

Key factors to consider for *Candida auris* screening in healthcare settings: a systematic review

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Abstract

Background

Candida auris is an emerging fungal pathogen that is often multidrug-resistant. It can persist on skin and in hospital environments, leading to outbreaks and severe infections for patients at risk. Several countries and institutions are working on establishing guidelines and recommendations for prevention. This review aims to assess the evidence on factors associated with *C. auris* colonisation or infection, the duration of such colonisation, possible colonisation sites, and the risk of secondary transmission to inform screening recommendations.

Methods

We systematically searched five databases for primary studies and systematic reviews of our four outcomes. We excluded studies on treatment, management, laboratory methods, drug resistance, and environmental screening. From each paper, we extracted relevant data and summarised them in tables. Main findings were described narratively.

Results

We selected 117 studies for inclusion. Most of the studies were observational studies. The duration of *C. auris* colonisation varied, with up to and beyond a year being common. The predominant sites of colonisation were the axillae and groin, with the nares and rectum being less common sites. The risk of secondary infection saw considerable variation across the studies, and these secondary cases primarily involved patients and not health care workers. Critical care settings, invasive medical devices, recent antimicrobial use, and comorbidities were often associated with *C. auris* colonisation and infection.

Conclusion

Our review highlights that, despite relevant findings on factors influencing *C. auris* colonisation and infection, substantial gaps remain in the evidence supporting screening practices. Most studies were conducted reactively, in outbreak settings, and lack systematic protocols. Given these limitations, screening guidelines are likely to be more successful if grounded in medical theory and yeast microbiology rather than relying solely on current studies. Rigorous, well-designed research is urgently needed to inform future *C. auris* screening and control efforts.

Background

Candida auris is a fungal pathogen that rapidly emerged globally. Initially isolated from the external ear canal of a Japanese patient in 2009 and retrospectively identified in South Korean blood samples dating back to 1996 (2-4). In the 2019 Antibiotic Resistance Threat Report by the U.S Centers for Disease Control and Prevention (CDC), *C. auris* was listed as an urgent threat and in 2022 the World Health Organization (WHO) classified it as a critical priority pathogen (5;6). The urgency communicated from these institutions stems from the rapid emergence of *C. auris*, its resistance to antifungal treatments, and its ability to cause outbreaks and severe, often fatal, infections in hospitalised patients, particularly those with underlying conditions(6).

C. auris can colonise and persist on the skin for longer periods and exhibits extended environmental survival on inanimate surfaces within healthcare settings. These characteristics contribute to transmission events and protracted outbreaks in healthcare settings, especially in intensive care units (ICU) (2;7). Furthermore, *C. auris* is capable of biofilm formation and can resist routine cleaning (8-10). Four major clades – South Asian (I), East Asian (II), South African (III) and South American (IV) – have accounted for the global spread of the pathogen (2). Clade I is the most prevalent. Genetic studies using whole genome sequencing (WGS) suggest a simultaneous emergence of these clades, which may have played a part in causing the rapid global spread. Recently one more clade; Iranian (V) has been identified, and a sixth clade is under investigation in Singapore (VI) (2;11). Variations in drug resistance and virulence, the ability to cause invasive disease, have been observed among different *C. auris* clades (2).

Since its discovery, *C. auris* has been reported in over 60 countries across six continents (8;12). The first identified case of *C. auris* in Europe, belonging to clade I, was imported from India in 2007 (13). Since then, several European countries have witnessed a significant increase in cases, causing outbreaks, especially in ICU (2). Between 2013 and 2021, 15 EU/EEA countries identified a total of 1812 cases (10). The first European outbreak occurred in 2015-2016 in an ICU in the United Kingdom with a total of 70 cases (14). Between 2019 and 2021, five European countries (Denmark, France, Germany, Greece and Italy) reported a total of 14 *C. auris* outbreaks, encompassing 327 cases (15).

As several national and local institutions are moving to either recommend or mandate screening against *C. auris* in their prevention effort, e.g., in guideline documents, there is a need to assess the evidence on some key factors to consider when developing screening strategies. These key factors are the associated factors of colonisation/infection, duration of colonisation, possible colonisation sites and risk of secondary cases. This systematic review aimed to comprehensively search for and narratively summarise the current literature on these key factors.

