *TEM* Transmission electron microscopy; *TNF*-*α* Tumor necrosis factor-alpha; *UPR* Unfolded protein response; *XTT* 2,3-bis-(2-methoxy-4-nitro-5-sulfophenyl)-2 H-tetrazolium-5-carboxanilide boxanilide

#### **Efects on** *Candida* **species**

*Candida* species belong to the normal microbiota of the oral cavity, gastrointestinal tract, and vagina. In the United States, *Candida* species are the fourth leading cause of nosocomial bloodstream infections, with mortality rates reached as high as 40% (Atiencia-Carrera et al. [2022\)](#page-23-13). *C. albicans* is the most important species, a pathobiont that can become pathogenic under certain circumstances. It possesses several virulence attributes, including yeast-to-hypha transition, hydrolytic enzyme secretion, tissue adhesion, and bioflm formation. The emergence of multi-drug resistant *Candida* species, such as *C. glabrata* and *C. auris*, has sparked a great deal of research into antifungal alternatives (Arendrup and Patterson [2017](#page-23-14)). In the current situation, AMPs may offer a fruitful avenue for developing new anticandidal drugs (Memariani et al. [2023](#page-25-16)).

There is now a rather signifcant and consistent body of data on anticandidal activities of LL-37 under diferent experimental conditions. In the case of *C. albicans*, concentrations ranging from  $0.8$  to  $64 \mu M$  were sufficient for both growth-inhibiting and killing actions of LL-37 (Table [1](#page-4-0)). According to Wong et al.  $(2011)$  $(2011)$ , LL-37  $(0.5-12 \mu M)$  exhibited similar or perhaps slightly greater anticandidal activity compared to its fragments, namely LL13–37 and LL17–32. LL-37 cleavage into shorter processed forms (such as RK-31 and KS-30) has been shown to confer additional fungicidal activity in ionic environments mimicking sweat (López-García et al. [2005](#page-24-7)). Based on analyses of truncated variants of LL-37, the stretches of 1–12 and 26–37 do not appear to have substantial anticandidal activity. It has been suggested that overall structural properties of LL-37, such as peptide length, are also important for antifungal potency, even in the absence of an obvious candidacidal domain (den Hertog et al. [2006](#page-24-12)).

*C. albicans* cells were reported to be killed by LL-37 in a dose- and pH-dependent manner (Tsai et al. [2014](#page-26-11); López-García et al. [2005](#page-24-7)). Furthermore, the candidacidal activity of LL-37 is unafected by the metabolic inhibitor sodium azide; thus, this activity is independent of cellular energy status (Ordonez et al. [2014](#page-25-13)). Nonetheless, LL-37 was considerably less active in vitro when exposed to physiological salt concentrations (Ciornei et al. [2005\)](#page-23-11). One study found that human body fluids (pus, saliva, and urine) decreased anticandidal activity of LL-37, whereas 50% of blood plasma completely abolished its activity (Durnaś et al. [2016](#page-24-9)).

Regarding localization of LL-37 in *C. albicans*, microscopic studies unraveled that fuorescein isothiocyanate (FITC)-labelled LL-37 remained connected to the cell perimeter (den Hertog et al. [2005;](#page-23-9) Ordonez et al. [2014](#page-25-13)). It appears that LL-37 is localized at the cell wall and cell membrane. As judged by freeze-fracture electron microscopy, untreated yeast cells showed a homogenous distribution of intramembraneous particles (IMPs), which are transmembrane proteins. Additionally, these untreated cells showed trough-shaped invaginations that are typical of freezefractured yeast cells. A sub-lethal concentration of LL-37  $(0.5 \mu M)$  led to formation of shallow craters and IMP-free patches in yeast membranes, while increasing the concentration to 2 µM resulted in developing of discrete vesicle-like structures in the membrane leafets (den Hertog et al. [2006](#page-24-12)). From these data, it can be concluded that sub-lethal concentrations of LL-37 induce morphological changes in the yeast membrane, while higher concentrations of the peptide are more destructive to the membrane, leading to weakening of the membrane leafets.

LL-37 is capable of inducing major morpho-structural deformities such as surface wrinkling, cell elongation, and crack-like break formations in yeast cells (Durnaś et al. [2016\)](#page-24-9). Experimental evidence also points to a correlation between membrane-permeabilizing activity of LL-37 and its candidacidal kinetics (López-García et al. [2005\)](#page-24-7). In support of this, confocal live-cell imaging of *C. albicans* cells divulged that LL-37 at its minimum fungicidal concentration (MFC) could induce propidium iodide infux and vacuolar expansion (Ordonez et al. [2014\)](#page-25-13). Rapid permeabilization and perturbation of *C. albicans* membrane, instantaneous release of vital cellular components such as nucleotides and proteins (with molecular masses of  $<$  40 kDa), detachment of the plasma membrane from the cell wall, and disintegration of the membrane bilayer into discrete vesicles by LL-37 would eventuate in yeast cell demise (López-García et al. [2005](#page-24-7); den Hertog et al. [2006;](#page-24-12) Sonesson et al. [2007;](#page-25-11) Ordonez et al. [2014\)](#page-25-13). Collectively, it appears that membrane disruption is an important mechanism by which LL-37 extirpates yeast cells.

