Systemic *Staphylococcus aureus* infection mediated by *Candida albicans* hyphal invasion of mucosal tissue

Lisa Marie Schlecht,1,2† Brian M. Peters,2,3† Bastiaan P. Krom,4 Jeffrey A. Freiberg,2,3 Gertrud M. Hänsch,5 Scott G. Filler,6 Mary Ann Jabra-Rizk7,8‡ and Mark E. Shirtliff2,8‡

1Department of Restorative Dentistry and Periodontology, Ludwig Maximilian University of Munich, Goethestrasse 70, 80336 Munich, Germany
2Department of Microbial Pathogenesis, University of Maryland – Baltimore, Dental School, 650 W. Baltimore Street, Baltimore, MD 21201, USA
3Graduate Program in Life Sciences, Molecular Microbiology and Immunology Program, University of Maryland – Baltimore, 660 W. Redwood Street, Baltimore, MD 21201, USA
4Department of Preventive Dentistry, Academic Centre for Dentistry Amsterdam (ACTA), University of Amsterdam and Free University Amsterdam, Gustav Mahlerlaan 3004, 1081 LA Amsterdam, the Netherlands
5Department of Immunology, Ruprecht Karls University Heidelberg, Im Neuenheimer Feld 305, 69120 Heidelberg, Germany
6Division of Infectious Diseases, Los Angeles Biomedical Research Institute at Harbor-UCLA Medical Center, 1124 W. Carson St, Torrance, CA 90502, USA
7Department of Oncology and Diagnostic Sciences, Dental School, University of Maryland – Baltimore, 650 W. Baltimore Street, Baltimore, MD 21201, USA
8Department of Microbiology and Immunology, School of Medicine, University of Maryland – Baltimore, 660 W. Redwood Street, Baltimore, MD 21201, USA

*Candida albicans* and *Staphylococcus aureus* are often co-isolated in cases of biofilm-associated infections. *C. albicans* can cause systemic disease through morphological switch from the rounded yeast to the invasive hyphal form. Alternatively, systemic *S. aureus* infections arise from seeding through breaks in host epithelial layers although many patients have no documented portal of entry. We describe a novel strategy by which *S. aureus* is able to invade host tissue and disseminate via adherence to the invasive hyphal elements of *Candida albicans*. In vitro and *ex vivo* findings demonstrate a specific binding of the staphylococci to the candida hyphal elements. The *C. albicans* cell wall adhesin Als3p binds to multiple staphylococcal adhesins. Furthermore, Als3p is required for *C. albicans* to transport *S. aureus* into the tissue and cause a disseminated infection in an oral co-colonization model. These findings suggest that *C. albicans* can facilitate the invasion of *S. aureus* across mucosal barriers, leading to systemic infection in co-colonized patients.

INTRODUCTION

Polymicrobial infections tend to be complex and result in aggressive forms of diseases that often exhibit increased resistance to antimicrobials and impact therapeutic measures (Brogden, 2003; Harriott & Noverr, 2009; Jenkinson & Douglas, 2002; Klotz *et al.*, 2007; Lynch & Robertson, 2008). Yet, despite the gravity of such infections, studies of mechanisms underlying polymicrobial infections are in their infancy.

Among the vast number of human pathogens, the bacterial species *Staphylococcus aureus* and the fungal species *Candida albicans* are currently the second and third most commonly isolated bloodstream pathogens (Goetghebeur
et al., 2007; Kleven et al., 2007; Perlroth et al., 2007). In particular, S. aureus has gained considerable attention from the medical community due to its involvement in the increasing number of nosocomial and community acquired infections resulting in nearly half a million hospitalizations and 50,000 deaths each year in the USA alone (Goetzheuer et al., 2007; Gordon & Lowy, 2008). This bacterial species is armed with an array of virulence factors including toxins and immunoavoidance strategies for invading and destroying host tissue during infection (Bien et al., 2011; Ferry et al., 2005). Despite its pathogenic potential, S. aureus is typically a non-invasive commensal and has been historically identified as a common nasopharyngeal resident, but is also found localized associated with moist skin areas of the axillae and groin. However, this microbial species has more recently been found to commonly exist in the oral cavity. S. aureus typically requires a breach in mucosal barriers to gain entry into the epithelium (Acton et al., 2009; Ohara-Nemoto et al., 2008; Smith et al., 2003; Zimmerli et al., 2009). Yet, it has been reported that a significant number of patients with staphylococcal bloodstream infections have no documented portal of entry (del Rio et al., 2009).

Similarly, C. albicans is the most frequently encountered pathogenic human fungal species and commonly colonizes host mucosal and moist skin surfaces (Calderone & Clancy, 2012; Cannon & Chaffin, 2001). However, under conditions of immune dysfunction, this opportunistic microbe can rapidly transition from commensal to pathogen, causing an array of infections ranging from localized mucosal to severe systemic infections with high morbidity and mortality rates (Calderone & Clancy, 2012; de Repentigny et al., 2004; Perlroth et al., 2007). Oral candidiasis or thrush is the most common opportunistic infection in HIV-infected population with 80–90% of these individuals developing oropharyngeal candidiasis during the course of their illness (de Repentigny et al., 2004; Fidel, 2006). In addition, recent longitudinal studies have shown that in the ageing population, C. albicans is even more frequently encountered in the oral cavity, especially in edentulous elderly populations (Budtz-Jorgensen et al., 1996; Kulak-Ozkan et al., 2002; Zaremba et al., 2006). The success of this species as an opportunistic pathogen is the result of its repertoire of virulence factors, including the ability to switch between a yeast and hyphal morphology, a property crucial to its pathogenicity (Calderone & Clancy, 2012).