Methods

Search and study selection

We systematically searched four databases on 2 February 2024: Embase, Cochrane Database of Systematic Reviews/ Cochrane Central Register of Controlled Trials, Web of Science, and Epistemonikos. The searches were complemented with hand-searches for grey literature and existing guidelines. The searches were performed by a specialist librarian (RAT), after internal peer review by another librarian. Search terms for *C. auris* combined with synonyms with appropriate truncations and abbreviations were used for searching title, abstract, author keywords, and controlled vocabulary. The search strategy was tailored to each database's search interface. The search strategy can be found in Appendix 1. Deduplication was performed in EndNote 20 (16).

Three researchers (LEØ, RR, MM) piloted the inclusion and exclusion criteria on an initial sample of 50 abstracts to identify relevant inclusion criteria (Table 1). Subsequently, two researchers (LEØ, MM) screened the remaining studies. We used EPPI-Reviewer 6 for screening (17). Disagreements or uncertainties were addressed through discussion with a third researcher (RR). Two researchers (LEØ, MM) performed single full-text screening. Inclusion conflicts were resolved through discussion between the researchers.

Data extraction and analysis

Two researchers (LEØ, MM) extracted relevant data on three of the main outcomes: duration of colonisation, risk of secondary cases, and colonisation sites. One researcher (ASD) extracted data regarding associated factors. For all studies we extracted information on the country of study, setting, participants, follow-up period, and reported outcomes. Additionally, depending on the specific outcome of interest, we also extracted relevant data and statistics (e.g., odds ratio).

For each outcome we created tables summarising the relevant studies. Each table lists the studies reporting on the specific outcomes, along with the variables relevant for the outcome. There was a limited number of studies featuring control groups that investigated associated factors or participant characteristics, and only these were included in the interpreting and assessing factors associated with infection or colonisation. We narratively summarised each of the systematic reviews separately, and then findings for each outcome from the primary studies, where similar studies or studies reporting on comparable aspects to each outcome were grouped together for easier comparison. To assist in the synthesis and discussion we employed a set of definitions (Table 2). Neither a meta-analysis or a critical appraisal/quality assessment of the studies was performed due to the qualitative heterogeneity in the primary studies – both in terms of design and context. However, we highlighted methodological shortcomings throughout the text to provide context for our findings.

Results

Included studies

We identified 2,371 unique references after deduplication (Figure 1). Title and abstract screening identified 291 relevant studies.

On full-text screening we included 117 studies. Studies were conducted in Asia (n=40), North America (n=29), Europe (n=21), South America (n=12), Africa (n=8), and Oceania (n=1). Six studies encompassed data from multiple countries. Publication dates ranged from 2016 to 2024. We included 114 observational studies, and three of these were systematic reviews. Reported outcomes were duration of colonisation (n=8), risk of secondary cases (n=15), colonisation sites (n=29), and associated factors/participant characteristics (n=112). Only a limited number of studies that investigated associated factors or participant characteristics featured control groups (n=14). An overview of the included studies is provided in Table 3.

Systematic reviews

We identified three systematic reviews (7;18;19). Two reviews, by Vaseghi et al. and Vinayagamoorthy et al. reviewed the literature on *C. auris* related to COVID-19 patients. The third review by Sekyere reviewed updates on *C. auris* in 2018.

Vaseghi et al. has carried out a systematic overview of the literature of COVID-19 associated *C. auris* infections (18). The relevant results of the review were underlying medical conditions and medical device interventions as risk factors/predictors for *C. auris*, reflecting a highly selected group of patients. The most frequent predisposing factors were found to be hypertension (15/996; 1.5%), followed by diabetes mellitus (12/996; 1.2%) and cardiovascular diseases (7/996; 0.7%). Central venous catheter (CVC) was found to be the most applied medical device (prevalence rate: 96%). The estimated odds ratios indicated that COVID-19 patients who received a CVC had 2.6 times the odds of catching *C. auris* co-infection.