There is also some indication that LL-37 may incur damage to the internal cell architecture in *C. albicans*. For example, transmission electron microscope studies of LL-37-treated yeasts revealed round electron-dense structures and mitochondrial distortion, reminiscent of what is observed during autophagy (Menzel et al. [2017](#page-25-15)). Condensed, yet fragmented nuclear fractions and membrane internalization were also detected in the peptide-treated yeast cells. However, there is still a great deal of mystery surrounding the molecular details underlying such efects.

Adhesion to both biotic and abiotic surfaces is crucial for *C. albicans* pathogenesis since it contributes to fungal persistence, flamentation, and bioflm formation (Martin et al. [2021\)](#page-25-17). Consequently, targeting *C. albicans* adhesion offers a promising strategy for disease prevention. A pair of articles published in 2011 demonstrated that LL-37 could inhibit the adhesion of *C. albicans* (Tsai et al. [2011a](#page-26-10), [b](#page-26-14)). In the frst study, LL-37 dose-dependently inhibited *C. albicans* attachment to polystyrene by binding directly to the cell surface and evoking cell aggregation. Moreover, sub-lethal concentrations of LL-37 decreased yeast cell adhesion not only to oral epidermal cells but also to murine bladder mucosa. Interaction of LL-37 with cell wall polysaccharides (such as mannan, chitin, and glucan) may explain the decreased adhesion of yeast cells (Tsai et al. [2011a](#page-26-10)). Cationic AMPs like LL-37 can interact electrostatically with negatively charged membrane carbohydrates (Chang et al. [2012\)](#page-23-12). Besides carbohydrates, proteins are major components of the *C. albicans* cell wall (Chaffin [2008](#page-23-15)). In a later work, LL-37 was shown to interact with cell wall proteins (Tsai et al. [2011b](#page-26-14)). Upon closer inspection, it became clear that LL-37 targets cell wall β-1,3-exoglucanase Xog1p, which is involved in *C. albicans* cell adhesion (Table [1](#page-4-0)). In fact, LL-37 afects Xog1p activity, thereby impairing cell wall remodeling. It was also suggested that deletion of *XOG1* reduced cellular exoglucanase activity, cell adhesion to polystyrene wells, and LL-37 binding to mutant *C. albicans* cells (Tsai et al. [2011b](#page-26-14)). In a related study, non-lethal concentrations of LL-37 precluded *C. albicans* adhesion to plastic by enhancing the β-1,3-exoglucanase activity of Xog1p (Chang et al. [2012](#page-23-12)). Increased β-1,3-exoglucanase activity could lead to abnormal cell wall glucan metabolism, resulting in the suppression of fungal adhesion without inducing perceptible changes in cell wall morphology (Chang et al. [2012](#page-23-12)).

Mechanistic studies provided additional insight into the efects of LL-37 on *C. albicans* cell wall and its cellular responses (see Table [1\)](#page-4-0). Recently, Hsu et al. [\(2021](#page-24-13)) observed that LL-37 could induce cell wall stress in *C. albicans*. In a separate study, LL-37 (20 µg/mL) diminished both *C. albicans* cell wall thickness and total polysaccharide content (i.e. glucan and mannan, but not chitin), suggesting that LL-37 alters cell wall architecture (Tsai et al. [2014\)](#page-26-11). In *C. albicans*, the majority of  $β-1,3$ -glucan is located in the inner cell wall and is masked by an outer layer of mannan fbrils (Childers et al. [2020\)](#page-23-16). Yeasts treated with LL-37 ( $\geq$  5 µg/mL) showed substantially more  $β-1,3$ -glucan exposed on the cell surface than the control, connoting that the peptide might disrupt cell wall reconstruction.

LL-37 was reported to activate the mitogen-activated protein (MAP) kinase Mkc1 signaling pathway (Hsu et al. [2021\)](#page-24-13). The MAP kinase Mkc1 participates in cell wall integrity of *C. albicans* (Ernst and Pla [2011\)](#page-24-14). LL-37 can also stimulate the unfolded protein response (UPR) pathway to adapt and respond to endoplasmic reticulum (ER) stress conditions. The UPR is the mechanism through which cells control ER protein homeostasis (Read and Schröder [2021](#page-25-18)). Moreover, LL-37 can trigger ER-derived reactive oxygen species (ROS) accumulation to cause oxidative stress and to infuence ER-related protein secretion (Hsu et al. [2021](#page-24-13)). ER-derived ROS are thought to be involved in toxicity of cell wall stress. Thus, there is a possible link between cell wall integrity, ER function, and ER-derived ROS production in fungal cells (Yu et al. [2016b\)](#page-26-15). Another point worth highlighting is that deletion of the transcription factor *SFP1* reduced the vulnerability of *C. albicans* to LL-37. Experiments on mutants lacking *SFP1* gene also suggest that this transcription factor plays a key role in cell wall maintenance, ER homeostasis, and oxidative stress response upon LL-37 treatment (Hsu et al. [2021\)](#page-24-13).