Several studies have reported the co-isolation of S. aureus and C. albicans from numerous biofilm-associated diseases such as periodontitis, denture stomatitis, cystic fibrosis, keratitis, ventilator-associated pneumonia and urinary tract and burn wound infections (Adam et al., 2002; Baena-Monroy et al., 2005; Costerton et al., 1985; Cuesta et al., 2010; Gupta et al., 2005; Pate et al., 2006; Tawara et al., 1996; Timsit et al., 2001; Valenza et al., 2008). Although these studies only reported associations and did not prove causation, the frequency with which S. aureus and C. albicans are co-isolated merits further study. More directly relevant to bacteraemia, a study by Klotz et al. (2007) investigating the incidence of candidal bloodstream infections in hospitalized patients reported that C. albicans was co-isolated with S. aureus in 20% of the cases. Further, animal studies by Carlson et al. (1983, 1985) demonstrated a significant increase in mortality in mice co-infected intraperitoneally with sublethal levels of C. albicans and S. aureus. This lethal synergism was also found in a more recent study by Peters & Noverr (2013) where co-infection led to a 40% mortality rate and increased microbial burden in the spleen and kidney. The interaction between S. aureus and C. albicans does not appear to be strain specific, and it is significantly higher than the interaction between C. albicans and other microbial species (Staphylococcus epidermidis, Streptococcus pyogenes, Pseudomonas aeruginosa, Escherichia coli and Bacillus subtilis) (Peters et al., 2010, 2012).

Collectively, these observations seem to indicate a potential synergy in virulence when these species co-exist in a host. These speculations were recently validated by our in vitro studies, where microscopic images revealed a complex physical interaction with S. aureus demonstrating high affinity to the hyphal elements of C. albicans (Perlroth et al., 2010, 2012). Further analysis revealed that S. aureus bound specifically to the hyphae form of C. albicans and not to the yeast form (Peters et al., 2010). The main C. albicans target for S. aureus binding was shown to be the agglutinin-like sequence 3 adhesin (Als3p). Purified recombinant Als3p has been shown to bind S. aureus in in vitro assays, and binding of S. aureus to the C. albicans hyphae is significantly reduced in a mutant of Als3p compared to WT or other adhesin-deficient mutant strains (Peters et al., 2012). However, previous studies did not confirm this specific interaction by restoration of the WT binding phenotype through complementation of the C. albicans Als3p gene.

Given the propensity of C. albicans to adhere to and penetrate tissue via its invasive hyphae, combined with the high in vitro affinity of S. aureus to the hyphae, it was feasible to speculate that co-colonization with C. albicans may provide S. aureus with the means to gain entry into the vascular system (Cannon & Chaffin, 2001; Sudbery et al., 2004). Since S. aureus has more recently been identified in the oral cavity along with C. albicans, we sought to test the effects of their co-colonization in the oral cavity using a standard murine model of candidiasis. Tongue histopathological analysis was performed and subepithelial penetration of the tissue by invasive C. albicans hyphae with adherent S. aureus was shown. This interaction was absent in mutants of the C. albicans Als3p hyphal protein but was restored when Als3p was restored through complementation. We developed a novel murine model of oral co-colonization to monitor the development and potential progression of mucosal co-colonization to systemic disease in an immunocompromised host. In this model, mice suffered disseminated staphylococcal disease with high morbidity and mortality only when co-colonized by S. aureus and C. albicans. While this ‘microbial
hitchhiking’ phenomenon has been identified in other in vitro systems (Edwards et al., 2006; Saito et al., 2012), this is the first report, to our knowledge, of systemic disease associated with multi-Kingdom interactions. The clinical implications are far-reaching, especially if this microbial infectious synergy occurs in other areas where co-colonization can commonly occur such as the intestinal tract, genital tract, infected and devitalized skin or axillary or groin areas of the skin. This study also provides crucial insight into one of the complex mechanisms behind polymicrobial interactions.

**METHODS**

**Strains.** The genotypes of the strains used can be found in the corresponding references: C. albicans strains SC5314 WT (SC5314) (Gillum et al., 1984), ALS3 mutant in SC5314 (als3Δ/Δ) (Phan et al., 2007), ALS3 mutant in SC5314 complemented (als3Δ/Δ ALS3) (Phan et al., 2007), the methicillin-resistant S. aureus WT strains M2 (Brady et al., 2006) and USA300 JE2 (Kennedy et al., 2010). In order to determine potential adhesions on S. aureus to which C. albicans was binding, 25 different S. aureus mutant strains were selected based on a review of microbial surface components recognizing adhesive matrix molecules in S. aureus (Clarke & Foster, 2006). The parent strain USA300 JE2 and the 25 S. aureus mutant strains that were used in the experiment were obtained from The Nebraska Transposon Mutant Library from Network on Antimicrobial Resistance in Staphylococcus aureus (NARS) and were constructed by the Center for Staphylococcal Research (CSR) at the University of Nebraska Medical Center (http://app1.unmc.edu/fgo/). A description of all strains used can be found in Table 1.

**Hyphal–bacterial attachment assay.** For all attachment assays carried out in order to identify the S. aureus adhesin responsible for C. albicans hyphal binding, an aliquot of a glycerol stock of C. albicans strain was grown and maintained on Sabouraud dextrose agar (BBL). Cultures were grown overnight in yeast–peptone–glucose (BBL) in an orbital shaker (120 r.p.m.) at 30 °C under aerobic conditions. Yeast cells were harvested and washed twice in sterile PBS. Hyphae formation was induced by first growing C. albicans as noted above on plastic Permanox slides (Electron Microscopy Sciences) in polystyrene six well plates (Corning) in 3 ml RPMI 1640 for 3 h. Nonadherent hyphae were removed by gently washing the slides in PBS, followed by the addition of 3 ml of fresh RPMI 1640.