Vinayagamoorthy et al. conducted a systematic review examining the prevalence, risk factors, treatment, and outcome of *C. auris* infections in COVID-19 patients (19). They found that hypertension (17/35; 48.6%) and diabetes mellitus (12/35; 34.3%) were the most prevalent underlying conditions among COVID-19-patients with *C. auris* candidemia. Regarding risk factors, the review identified broad-spectrum antibiotic usage (35/35; 100%), ICU stay (33/35; 94.3%), mechanical ventilation (24/35; 86.6%) and CVC (28/35; 80%) were most frequently found. However, the authors found no significant differences in underlying disease and risk factors among *C. auris* non-candidemia/colonisation and *C. auris* candidemia cases.

Sekyere authored a systematic review in 2018, an update on different aspects of *C. auris*; molecular epidemiology, virulence and pathogenicity, resistance, crude mortality rates and infection prevention and control (7). The review describes and summarises findings from primary literature up to July 2017 but does not include any assessment of the risk of bias of the included studies and does not collate data or make interpretations regarding our outcomes of interest.

Primary studies

Duration of *C. auris* colonisation

We included eight studies reporting on duration of *C. auris* colonisation (Table 4). The studies were from USA (n=5), UK (n=1), India (n=1), and South Korea (n=1), and were published between 2016 and 2023. The combined study population consisted of adult patients with a median age ranging from 51-72 years. Included participants were hospitalised in different types of hospitals and often with several underlying medical conditions. The assessment on colonisation duration were mainly done within the healthcare settings, only one study followed the patients after discharge to the community (20).

The number of positive *C. auris* patients followed up with one or several screening tests varied from three to 75 patients among the studies. In some studies patients were lost to follow-up so the final number of patients in the included studies were three to 60 patients. Two of the studies followed less than ten patients (21;22). Follow-up time and number of screening tests taken of each patient varied between studies and among patients. Most studies followed some of the patients for at least 6 months, although follow-up time varied from a few days to 20 months.

Seven studies looked at the length of colonisation among patients in hospitals (14;21-26). The duration of colonisation varied between studies and patients, ranging from days to years, with long-term colonisation of a few months to over a year being commonly observed. Eyre et al. followed 60 patients for up to 6 months with weekly screening and at discharge. They found the median duration of colonisation to be 2-3 months. Clearance was defined as two or three consecutive negative cultures (14). Pacilli et al. followed 51 patients with screening every week

and found the duration of colonisation to be up to 10 months in some patients, but were unable to ascertain their definition of colonisation clearance (25). Adams et al. took follow-up samples of 38 patients taken at least one week apart and found a duration of colonisation ranging from days and up to >200 days (23).

Bergeron et al. looked at colonisation among patients after discharge to the community with a follow-up time ranging from 0 to 20 months, taking samples every three months. They found that 62% of the patients did not remain colonised in the follow-up cultures after discharge to the community. They defined 'serial negative' as two consecutive negative cultures. The median time for patients to become 'serial negative' was 8.6 months (interquartile range: 5.7-10.8) (20).

Numerous studies have demonstrated that patients can experience one or more negative screening result, before subsequently receiving a positive one (24-26). Pacilli et al. observed that in 55% of the patients with one or more negative screenings, a later sample became positive (25). In two separate studies, Arenas et al. and Bergeron et al. found that 34% and 25% of colonised patients respectively received a positive result after at least one negative result.

Three studies lacked a pre-defined, standardized interval for the follow-up screening (21-23). Although the other studies had defined screening intervals, the time frames varied among the patients involved. Colonisation clearance was not clearly defined in five of the studies (21;22;24-26). All the studies, except one, obtained follow-up samples at various sites, primarily the groin and axilla. The exception conducted screenings only from external ear discharge (22).

Risk of secondary cases

We included 15 studies that reported on the risk of secondary cases of *C. auris* (Table 5). These were conducted in Australia, Canada, Columbia, India, Italy, Saudi Arabia, Republic of Korea, Spain, UK and USA. Studies were published between 2017 and 2024. The studies reported on outbreak investigations and surveillance screening. The study settings were hospitals, mainly ICUs, and two studies in nursing facilities with ventilator-capability (27;28). Index *C. auris* cases ranged from one to 50 adults, depending on study design, number of hospitals included, and the study period. The total number of screened persons ranged from 17 to 960. Screened persons were mainly patients, with seven studies including healthcare workers (HCWs) and/or family members and visitors.