Genome-wide analysis of LL-37-treated *C. albicans* cells made it clear that exposure to LL-37 (5 µg/mL) caused significant changes in the expression levels of 83 genes  $(>1.5$ fold change,  $p < 0.05$ ), of which 59 were downregulated while the remainders were upregulated. Based on *C. albicans* genome annotation, these genes infuence a wide gamut of biological processes including, but not limited to, RNA metabolism, ribosome biogenesis, cell cycle, cell wall organization, stress responses, and flamentous growth (Tsai et al. [2014\)](#page-26-11). For instance, treatment of *C. albicans* with LL-37 caused upregulation of *NRG1*, *KRE6*, and *TPO3*. The product of *NRG1* was suggested to play a part in the regulation of stress responses, yeast-to-hypha morphological switch, and bioflm establishment (Murad et al. [2001](#page-25-19); Tsai et al. [2014](#page-26-11)). *KRE6* contributes to the synthesis of β-1,6-glucan (Han et al. [2019](#page-24-15)). *TPO3* encodes a polyamine transporter, required for yeast resistance to the polyamine spermine toxicity (Fernandes et al. [2005\)](#page-24-16). On the other hand, expression levels of *HGT12*, *GAP2, RHR2*, and *TRY4* were shown to be downregulated in response to LL-37 treatment (Tsai et al. [2014](#page-26-11)). *HGT12* encodes a protein that transports fructose, mannose, and glucose specifcally during macrophage infection (Luo et al. [2007\)](#page-24-17). *GAP2* encodes a general amino acid permease (Kraidlova et al. [2016\)](#page-24-18). *RHR2*, which encodes the enzyme glycerol-3-phosphatase, is required for bioflm production in vitro and in vivo (Desai et al. [2013](#page-24-19)). *TRY4* is needed for yeast cell adherence (Finkel et al. [2012](#page-24-20)).

The phenotypic plasticity between the two morphological phenotypes, yeast and hyphae, allows *C. albicans* cells to adapt to and persist in diferent environments. Indeed, the yeast-to-hyphae transition is essential for tissue invasion, escape from phagocytes, and bioflm formation (Wooten et al. [2021](#page-26-16); Kong and Jabra-Rizk [2015](#page-24-21)). According to Wong et al. [\(2011](#page-26-9)), *C. albicans* morphogenesis was afected by LL-37 or its fragment (LL13–37), as hyphae became thinner and budding appeared less robust. The exact mechanisms behind these observations need to be elucidated in future studies.

Aside from *C. albicans*, other species of *Candida* were reported to be susceptible to LL-37 treatment. These include *C. auris*, *C. krusei*, *C. norvegensis*, *C. parapsilosis*, and *C. tropicalis* (Kamysz et al. [2012](#page-24-5); Rather et al. [2022;](#page-25-14) Scarsini et al. [2015;](#page-25-12) Sigurdardottir et al. [2006\)](#page-25-10). According to a recent study, LL-37 exhibited fungicidal activity against 10 clinical isolates of *C. auris*, some of which were resistant to conventional antimycotics (Table [1\)](#page-4-0). Kinetics studies also

suggest that 8-h exposure to MFC of LL-37 was sufficient for complete killing of an MDR *C. auris* strain (Rather et al. [2022\)](#page-25-14). Moreover, LL-37 was shown to permeabilize plasma membrane, arrest cell cycle at S phase, and induce oxidative stress in *C. auris* (Table [1\)](#page-4-0), indicating multifaceted mechanisms of action of LL-37. When combined with fuconazole, amphotericin B, and caspofungin individually, LL-37 showed synergistic efects against 80%, 100%, and 100% of the above-mentioned *C. auris* strains, respectively (Rather et al. [2022](#page-25-14)). Therefore, LL-37 in combination with the current antifungal drugs could be suggested as a possible treatment for *C. auris* infections.

Nanoparticles might serve as both AMP releasers and protection agents (Maximiano et al. [2022](#page-25-20)). In this regard, Niemirowicz et al. [\(2017\)](#page-25-21) observed that immobilization of LL-37 on the surface of magnetic nanoparticles (MNPs) substantially increased fungicidal activity of LL-37 toward laboratory and clinical strains of *C. albicans*, *C. glabrata*, and *C. tropicalis* in the presence of body fuids (e.g., saliva, urine, plasma, pus, and cerebrospinal fuid). They also exhibited low cytotoxicity to human osteoblast cells. These functionalized MNPs disrupted the integrity of fungal plasma membrane and triggered ROS generation, resulting in cell death (Niemirowicz et al. [2017\)](#page-25-21). It appears that high antifungal activity and biocompatibility of these LL-37-coated MNPs make them attractive candidates for the treatment of *Candida* infections.

#### **Efects on** *Colletotrichum higginsianum*

Species of the genus *Colletotrichum* cause devastating anthracnose diseases in various agricultural and horticultural crops (da Silva et al. [2020\)](#page-23-17). *C. higginsianum* is one of the most prominent *Colletotrichum* species. In one study, Jung and coworkers ([2012\)](#page-24-22) demonstrated transgenic expression of LL-37 with Met37Leu substitution in Chinese cabbage, an important vegetable crop in Asia. The leaves of the transgenic plants were then exposed to *Colletotrichum higginsianum* KACC 40807 to examine whether LL-37 expression could confer them resistance to this fungal pathogen. Transgenic plants exhibited higher resistance to *C. higginsianum* than the non-transgenic control plants, as the average size of disease lesions decreased in the transgenic plants (Jung et al. [2012](#page-24-22)). In light of the adverse efects that fungi have on many economically important crops, transgenic strategies such as constitutive expression of AMPs could be useful in enhancing plant resistance to phytopathogens.