Starter cultures of the WT S. aureus strain JE2 and 25 different S. aureus mutants strains were grown in trypticase soy broth (TSB; Remel) and incubated overnight at 37 °C. Erythromycin (10 μg ml⁻¹) was added into the TSB medium for the S. aureus mutant strains. Fresh exponential-phase S. aureus starter cultures were grown by diluting the overnight culture 1:100 in fresh TSB for 3 h. Exponential-phase S. aureus cell suspensions were washed in PBS, diluted to an OD₆₀₀ of 0.1, and added to SC5314 C. albicans biofilms (WT and als3Δ/Δ). Dual-species biofilms were grown in RPMI 1640 buffered with HEPEs and supplemented with l-glutamine (Invitrogen). Plates were placed on a rotary shaker to distribute the bacteria evenly and incubated for 1 h at 37 °C. Following incubation, non-adherent cells were removed by gently washing the slides in PBS and then examined using phase-contrast microscopy under a 100× oil-immersion objective. The total number of bacterial cells per field and attached bacteria per hyphae were counted. Per cent attachment was calculated by dividing the number of attached bacteria by the total number of bacteria. A total of ten random fields per coverslip were analysed. Each assay was done in triplicate.

**Real-time adhesion analysis.** Real-time adhesion was visualized using the Bioflux 200 system (Fluxion) combined with an EVOS FL digital fluorescence microscope (AMG). To analyse adhesion of S. aureus to hyphae of SC5314 C. albicans in real-time, a GFP labelled S. aureus (S. aureusGFP) strain was used (Li et al., 2011). C. albicans suspended at 10⁷ cells ml⁻¹ in PBS was allowed to adhere to glass under static conditions at 37 °C. Following 2 h incubation, non-adherent cells were removed by flow with 0.2 Pa and yeast nitrogen base pH 7 containing 0.5 % D-glucose (YNB) was flowed through the channel. The flow was stopped and the channel was incubated at 37 °C for 3 h to allow hyphae to form (Jarosz et al., 2009), then YNB was removed by flow (0.2 Pa). Pilot experiments using different shear rates showed that hyphae remained attached to the glass surface up to a maximum of 2 Pa (not shown). Overnight cultures of S. aureusGFP, grown at 37 °C while shaking at 150 r.p.m., were harvested and resuspended in PBS. This suspension was flowed over the adherent hyphae of C. albicans at 0.2 Pa and images were obtained using an EVOS FL digital fluorescence microscope using 510× objective and the appropriate filter set. Images were taken every 10 s for a total of 5 min and a movie was created at 2 frames s⁻¹.

**Microscopic analysis.** Peptide-nucleic acid fluorescent in situ hybridization (PNA-FISH) staining and confocal scanning laser microscopy was utilized to visualize the architecture of mixed biofilms in vitro as described previously (Peters et al., 2010). PNA-FISH employs fluorescent-labelled PNA probes to target the species-specific rRNA sequences in a specific FISH assay that enables whole cell visualization. Hybridization was performed following the manufacturer’s protocol (Advandx) using a cocktail of Cy2-labelled S. aureus and FITC-labelled C. albicans PNA probe mixtures. Briefly, dual-species biofilms were grown on glass coverslips in polystyrene six well plates (Corning). S. aureus and C. albicans were diluted in PBS to an OD₆₀₀ of 0.1 and 1.0, respectively. This represented approximately 1 × 10⁵ cfu ml⁻¹ for S. aureus and 2 × 10⁵ cfu ml⁻¹ for C. albicans. Fifty microlitres of each cell suspension (representing a total of 5 × 10⁵ cfu of S. aureus and 1 × 10⁶ cfu of C. albicans) was added to wells containing 5 ml of RPMI 1640 buffered with HEPEs and supplemented with l-glutamine (Invitrogen) and 5 % heat-inactivated FBS (HyClone) and plates were incubated for 24 h at 37 °C. Following incubation, coverslips were gently rinsed with PBS to remove non-adherent cells. Imaging was performed by confocal scanning laser microscopy with a Zeiss LSM 510 confocal microscope (Carl Zeiss) using FITC filter sets.

In addition, microscopy was also performed on excised mouse tongues using a previously described ex vivo model (Kamai et al., 2002; Peters et al., 2012). Briefly, tongues were excised from euthanized CD1 mice and placed into polystyrene well plates containing 5 ml of RPMI 1640 per well. S. aureus and C. albicans were added in an identical manner as in the in vitro attachment assay: 50 μl of cell suspensions of each microbe for a total of 5 × 10⁶ cfu of S. aureus and 1 × 10⁶ cfu of C. albicans. Tones were then washed several times in sterile PBS, transferred to fresh RPMI 1640 and incubated overnight at 37 °C with 5 % CO₂. Tones were then fixed, embedded in paraffin and tissue sections stained with PNA-FISH probes and examined by confocal microscopy. Fluorescent microscopy could not be performed on tissue recovered from animals infected in vivo due to interference in the hybridization process by host erythrocytes and inflammatory cells.

**Murine in vivo model of co-infection.** Strains were grown on appropriate growth media and mid exponential-phase cultures were used in experiments. Animal studies were approved by the University of Maryland Animal Care and Use Committee. The animal model for oral co-infection was designed based on an established protocol for oral candidiasis (Dwivedi et al., 2011). Briefly, oral bacterial flora was suppressed by the addition of 300 μg ml⁻¹ ampicillin into the drinking water and mice (C57BL/6) were immunosuppressed by three subcutaneous injections of 225 mg kg⁻¹ cortisone acetate, one
Table 1. Strains used in this study

<table>
<thead>
<tr>
<th>Strain</th>
<th>Designation</th>
<th>Genotype</th>
<th>Reference</th>
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<tbody>
<tr>
<td>S. aureus M2</td>
<td>WT (SA)</td>
<td>ST30, spa type T019 and agrIII</td>
<td>Ali et al. (1997); Brady et al. (2006); Brady et al. (2007); Brady et al. (2011); Jabara-Rizk et al. (2006); Leid et al. (2002); Peters et al. (2010); Peters et al. (2012); Prabhakara et al. (2011a, b); Shirtliff et al. (2002)</td>
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<td></td>
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<td>Kennedy et al. (2008); Kennedy et al. (2010); <a href="http://appl.unmc.edu/fgx/">http://appl.unmc.edu/fgx/</a></td>
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<tr>
<td>S. aureus JE2</td>
<td>JE2</td>
<td>USA300 JE2 – a plasmid cured strain from WT USA300-LAC</td>
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<tr>
<td>NE1</td>
<td>ΔSAUSA300_1327 – Cell Wall Protein (protein G-related albumin-binding (GA) module related to streptococcal emb adhesin)</td>
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<tr>
<td>NE26</td>
<td>ΔSAUSA300_0224 – coa (staphylocoagulase precursor)</td>
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<tr>
<td>NE33</td>
<td>ΔSAUSA300_2589 – sasA (Staphylococcus aureus surface protein A and LPXTG-motif cell wall surface anchor family protein)</td>
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<tr>
<td>NE98</td>
<td>ΔSAUSA300_0548 – sdrE (SdrE protein binds host Factor H)</td>
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<td>NE186</td>
<td>ΔSAUSA300_2441 – fnbA (fibronectin binding protein A)</td>
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<td>NE286</td>
<td>ΔSAUSA300_0113 – spa (immunoglobulin G binding protein A)</td>
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<td>ΔSAUSA300_1029 – sasE (iron transport associated domain protein)</td>
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<td>ΔSAUSA300_2565 – clfB (clumping factor B)</td>
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<td>NE1190</td>
<td>ΔSAUSA300_2256 – atl (Bifunctional autolysin Atl [N-acetyl muramoyl-l-alanine amidase/Endo-beta-N-acetylglucosaminidase)</td>
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<td>NE1289</td>
<td>ΔSAUSA300_0547 – sdrD (SdrD protein)</td>
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<td>NE1558</td>
<td>ΔSAUSA300_0774 – emp (secretory extracellular matrix and plasma binding protein)</td>
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<td>NE1561</td>
<td>ΔSAUSA300_1370 – elbpS (cell surface elastin binding protein)</td>
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<tr>
<td>C. albicans</td>
<td>SC5314</td>
<td>URA3 AL53 ARG4 HIS1 URA3 AL53 ARG4 HIS1</td>
<td>Gillum et al. (1984)</td>
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<tr>
<td>SC5314</td>
<td></td>
<td></td>
<td>Phan et al. (2007)</td>
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<tr>
<td>C. albicans</td>
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<td>ura3Δ:::imm434::URA3-IR01 als3::ARG4 arg4::hisG his1::hisG</td>
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<tr>
<td>CAYF178U</td>
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<td>ura3Δ:::imm434:::UR3-IR01 als3::ARG4 arg4::hisG his1::hisG</td>
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<tr>
<td>C. albicans</td>
<td>als3A/Δ ALS3</td>
<td>ura3Δ:::imm434::UR3-IR01 als3::ARG4::ALS3 arg4::hisG his1::hisG</td>
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<td>CAQTP178U</td>
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<td>ura3Δ:::imm434::ALS3 arg4::hisG his1::hisG</td>
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given prior to inoculation and the other two given following inoculation 2 days apart. Anaesthetized animals were orally administered with standardized cell suspensions of C. albicans (100 μl of a 6 × 10^6 c.f.u. ml⁻¹ suspension administered on a small cotton pad), S. aureus (50 μl of a 1 × 10^6 c.f.u. ml⁻¹ suspension), or in combination (four mice per group in triplicate) on days 1 and 3, and were continually exposed to C. albicans (6 × 10^6 c.f.u. ml⁻¹) through drinking water. During the course of the experiments, animals were weighed every 3 days, and on day 6 post-infection, were euthanized and tongues and kidneys were harvested. Tissue homogenates were assessed for microbial burden (cells g⁻¹ tissue) by culturing on selective microbial media. Mice exhibiting greater than 20% weight

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loss were euthanized and considered deceased, as established as a humane end point by the University of Maryland Institutional Animal Care and Use Committee.

**Statistical analysis.** Experiments were performed in triplicate. Data analysis was performed using the two-tailed Student’s t-test, the Log Rank Test, or the Mann–Whitney U Test (two tailed), where appropriate. Values of \( P<0.05 \) were considered statistically significant.

**Ethics statement.** The experiments in this study were approved under Protocol 1111010 of the Dental School IACUC committee and adhered to Public Health Service (PHS) Policy on Humane Care and Use of Laboratory Animals (Animal Welfare Assurance A3200-01) and United States Department of Agriculture Animal Welfare Act & Animal Welfare Regulations.

**RESULTS**

**Hyphal–bacterial attachment assay: in vitro analysis of polymicrobial biofilm development using confocal and time lapse microscopy**

As colonization and biofilm formation is a prerequisite for the development of the pathogenic process, in vitro studies were performed in order to visualize the interaction between *S. aureus* and *C. albicans* strains as they co-existed in a polymicrobial biofilm. Mixed-species biofilms of *S. aureus* and *C. albicans* mutant and complemented strains were grown in vitro and visualized by PNA-FISH staining. Microscopic images of the mixed biofilms paralleled those from our previous studies (Peters et al., 2010, 2012) where a significant decrease in *S. aureus* adherence to the hyphae of the *C. albicans* strain lacking the Als3p (als3Δ/Δ) was observed compared to the strains expressing the receptor. Additionally, there was no appreciable difference between the WT *C. albicans* or the als3Δ/Δ ALS3 complemented strain (data not shown).