#### **Efects on dermatophytes**

Dermatophytes are a group of closely related keratinophilic fungi that invade keratinous tissues. Infections caused by these pathogens (tinea or ring-worm) usually tend to involve

the hair, nail, or skin of the host. Dermatophytes can be classifed in three genera, namely *Epidermophyton*, *Microsporum*, and *Trichophyton* (Aref et al. [2022](#page-23-18)). Some dermatophytes have been reported to be susceptible to LL-37 (López-García et al. [2006](#page-24-10)). For instance, LL-37 was found to be active as fungicide against diferent strains of *Trichophyton mentagrophytes* and *Trichophyton rubrum*, but not *Microsporum canis* CECT 2797 in vitro (see Table [1](#page-4-0)). Based on immunohistochemical studies, elevated LL-37 expression was found in the epidermis of patients with tinea corporis or tinea versicolor in comparison to healthy human skin. Besides this, LL-37 expression was co-localized with the fungus in the stratum corneum. Exposure to *T. rubrum* for 40 h also induced the mRNA expression of LL-37 in cultured normal human keratinocytes (NHKs) (López-García et al. [2006\)](#page-24-10). This is not surprising since, as mentioned earlier, keratinocytes are the most abundant cells in the epidermis and play a crucial role in the initial response to dermatophytes. In fact, these cells secret AMPs, such as cathelicidins and defensins, which have fungicidal activity (Celestrino et al. [2021\)](#page-23-19). Doubtlessly, human-derived AMPs such as LL-37, human β-defensin 2 (hBD-2), ribonuclease 7 (RNase 7), and psoriasin are ideally suited for developing novel therapeutics for dermatophytosis (Fritz et al. [2012](#page-24-23); Mercer and O'Neil [2020](#page-25-22)).

#### **Efects on** *Fusarium* **species**

*Fusarium* species are hyaline saprophytic molds that are frequently reported as agents of opportunistic infections in humans. Besides this, mycotoxins produced by *Fusarium* show varying levels of toxicity to humans and animals after consumption of contaminated grain (Jacobs and Walsh [2023](#page-24-24)). In a study performed by van der Weerden et al. ([2010\)](#page-26-13), two agronomically important species of *Fusarium* exhibited exquisite susceptibility to LL-37. In this respect, the half-maximal inhibitory concentrations  $(IC_{50})$  values of LL-37 against *F. graminearum* and *F. oxysporum* f. sp. *Vasinfectum* were 1 and 2.5  $\mu$ M, respectively. The same authors also furnished evidence that LL-37 has fungicidal activity on *F. oxysporum* f. sp. *vasinfectum* hyphae. Kinetics studies also revealed that LL-37 induced rapid permeabilization of hyphal membrane (van der Weerden et al. [2010\)](#page-26-13). This fnding supports the hypothesis that LL-37 functions primarily through direct interaction with and disruption of the fungal plasma membrane. A second study involving genetically engineered Chinese cabbage found that transgenic expression of LL-37 conferred enhanced resistance to *Fusarium oxysporum* f. sp. *Lycopersici* KACC 40032 (Jung et al. [2012\)](#page-24-22). Considering these encouraging results, transgenic plants expressing AMPs, like LL-37, are likely to enhance resistance against fungal pathogens and inhibit production of mycotoxins.

#### **Efects on** *Malassezia* **species**

*Malassezia* species are lipophilic yeasts that belong to the normal skin fora. One of the most commonly encountered species is *M. furfur*. It can become pathogenic under certain conditions. This phenomenon is infuenced by a unique host-agent interaction that triggers the production of several virulence factors, such as various lipase enzymes, indoles, ROS, azelaic acid, hyphae formation, and bioflm formation (Kurniadi et al. [2022](#page-24-25)). *M.fufur* is associated with a variety of dermatological conditions, notably seborrheic dermatitis and tinea versicolor (Rhimi et al. [2020](#page-25-23)).

López-García et al. [\(2006](#page-24-10)) demonstrated that treatment of *M. furfur* with diferent concentrations of LL-37 led to delay or complete inhibition of fungal growth. Furthermore, NHKs that were exposed *M. furfur* for 24 h had a higher expression level of LL-37 mRNA in comparison to the untreated NHKs (López-García et al. [2006\)](#page-24-10). In another work, an 18-h treatment with *M. sympodialis* triggered LL-37 secretion from monocyte-derived dendritic cells (MDDCs) obtained from atopic eczema (AE) patients (Agerberth et al. [2006](#page-23-20)). Contrarily, the exposure of MDDCs retrieved from the healthy individuals to *M. sympodialis* had no or a negative impact upon the amount of secreted LL-37. While MDDCs from AE patients showed an initial transcriptional upregulation followed by a gradual downregulation of LL-37 transcription after 1-h exposure to *M. sympodialis*, the LL-37 transcription in MDDCs from healthy individuals was uninfuenced by *M. sympodialis* (Agerberth et al. [2006](#page-23-20)). Hence, it seems reasonable to believe that *M. sympodialis* could instigate innate immune responses diferently in AE patients and healthy individuals. Another conclusion is that increased secretion of LL-37 from the MDDCs in AE patients may refect the severity of their infammatory response to this yeast. In future studies, detailed molecular investigations will be needed to parse out the protective and therapeutic roles of LL-37 in patients with skin diseases caused by *Malasezzia* species.