Importantly, the initial adherence of *S. aureus* to the hyphae leading to the development of a mature biofilm was monitored and captured in real-time by fluorescent microscopy in a biofilm flow system. A movie was created of compiled images taken every 10 s over a 5 min time frame (Video S1, available in the online Supplementary Material). As can be seen, immediately upon entry into the flow cell, *S. aureus* rapidly and specifically adheres to the hyphae attached to the surface of the flow cell. When a higher cell density of *S. aureus* is flowed through the system, a more rapid and dramatic adhesion is seen resulting in development of a mature mixed-species biofilm within 5 min of initiation of the adherence process.

In order to determine the specific staphylococcal factor responsible for the hyphal binding, WT *S. aureus* strain JE2 and 25 different *S. aureus* strains mutated in previously described adhesins were individually added to SC5314 *C. albicans* biofilms (see Fig. 1, Table 1 for strain designations). The percentage of cells attached to the hyphae of SC5314 was determined for each mutant and compared to the hyphal attachment percentage of WT *S. aureus* co-cultured with either SC5314 or the SC5314 als3Δ/Δ. It was found that the percentage of WT JE2 cells binding to hyphae was that same as that seen for the staphylococcal strain M2 (84 % vs 82 %

**Fig. 1.** Hyphal binding assay for determining the *S. aureus* adhesin responsible for *C. albicans* hyphae binding. The WT *S. aureus* strain JE2 and 25 different *S. aureus* mutants strains in previously described adhesins, were grown in TSB, added to *C. albicans* hyphae, and incubated for 3 h. Non-adherent hyphae were removed by gently washing the slides in PBS, and then examined using phase-contrast microscopy under a 100× oil-immersion objective. The total number of bacterial cells per field and attached bacteria per hyphae were counted. Attachment (%) was calculated by dividing the number of attached bacteria by the total number of bacteria. A total of 10 random fields per coverslip were analysed in triplicate (\( n=3 \)). Error bars indicate SD. * denotes statistically significant (\( P<0.05 \)) reductions in binding ability compared to the WT *S. aureus* and *C. albicans* attachment (JE2 to SC5314) as evaluated by a two-tailed Student’s t-Test.
respectively) (Peters et al., 2012). The use of JE2, a S. aureus strain that is phylogenetically divergent from the M2 strain (Diep et al., 2006; Harro et al., 2013), provides broader support for the idea that this S. aureus–C. albicans interaction is species-specific and not just strain specific.

Several of the staphylococcal mutants tested had a statistically significant reduction in their ability to bind C. albicans, including NE728 (Δ in fibronectin binding protein B) with 62% attachment, NE800 (Δ in sasF, a putative surface anchored protein) with 61% attachment and NE1190 (Δ in Atl, a putative N-acetylmuramoyl-L-alanine amidase) with 52% attachment. In addition, five other adhesin mutants showed a similarly reduced ability (52–65% attachment) to bind C. albicans, although these differences were not statistically significant due to larger SD.

The creation of single, double, triple, or octuple mutants in these adhesins has been shown to eliminate the ability of S. aureus to both form biofilms and survive in vivo (Bose et al., 2012; Chen et al., 2013; Kenny et al., 2009; Mazmanian et al., 2000; Palmqvist et al., 2005). Therefore, these S. aureus mutants are no longer able to systemically spread in cases of co-infection with C. albicans regardless of the mechanism of deep tissue delivery. Since it cannot be concluded whether a lack of systemic disease by S. aureus is a product of reduced C. albicans hyphal binding or an inability to survive within the host, subsequent studies to determine the combination of staphylococcal adhesins required for hyphal interactions in vivo were not possible.

**Microscopic analysis**

To investigate the role of Als3p in the invasive mechanism of co-colonization, experiments were performed where both micro-organisms were allowed to interact on excised tongues infected ex vivo. Similarly to the images of abiotic surfaces, S. aureus was seen strongly adhering to the C. albicans hyphae with the Als3p receptor (WT SC5314 and als3ΔΔ ALS3; Fig. 2b, f) but only minimally to the hyphae lacking the receptor als3ΔΔ (Fig. 2d). However, in all three C. albicans strains, S. aureus and C. albicans were seen forming a polymicrobial biofilm on the surface of the tongue (indicated by the white arrows in Fig. 2a, c, e). Importantly, in addition to mere co-colonization, this model demonstrated tissue co-penetration of S. aureus along with the invasive hyphae of C. albicans into the subepithelium (Fig. 2a, b, e, f), a process dependent on Als3p as S. aureus did not co-penetrates with als3ΔΔ (Fig. 2c, d). We did notice that the staphylococcal hyphal binding was markedly reduced in these studies compared to the in vitro analysis of polymicrobial biofilm development using confocal microscopy.

![Microscopic images](http://mic.sgmjournals.org/173)

**Fig. 2.** Microscopic images (low and high magnification) of sections of tongues infected and stained with probes specific to S. aureus (red) and C. albicans (green) demonstrating hyphal invasion of tissue and bacterial presence. Hyphae of Als3p-expressing C. albicans strains (WT SC5314 and complemented strain als3ΔΔ ALS3) are seen penetrating the epithelium with S. aureus (SA) adhering to and thus co-invading the tissue with the hyphae (a, b, e, f). In contrast, although the hyphae of the C. albicans Als3p mutant (als3ΔΔ) penetrated the tissue and SA adhered to the border of the tongues, no bacteria were seen adhering to the hyphae or detected in the subepithelium (c, d). White arrows denote tongue outer surface and scale bars represent 10 μm.
microscopy. These differences may have been due to salivary components and structural complexities of the tongue environment, as well as the tongue’s ability to produce host defence factors, such as β-defensins (Weinberg et al., 1998).

**Murine in vivo model of oral co-colonization**

An animal model of microbial co-colonization was developed to investigate the pathogenic implications of microbial interactions on mucosal tissue in immunocompromised hosts. Mouse oral cavities were inoculated with both *S. aureus* and *C. albicans* alone or in combination, and tongues and kidneys were harvested from euthanized animals. In addition, the *C. albicans* als3Δ ALS3 complemented strain were inoculated as well, either alone or in combination with *S. aureus*. Clinical presentation of the harvested tongues was consistent with advanced candidiasis and diagnosis was confirmed by histopathology.

None of the animals colonized with *S. aureus* alone exhibited significant symptoms of disease or weight loss, and all survived until the conclusion of the experiment (Fig. 3). Mice infected with *C. albicans* alone exhibited symptoms of oral candidiasis and half of the mice required early euthanization due to significant weight loss (Fig. 3). However, none of these mice exhibited symptoms of systemic infection, suggesting the weight loss was solely due to the oral candidiasis, and not because of an invasive infection. There was no significant difference in the survival among all three of the *C. albicans* strains administered alone (data not shown).

As opposed to the animals orally inoculated with either single species, those simultaneously inoculated with *S. aureus* and *C. albicans* containing an intact Als3p (WT SC5314 or SC5314 als3Δ Δ ALS3 complemented) exhibited signs of systemic infection, including dehydration and lethargy. Additionally, the mice in this group showed significant loss of body weight, requiring early euthanization and halting of experiments at 6 days post-inoculation (dpi), as per the University of Maryland Institutional Animal Care and Use Committee humane end point guidelines. Significantly, all of these animals succumbed to their infection prior to the end of the experiment as determined by the humane end points (Fig. 3). In contrast, none of the animals in the group co-colonized with *S. aureus* and *C. albicans* lacking Als3p exhibited evidence of systemic infection and the majority (83%) of these mice survived until the conclusion of the experiment (Fig. 3).

In order to diagnose the cause of morbidity in the sick animals, the tongues and kidneys were harvested and cultured to identify microbial presence. There was no significant difference in c.f.u. of *C. albicans* recovered from the tongues, regardless of which *C. albicans* strain was used and whether it was inoculated alone or co-inoculated with *S. aureus*, suggesting that *C. albicans* does not exhibit any deficiency...
in colonizing the tongue in the absence of Als3p (Fig. 4b). *S. aureus*, on the other hand, exhibited enhanced colonization of the tongue when co-inoculated with any of the *C. albicans* strains as compared to *S. aureus* given alone (Fig. 4a).

However, the clinical symptoms indicating systemic disease were corroborated by the recovery of *S. aureus* and *C. albicans* from the kidneys in strains with a functional Als3p protein compared to the als3Δ/Δ (Fig. 4c, d). High numbers

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**Fig. 4.** Microbial burden in the tongue and kidneys in mice orally colonized with either *S. aureus* or *C. albicans* WT (SC5314), Als3p mutant (als3Δ/Δ), and Als3p complemented (als3Δ/Δ ALS3) individually, or in combination. Three days post-infection, tissue was extracted, homogenized and cultured for assessment of microbial presence based on number of organisms recovered per gram of tissue. Number of microbes recovered is reported as log_{10} of c.f.u. per gram of respective tissue. (a, c) *S. aureus* recovered from the tongues (a) and kidneys (c) of infected mice. (b, d) *C. albicans* recovered from the tongues (b) and kidneys (d) of infected mice. Both microbes were recovered from tongues of mice under all conditions tested. However, *S. aureus* was only recovered from kidneys of mice co-colonized with either WT *C. albicans* or mutant *C. albicans* that had been complemented for Als3p expression. All experiments were performed in triplicate in groups of four mice per group. In addition to all data points, the mean of the log of c.f.u./gram is shown. Error bars indicate 95% confidence intervals. Significance was determined using the Mann–Whitney U Test to compare each polymicrobial condition to the monomicrobial control infection. Asterisks denote statistical significance versus the mono-microbial control infection according to the Mann–Whitney U Test. * indicates $P<0.05$ and *** indicates $P<0.001$. 

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Systemic *S. aureus* infection mediated through *C. albicans* hyphal invasion
of *S. aureus* were recovered from mice co-infected with *C. albicans* expressing intact Als3p (WTSC5314 or SC5314 al33A/Δ ALS3 complemented) and no *S. aureus* was found in the kidneys of mice inoculated without *C. albicans* or with *C. albicans* lacking Als3p (Fig. 4c). Additionally, there were significant c.f.u. of *C. albicans* recovered from the kidneys of mice co-inoculated with *S. aureus* and the WT *C. albicans*. This is in contrast with mice inoculated with *C. albicans* alone or co-inoculated with *S. aureus* and *C. albicans* lacking Als3p, where most mice had no *C. albicans* present in their kidneys (Fig. 4d).

The data presented in Fig. 4 suggests that, as seen in Fig. 2, *S. aureus* and *C. albicans* are able to form a dense polymicrobial biofilm on the epithelial surface of the tongue with or without the expression of Als3p. However, *S. aureus* is unable to enter the bloodstream and disseminate *C. albicans* in vitro is unable to enter the bloodstream and disseminate *S. aureus* and the WT *C. albicans*. The data presented in Fig. 4 suggests that, as seen in Fig. 2, *S. aureus* was found in the kidneys of mice inoculated without *C. albicans* or with *C. albicans* lacking Als3p (Fig. 4c). Additionally, there were significant c.f.u. of *C. albicans* recovered from the kidneys of mice co-inoculated with *S. aureus* and the WT *C. albicans*. This is in contrast with mice inoculated with *C. albicans* alone or co-inoculated with *S. aureus* and *C. albicans* lacking Als3p, where most mice had no *C. albicans* present in their kidneys (Fig. 4d).