#### **Efects on** *Pythium insidiosum*

The *Pythium* genus contains some notorious plant pathogens. They belong to the order oomycetes. Only *P. insidiosum* has been reported to cause disease in mammals, particularly in tropical and subtropical areas of the world. The pathogen is able to cause cutaneous, subcutaneous, intestinal and, less commonly, systemic infections. Infection is not contagious; there have been no reports of animal-animal or animal-human transmission (Daly et al. [2022\)](#page-23-21). In a recent study focusing explicitly on antifungal activity of LL-37 and other AMPs (MSI-78 and magainin-2) against 14 strains of *P. insidiosum*, LL-37 exhibited growth inhibitory efects (Table [1\)](#page-4-0), with minimum inhibitory concentration (MIC) values in the range of 20–40 µg/mL (Denardi et al. [2022](#page-24-11)). Future studies should examine these effects and the direct inhibition of *P. insidiosum* growth using in vivo models.

#### **Efects on** *Rhizoctonia solani*

*Rhizoctonia solani* is one of the most widespread soilborne pathogens, causing massive damage to economically important crops worldwide. It is an aggressive basidiomycete necrotrophic plant pathogen with a wide host range. Symptoms associated with *R. solani* infections are diverse and change depending on the host: they include hypocotyl, crown, stem and root rot, blights, wire stem, and damping off (Dell'Olmo et al. [2023\)](#page-23-22). The antifungal properties of LL-37 against *R. solani* are rarely explored. According to one study, the transgenic expression of LL-37 in geneticallymodifed Chinese cabbage reduced the average size of *R. solani* lesions on plant leaves (Jung et al. [2012\)](#page-24-22). Since the pathogen has an almost unlimited host range, LL-37 and its derivatives are still awaiting further research in a wider variety of genetically modifed plants.

#### **Effects on Saccharomyces cerevisiae**

*S. cerevisiae* is a model organism for understanding cellular processes in higher eukaryotes (Memariani and Memariani [2020](#page-25-8)). One study investigated the in vitro antifungal activity of LL-37 against three clinical strains of *S. cerevisiae*, which were isolated from vaginal infections (Scarsini et al. [2015](#page-25-12)). MIC values of LL-37 for these strains were reported to be 2 µM, suggesting that LL-37 had a potent growth-inhibitory activity. However, cellular and molecular mechanisms behind these observations remain unclear.

# **Antifungal efects of LL‑37 on fungal bioflms**

Bioflms are syntropic conglomerations of microorganisms that reside in a matrix of extracellular polymeric compounds attached to a surface. The formation of bioflms is one of the mechanisms responsible for antifungal drug resistance (Radojević et al. [2023\)](#page-25-24). Similar to bacteria, bioflms bestow upon fungi a protective shelter, creating a high-level barrier against most antimicrobials. Due to the lack of efectiveness and adverse efects of existing antifungal medications, safer drugs are exigently needed. The multifunctional properties of AMPs as new therapeutics further reinforce their potential role for prevention and treatment of fungal bioflms (Oshiro et al. [2019](#page-25-25)).

Over the past decade, several studies have been conducted to investigate whether LL-37 affects different stages of fungal bioflm formation (Table [3](#page-17-0)). According to Scarsini et al.



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<span id="page-17-0"></span>Table 3 Antibiofilm activities of the human cathelicidin LL-37 against different fungal pathogens



**Table 3**

 $\underline{\textcircled{\tiny 1}}$  Springer

[\(2015](#page-25-12)), short-term exposure to LL-37 (64  $\mu$ M) was sufficient to reduce the number of viable *C. albicans* cells that adhered to polystyrene microtiter plates by 80%. Additionally, LL-37 exhibited anti-adhesive activity when it was added to the Sabouraud medium immediately after seeding yeasts onto uncoated silicone elastomer (SE) disks or, alternatively, when yeasts were dispensed on LL-37-coated SE disks and incubated in the peptide-free medium (Scarsini et al. [2015](#page-25-12)). The latter activity occurred in a concentration-dependent manner. LL-37 is also capable of suppressing the attachment of yeasts cells to biotic surfaces (Tsai et al. [2011a\)](#page-26-10). This would result in a reduction in the number of fungal cells actually participated in the initial stages of bioflm production. In another study, LL-37 strongly suppressed adhesion of *C. albicans*, *C. glabrata*, and *C. tropicalis* to microtiter wells (Niemirowicz et al. [2017](#page-25-21)). Interestingly, the observed anti-adhesive ability of LL-37 was enhanced when it was immobilized on MNPs, suggesting a synergistic efect between MNPs and LL-37. As hinted earlier in this review, the interactions of LL-37 with both cell wall carbohydrates and proteins (Tsai et al. [2011a](#page-26-10), [b\)](#page-26-14), as well as the increased β-1,3-exoglucanase activity of Xog1p, (Chang et al. [2012\)](#page-23-12) are so far proposed mechanisms responsible for anti-adhesive effects of LL-37.

It has been shown that LL-37 could decrease the formation of *C. albicans* bioflm in the presence or absence of DNA after 24 h of incubation (Durnaś et al. [2016;](#page-24-9) Luo et al. [2017\)](#page-24-27). However, LL-37 failed to maintain its inhibitory activity after 48 h of incubation as the bioflm mass formed at this time was comparable to that of the non-treated control (Durnaś et al. [2016\)](#page-24-9). Prevention of initial microbial adhesion by LL-37 appears to be the main reason for this suppressive effect. A second reason may be changes in fungal gene expression. A DNA microarray analysis has indicated that LL-37 afects the expression levels of several bioflm-related genes (Tsai et al. [2014\)](#page-26-11). Another important observation was a noticeable decline in the metabolic activity of bioflm-producing cells after treatment with LL-37 (Luo et al. [2017\)](#page-24-27). In a separate study on a clinical *C. tropicalis* isolate, Chen et al. [\(2021\)](#page-23-23) observed a dose-dependent decrement in the metabolic activity of bioflm-forming cells after incubation with high concentrations (100–500 µg/mL) for 24 or 48 h. This reduction was not observed when *C. tropicalis* was exposed to low concentrations (0.5–40 µg/mL) of LL-37.

Luo et al. ([2017](#page-24-27)) highlight the effectiveness of LL-37 in inhibiting the maturation of early *C. albicans* bioflms. Nevertheless, available evidence indicates no inhibitory efects of LL-37 on metabolic activity of bioflm-encased cells (Scarsini et al. [2015;](#page-25-12) Luo et al. [2017](#page-24-27)). In another work, restriction of the growth of mature *Candida* bioflms was reported in the presence of LL-37, alone or when immobilized on MNPs (Niemirowicz et al. [2017\)](#page-25-21). A recent study also demonstrated that 100 µg/mL of LL-37 was inefective

against dual-species bioflms formed by *Candida albicans* and one of the four clinically important Gram-negative bacteria (Hacioglu et al. [2020\)](#page-24-26). In view of this, it will be of interest to explore if LL-37 at higher concentrations, alone or in combination with the current antifungal drugs, can decrease the viability of *C. albicans* cells enclosed in bioflms.

## **Antifungal mechanisms of action for LL‑37**

Considering the relatively large amount of experimental data on molecular mechanisms responsible for antifungal activity of LL-37, and for the reader's convenience, this section brings together and summarizes antifungal mechanisms of action of this peptide.

Two decades of research have expanded our understanding of how LL-37 exerts its growth-inhibiting and/or killing actions on a variety of fungal pathogens. In this connection, diferent research groups have made use of *C. albicans* as a model organism to gain molecular-levels insights into antifungal effects of LL-37. There is now sufficient experimental data to corroborate the multi-pronged nature of the attack of LL-37 on fungal cells. Fungal cell wall serves as a main target for antimicrobial action of LL-37. Interaction with cell wall components such as the major *β*-1,3-exoglucanase (Tsai et al. [2011a;](#page-26-10) Chang et al. [2012](#page-23-12)), reduction of both cell wall thickness and total polysaccharide content (Tsai et al. [2014](#page-26-10)), inhibition of the cell wall reconstruction, and disruption of the cell wall integrity (Luo et al. [2019](#page-24-4)) have been well described in diferent studies. Induction of various structural changes in fungal plasma membrane, rapid membrane permeabilization, and subsequent release of vital cellular components are the other mechanisms by which LL-37 afects fungal cell viability (López-García et al. [2005](#page-24-7); den Hertog et al. [2006](#page-24-12); Sonesson et al. [2007](#page-25-11); Ordonez et al. [2014\)](#page-25-13).

Aside from altering the cell wall and plasma membrane, LL-37 has a number of intracellular targets as well. In particular, expression levels of a wide array of genes were changed in response to LL-37 treatment (Tsai et al. [2014](#page-26-11)). Moreover, LL-37 was shown to affect signaling pathways related to ER stress response and cell wall integrity (Hsu et al. [2021](#page-24-13)). Inhibition of cell cycle progression, elevation of intracellular ROS levels, stimulation of oxidative stress, disruption of ER homeostasis, and formation of autophagy-like structures were also observed in LL-37-exposed fungal cells (Rather et al. [2022](#page-25-14); Hsu et al. [2021](#page-24-13); Menzel et al. [2017\)](#page-25-15). A summary of antifungal mechanisms of LL-37 is schematically illustrated in Fig. [1.](#page-20-0)

Evidence also began to emerge that LL-37 could reduce fungal adhesion to biotic and abiotic surfaces (Tsai et al. [2011a;](#page-26-10) Chang et al. [2012;](#page-23-12) Scarsini et al. [2015\)](#page-25-12), excessive infammation (Luo et al. [2019\)](#page-24-4), invasion and cytotoxicity on