The data presented in Fig. 4 suggests that, as seen in Fig. 2, *S. aureus* and *C. albicans* are able to form a dense polymicrobial biofilm on the epithelial surface of the tongue with or without the expression of Als3p. However, *S. aureus* is unable to enter the bloodstream and disseminate in the absence of Als3p, ostensibly due to the lack of binding to penetrating hyphae as shown in Fig. 2. Collectively, these findings demonstrate that co-colonization of the oral mucosa by *C. albicans* and *S. aureus* in immunocompromised animals may lead to systemic *S. aureus* infections with high morbidity and mortality.

**DISCUSSION**

Polymicrobial diseases represent the clinical manifestations induced by the presence of multiple microbial species that may act synergistically to cause complex infectious processes (Brogden & Gerberding, 2002; Pittet et al., 1993; Tuft, 2006). Yet, despite the gravity of such infections, areas of study in polymicrobial diseases and particularly those involving vastly diverse pathogens such as fungi and bacteria are in their infancy (Peleg et al., 2010; Shirilff et al., 2009). *C. albicans* and *S. aureus* are frequent colonizers of human mucosal surfaces and exhibit a strong ability to adhere to host tissue and develop drug tolerance. However, studies investigating the implications of their interaction as they co-colonize host mucosal tissue have not been previously performed.

*S. aureus* avidly and specifically adheres to hyphae of *C. albicans* in vitro, as illustrated using static and time lapse microscopy (supplementary movie V1). Adhesion is followed by tissue penetration of *S. aureus* along with the invasive hyphae (Fig. 2). Although no single adhesin of *S. aureus* was found to be solely responsible for hyphal binding, three staphylococcal adhesin mutants (AfnpB, AsasF, and Δ ATL) were found to have significantly reduced hyphal binding compared to the WT strain (Fig. 1). FnPB (fibronectin binding protein B) is one of two important fibronectin binding proteins in *S. aureus*. FnPB is known to be upregulated in host tissues, and helps facilitate binding to eukaryotic cells (Menzies, 2003). Interestingly, the other structurally related *S. aureus* fibronectin binding protein, FnPA, did not appear to be involved in hyphal binding (Fig. 2), suggesting that the minor structural differences between FnPB and FnPA may influence the ability to bind *C. albicans* hyphae. SasF (staphylococcus aureus surface protein F) is a highly conserved cell surface-associated adhesin (McCarthy & Lindsay, 2010). SasF has been shown to be upregulated in response to linoleic acid (Kenny et al., 2009), which is one of the major endogenous fatty acids in *C. albicans* (Nigam et al., 2011). The third mutant with significantly reduced binding was a mutation of Atl, an uncharacterized protein that is annotated as a putative N-acetylmuramoyl-L-alanine amidase, and likely functions as an *S. aureus* autolysin (Diep et al., 2006).

In addition, five other staphylococcal mutants had similar reductions in binding (although these were not statistically significantly different from the WT strain). This was not surprising considering the redundant nature of adhesin binding partners in *S. aureus* (Clarke & Foster, 2006). Interestingly, neither the JE2 WT strain binding to the Als3p deficient mutant nor any of the *S. aureus* mutants binding to the WT *C. albicans* showed a reduction in binding to less than 50%. This may be due to the expression of other proteins on *C. albicans* hyphae that can have minor roles in *S. aureus* adherence. One such protein is Als1, which was shown in an earlier study to have a role, albeit a much smaller role compared to Als3p, in binding *S. aureus* in vitro (Peters et al., 2012). However, the clear difference between the *C. albicans* als33A/Δ mutant and the WT strain, both in terms of hyphal binding as shown in Fig. 2 and dissemination as shown in Fig. 4, suggest that differential in vivo regulation of these other *C. albicans* proteins may reduce their contributions to *S. aureus* binding during an actual infection.

This interaction with staphylococcal adhesins and Als3p may not be surprising since a number of *S. aureus* adhesins are predicted to have significant 3D homology to Als3p and other Als proteins (Nobile et al., 2008; Salgado et al., 2011). This homology is also demonstrated in cross protection studies in which immunization with *C. albicans* Als3p has been show to provide protection from *S. aureus* challenge in animal models of infection (Ibrahim et al., 2013; Lin et al., 2009). Since the self–self binding and clumping due to Als proteins have been well documented, the binding of staphylococcal adhesins to Als3p may mimic this self-agglutination (Lipke et al., 2012; Ramsook et al., 2010).

In order to determine the in vivo implications of this Als3p-dependent interaction, we developed a novel murine model to demonstrate the potential progression of mucosal co-colonization into disseminated systemic disease. In our animal model, mice co-colonized with *C. albicans* and *S. aureus* succumbed to systemic bacterial infection, *S. aureus* was recovered from the kidneys, and Als3p was crucial for this systemic dissemination (Fig. 3 and 4). As expected, colonization with *S. aureus* individually did not result in death or any signs of significant morbidity, as *S. aureus* typically requires a breach in host surface barriers to invade (Acton et al., 2009; Smith et al., 2003; Veeh et al., 2003).

While the enhanced colonization of the tongue by *S. aureus* in the presence of all three *C. albicans* strains (Fig. 4a) may not correlate to the pattern of colonization seen in the
kidney (Fig. 4c), this is likely to reflect the fact that the C. albicans factors responsible for co-colonization are different from the one required for hyphal binding. As shown in an earlier study, the co-culture of C. albicans and S. aureus together causes reciprocal changes in protein expression (Peters et al., 2010). Additionally, although S. aureus has reduced binding to C. albicans lacking Als3p, it does not show a reduction in polymicrobial biofilm formation (Peters et al., 2012). Instead, what is likely to be happening in vivo is that S. aureus and C. albicans are still able to form a dense biofilm on the epithelial surface of the tongue, but are unable to attach to penetrating hyphae. This is what is observed in Fig. 2.