<span id="page-20-0"></span>**Fig. 1** Schematic representation of the molecular mechanisms underlying antifungal efects of the human cathelicidin LL-37

human cells (Luo et al. [2019](#page-25-17)), biofilm formation and maturation (Durnaś et al. [2016](#page-24-9); Luo et al. [2017](#page-24-17)), and yeast-to-hyphal dimorphic switch (Luo et al. [2019](#page-24-4); Wong et al. [2011](#page-26-9)). Indeed, these fndings bear testimony to the notion that LL-37 may act as a potential anti-virulence peptide. In essence, quelling virulence behavior and locking fungal pathogens in a vegetative non-bioflm-producing lifestyle have been propounded as a new paradigm for the development of potential antifungal therapeutics (Reen et al. [2016;](#page-25-26) Gauwerky et al. [2009\)](#page-24-28). This may make fungal pathogens less infective and more vulnerable to conventional therapy. In light of the above, it seems reasonable to embark upon in-depth investigations to assess how LL-37 interferes with fungal virulence attributes in vivo.

# **Potential applications and future research avenues**

Due to its apparent multifunctionality, cathelicidins have been the focus of in-depth research in various felds such as microbiology, immunology, oncology, and biotechnology.

The antimicrobial properties of LL-37 go beyond its role in innate immune responses and infammation (Alford et al. [2020](#page-23-24)). Potential toxicity, susceptibility to protease degradation, and other limitations may hinder the clinical translation of LL-37, but much research is being undertaken to address them. Thus far, there have been clinical trials of LL-37 in patients with melanoma (via intra-tumoral injections) and leg ulcers (via topical route). However, no clinical trials have been conducted on antifungal efects of LL-37 (Lu et al. [2022](#page-24-4); Dijksteel et al. [2021\)](#page-24-29). In this section, we briefy discuss innovative strategies, especially various drug delivery systems, for overcoming the above-mentioned challenges and how LL-37 might be used in the future. Potential biomedical applications of LL-37 against fungal pathogens are schematically illustrated in Fig. [2](#page-21-0).

# **Combination therapy with antifungal drugs or other AMPs**

In view of the unique properties and activities of LL-37, it could be a promising antifungal agent when combined with



<span id="page-21-0"></span>**Fig. 2** Schematic representation of potential biomedical applications of the human cathelicidin LL-37 for the prevention and treatment of various fungal diseases

antifungal drugs. By combining LL-37 with existing antifungal drugs or even other AMPs, we are able to reduce the likelihood of developing drug resistance in fungal pathogens during infections. On the other hand, antifungal drugs can also cause adverse reactions including hypokalemia, infusion reaction, nephrotoxicity, hepatotoxicity, and gastrointestinal problems. Because drug toxicity is highly concentration-dependent, one way to diminish the cytotoxic efects of antifungal drugs is to combine them with AMPs like LL-37 (Fernández de Ullivarri et al. [2020](#page-24-30)). A low concentration of LL-37 could disrupt fungal cell membranes and alter their permeability, enabling other drugs with lethal efects to enter the cell. In this respect, LL-37 has recently been shown to synergize with several antifungal drugs, such as fuconazole, amphotericin B, and caspofungin in vitro (Rather et al. [2022](#page-25-14)). Nevertheless, the efectiveness of LL-37 combined with such drugs needs to be tested in animal models of fungal infections in future studies.

#### **Chemical modifcations and peptidomimetics**

A potential problem associated with LL-37 is that it is easily degraded by proteolytic enzymes found in the digestive system, blood plasma, and microbial pathogens (Sieprawska-Lupa et al. [2004\)](#page-25-27). Therefore, various chemical modifcations of LL-37 can be made to improve its antimicrobial action and decrease its susceptibility to proteolytic degradation. Some examples of these approaches include the introduction of D-amino acids, cyclization, hybridization, lipidation, amidation or acetylation of the terminal regions (Memariani et al. [2017\)](#page-25-28). In order to enhance stability of LL-37 in the serum, tryptophan or β-naphthylalanine endtagging of the terminal regions of the peptide can also be considered (Lu et al. [2022](#page-24-31); Gan et al. [2021](#page-24-32); Dijksteel et al. [2021](#page-24-33)). Apart from this, some shorter analogs or fragments of LL-37 have been shown to exhibit enhanced antimicrobial activities (Kamysz et al. [2020](#page-24-34); Yun et al. [2020\)](#page-26-17). These shorter LL-37 derivatives could more readily penetrate fungal membranes and bioflm matrices.

It is also worth mentioning peptidomimetics, which have the advantage of circumventing the limitations of AMPs used in therapy. There are several advantages over AMPs, including enhanced stability, cell specifcity, and better tolerability. Additionally, the synthetic fexibility of these molecules allows fast modifcations of their structure in order to create novel antimicrobial peptidomimetics with particular pharmacological properties. A number of antimicrobial peptidomimetics have been developed so far, such as β-peptides, peptoids, arylamide oligomers, β-turn mimetics, and AApeptides (Méndez-Samperio [2004](#page-25-29)). In a recent study, cathelicidin-mimetic antimicrobial peptoids based on the LL-37 structure were shown to successfully eradicate *Staphylococcus aureus* strains (Benjamin et al. [2022](#page-23-25)). Further studies with these peptoids against fungal pathogens are warranted.

# **Use of drug delivery systems and diferent formulations**

As mentioned earlier, LL-37 becomes less potent when exposed to proteases secreted by host cells or microbes (Sieprawska-Lupa et al. [2004\)](#page-25-27). Furthermore, LL-37 binds easily to anionic serum proteins, resulting in rapid clearance from bloodstream circulation. In order to overcome these challenges, various delivery systems such as inorganic nanomaterials (e.g., metal nanoparticles, mesoporous silica, and hydroxyapatite), polymeric materials, and liposomes have been developed to improve the efficacy of LL-37 (Lin et al. [2020](#page-24-35)).

For instance, conjugating silver or gold nanoparticles with LL-37 was shown to enhance microbicidal properties of LL-37 (Lin et al. [2020\)](#page-24-35). An excellent example of polymeric materials is poly (lactic-co-glycolic) acid (PLGA). It is among the well-documented Food and Drug Administration (FDA)-approved polymers used for drug delivery systems. PLGA also displays good biocompatibility with a tailored biodegradation rate (Elmowafy et al. [2019\)](#page-24-29). LL-37 encapsulated in PLGA nanoparticles was found to enhance wound healing in dermal tissue when compared to LL-37 alone (Lin et al. [2020](#page-24-35)). There are other polymeric materials that are eligible to be used for enhanced LL-37 delivery, including poly (ethyl acrylate-co-methacrylic acid) microgels, degradable anionic dendritic nanogels (DNGs), composite microgel particles based on poly-γ-glutamic acid (γ-PGA) and chitosan, sodium alginate, and collagen/hyaluronic acid polyelectrolyte multilayers (PEMs) (Cassin et al. [2016](#page-23-26); Nordström et al. [2018;](#page-25-30) Lin et al. [2020\)](#page-24-35). As for lipidbased drug delivery systems, polyethylene glycol (PEG) coated liposomes might be served as a promising delivery system for AMPs including LL-37 (Gbian and Omri [2022](#page-24-36)). The PEG coating forms a hydration layer that inhibits the liposomes from being recognized by the reticuloendothelial system. Therefore, when LL-37 is bound to liposomes, the lipid and surrounding PEG chains provide protection against enzymatic degradation (Lin et al. [2020](#page-24-35)).

### **Treatment of superfcial infections and keratitis**

LL-37 and its derivatives are suitable for topical applications to treat superficial fungal infections of the skin, hair or nails and could be used as cosmetic ingredients to deter skin pathogens and maintain skin health. They can be used in different formulations such as ointments, creams, lotions, gels, shampoos, or wound dressings (Rodríguez-Castaño et al. [2023](#page-25-31)). Fungal keratitis has also been seen to increase due to escalating number of new contact lens wearers worldwide in recent years. A new line of research would be the study of LL-37 as eye drop formulations for the treatment of fungal keratitis (Wu et al. [2017\)](#page-26-18). Certainly, these new formulations need to be evaluated in vivo.

## **Plant‑based expression systems and transgenic plants**

There is no doubt that plants are one of the most promising platforms for large-scale and cost-efective commercial production of AMPs (Mirzaee et al. [2021](#page-25-32)). Owing to many advantages over other prokaryotic and eukaryotic expression systems, plants are excellent hosts for the production of recombinant proteins. It is possible to store or lyophilize plant-based therapeutic products for a longer shelf life without the need for low temperatures to ensure stability and activity. The main advantage of plant-based expression system is the ability to perform post-translational modifcations, which may be essential for protein folding and biological functions of AMPs (Shanmugaraj et al. [2021](#page-25-33)).

AMPs can be produced in plants by a variety of genetic approaches, such as whole plants, tissue specifc expression, tissue culture, or transient expression. The tobacco plant (*Nicotiana tabacum*) is the most commonly used transgenic expression system (Fernández de Ullivarri et al. [2020](#page-24-30)). Transgenic plants expressing LL-37 hold opportunities for fghting fungal phytopathogens. In addition to antifungal activity, LL-37 may also be capable of protecting crops from mycotoxin contamination by inhibiting mycotoxin biosynthesis, which opens new avenues for their use in agriculture and food industry. Clearly, this direction of research appears to be worthy of further pursuance.

## **Conclusion**

Fungal pathogens pose a formidable threat to humans, wildlife, and agriculture. The dearth of effective antimycotics in the pipeline along with the emergence of drugresistant strains highlights the importance of antifungal drug discovery and development. LL-37, the sole human cathelicidin, has been shown to exert potent growth-inhibitory activity at micromolar concentrations against diferent clinically and agronomically relevant fungal strains. Furthermore, accumulating data reveal multi-pronged mechanisms of action that rely on afecting fungal cell wall and plasma membrane as well as targeting intracellular components. The promise of LL-37 as an antifungal peptide can only be fulflled through a thorough investigation of its in vivo efficacy and safety, and we are therefore likely to witness continued progress in this feld in the coming years.

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## **Declarations**

**Conflict of interest** The authors declare no conficts of interest.

**Ethical approval** Not applicable.

**Consent to participate** Not applicable.

**Consent for publication** Both authors gave fnal approval for publication.

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