It is important to note that the mutant strain lacking Als3p did not exhibit a defect in hyphal formation (Fig. 2). This is significant, since we propose that Als3p does not affect C. albicans pathogenesis when present as a mono-species infection, but instead is important for synergy with S. aureus. Also, while the mutant lacking Als3p had reduced colonization of the kidneys in co-colonization experiments, Als3p has previously been shown to be dispensable for C. albicans pathogenesis in an intravenous challenge model (Cleary et al., 2011). This suggests that the increased presence of the WT C. albicans in the kidneys in comparison to the mutant is also mediated by this synergy with S. aureus. As mentioned previously, S. aureus can produce an array of virulence factors (Bien et al., 2011; Ferry et al., 2005) that are likely to be helping to further mediate tissue lysis and facilitate dissemination of both S. aureus and C. albicans into the bloodstream. The fact that deletion of Als3p does not alter the formation of hyphae (a necessary prerequisite for S. aureus attachment; Peters et al., 2010), nor affects the virulence of C. albicans in the bloodstream, suggests that its role in our model is solely due to S. aureus attachment. Therefore, the inability of the mutant to mediate a bacterial or fungal systemic disease further confirms the specificity of Als3p in the invasion process.

As our animal model involved the establishment of a polymicrobial infection in mice receiving immunosuppression, it is most directly relevant to cases of co-colonization in immunocompromised individuals. Immunocompromised hosts represent a significant and appropriate patient population to model, as these patients frequently suffer from infections and diseases of the oral mucosa and bloodstream that involve C. albicans and S. aureus (Bassetti et al., 2012; Delorenze et al., 2013; Dongari-Bagtzoglou et al., 2009; Marukutira et al., 2014; Olczak-Kowalczyk et al., 2012; Stammler Jaliff et al., 2014; Yehia et al., 2011). Additionally, a recent pair of studies found that among HIV positive individuals, S. aureus could be isolated from the oral cavity of 92% of individuals while C. albicans was isolated from 73% of the study subjects (Back-Brito et al., 2009, 2011), suggesting our model is highly relevant clinically. Furthermore, due to the continued rise in the prevalence of HIV (Hall et al., 2008) and the continued increase in patients living with transplants and receiving immunosuppression (Hall et al., 2008; Port et al., 2007), the population of immunocompromised patients at risk for co-colonization with S. aureus and C. albicans continues to expand.

While this ‘hitchhiking’ phenomenon of systemic infection stemming from staphylococcal–candidal interaction has yet to be established in a human host, we propose that this may be due to a failure to look for it. It is feasible to speculate that in a significant number of the 40–50% of cases of staphylococcal bloodstream infections with no clearly established portal of entry (del Río et al., 2009), oral candidiasis may have been the underlying cause. Should this phenomenon occur in a vulnerable human host harbouring both species, as often occurs on mucosal surfaces, the medical consequences are likely to be significant, as reflected by the high rate of morbidity and mortality observed in our co-colonized animals (Fig. 3).

Although this study focused on C. albicans and S. aureus, it is important to note that in the oral cavity, C. albicans co-exists with the myriad of bacterial species commonly residing the various niches of this complex environment (Bagg & Silverwood, 1986; Brehm-Stecher & Johnson, 2003; Holmes et al., 1995, 1996; Jenkinson et al., 1990; Klotz et al., 2007; Silverman et al., 2010). The oral cavity is colonized by an ever-changing population (Lazarevic et al., 2010) of over 900 bacterial species and therefore, it may also be conceivable that similar phenomena with clinical relevance may also occur between C. albicans and oral bacteria (Zaura et al., 2009). This has been seen in a recent study in which Streptococcus oralis colonization of the oral and gastrointestinal tract was augmented in the presence of C. albicans and resulted in increased size and frequency of thrush lesions in a murine model of dual infection (Xu et al., 2014). As our knowledge of interspecies interactions on niches expands, the role of C. albicans in pathogenesis might prove to be more intricate than currently recognized.

A potential limitation of the study is that this interaction was only evaluated in oral cavity instead of in other body locales where these microbes, particularly S. aureus, have been isolated, including the nasopharynx, moist skin areas and the genital tract. While the model used in this study has relevance, since both of these microbes have been co-isolated in the oral cavity, we look forward to future studies where we can evaluate this interaction in the mouse nasopharynx and skin models. Also worth noting is the possibility of gastrointestinal (GI) colonization to contribute to this ‘hitchhiking’ phenomenon. Although our study focused on the oral mucosa, based on the oral administration of the microbes there was potential for the co-colonization of the GI tract to occur as well. C. albicans and S. aureus have both been shown to be able to colonize the GI tract (Acton et al., 2009; Prieto et al., 2014), and GI candidiasis can occur in immunocompromised individuals, although it is much less common than oral candidiasis (Vazquez & Sobel, 2002). Although our current study failed to examine this potential route of invasion, we feel that based on the requirement that Als3p be present in order to
produce systemic *Staphylococcus aureus* bacteraemia, any dissemination occurring through the gut mucosa is likely to be occurring through the same proposed model of Als3p binding and hitchhiking. We hope to clarify the potential role this important mucosal site may play in this phenomenon in future studies.

In summary, this study elucidates a synergistic interaction between the bacterial pathogen *Staphylococcus aureus* and the opportunistic fungal pathogen *Candida albicans* during polymicrobial biofilm growth in the oral cavity, for which we propose the term ‘microbial hitchhiking’. The interactions between these diverse and important commensals and opportunistic pathogens hold significant clinical implications, and therefore characterizing their complex interactions is a major step in understanding the nature of their co-existence in the host. Although retrospective and prospective clinical studies are warranted, our findings advocate screening of critically ill patients for oral candidal colonization as a measure for the prevention of systemic bacterial infections.

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