Various studies identified an inconsistent range of secondary cases, from as few as one case to as many as 140. While seven studies reported more than 50 secondary cases, three studies observed zero to three secondary cases, despite screening between 180 and 600 patients (29). Secondary cases were mainly reported in patients.

Four studies detected positive cases among HCWs, identifying between one and four positive individuals from a pool of six to 258 screened persons (30-33). Schelenz et al. found one positive HCW out of 258 screened in an outbreak where HCW had been caring for a positive patient colonised with *C. auris* (33). Escandon et al. found two HCWs that had positive hand/groin samples out of six screened (31). The two last studies found one and four positive HCWs (hands), respectively, when performing Point-prevalence surveys (PPS) in the units where there had been a positive case (30;32). One out of two studies screening family members found one positive family-member (23).

Not all studies distinguished whether the secondary cases resulted from direct or indirect exposure. Some studies clearly defined direct exposure and contact tracing, while in several others, the results were presented alongside the number of detections of *C. auris* in broad surveillance surveys. In a comprehensive approach, four studies carried out contact tracing, screening patients and HCWs who had known exposure to a confirmed case. This exposure

included scenarios such as direct contact, overlapping stays in the ICU, or other connections within the same ward (31;34-36). These studies screened 17 to 960 exposed persons and found one to eleven positive cases. Lee et al. concluded that the proportion of secondary cases of *C. auris* from close contacts was relatively high (25%) (32). However, in a study by Rossow et al. they did not find an association between *C. auris* colonisation and residing in a room with a positive case (27).

Six studies reported results from PPS or surveillance screening (14;25;27;29;30;37). The authors reported screening of 101 to 900 persons and found 0 to 140 positives. Four studies did a combination of PPS, surveillance, and contact tracing (23;32;33;38). They screened 258 to 718 persons and found 1 to 62 positive cases. We were not able to find a denominator in three of the studies, and several studies had defined up to 50 primary cases in different hospitals and did surveillance screening on the wards where the cases were admitted (23;31;34). Six out of 15 studies did WGS, confirming genetically distinct clusters.

Associated factors of *C. auris* infection or colonisation

A total of 112 studies reported on factors associated with colonisation or infection with *C. auris* (Table 3). These studies were conducted in 30 different countries from all inhabited continents, whereas two studies included more than one country and two did not specify country of sampling. Most studies primarily focused on detailing patients' medical profiles or conditions without a control group and described critically ill patient populations or those with severe underlying medical conditions. The predominant settings were ICUs.

Fourteen of the incorporated articles include a control group and investigate factors associated with either colonisation or infection with *C. auris* (Table 6) (27;39-51). The studies were predominantly small-scale ($n < 100$), based on data from outbreak investigations in heterogeneous populations. These investigations commonly employed bivariable screening to identify potential explanatory covariates, which were subsequently included in multivariable regression models using stepwise selection techniques without theoretical models informing covariate selection.

Two studies examined the incidence of *C. auris* in relation to international travel (52). A case-series by Hamprecht et al. reported on the occurrence of *C. auris* in seven patients in Germany 2015-2017, of which six patients had previously been treated in healthcare centres in the Middle East, Asia, Africa, or the United States (53). In a study of healthy travellers by Turbett et al. (52), a total of 94 individuals were screened (pre-travel and post-travel) using self-collected axillary-inguinal groin swabs for the presence of *C. auris*. Travel destinations included all major regions of the world, with eastern Africa (31/94, 33%) as the most common region visited, and the predominant reason for travel was leisure (71/94, 76%). No *C. auris* was isolated from the samples. Few travellers (5%) reported providing or receiving medical care while traveling, indicating a low incidence of contact with healthcare systems during travel.

The majority of studies compared outcomes between patients with *C. auris* and those with other types of candidaemia. The research by van Schalkwyk et al. stands out due to its large scale, encompassing a national survey conducted over two years in an endemic region (51). This study evaluated a predefined hypothesis, among others, demonstrating a substantial increase in *C. auris* candidaemia. Rossow et al. concentrated their research on individuals colonized by *C. auris*, comparing them to non-colonized controls from identical exposed cohorts. They identified factors associated with colonization, including the use of specific invasive medical equipment, recent use of antimicrobials, recent hospitalizations, and colonization with other Multi-Drug Resistant Organisms (MDROs). (27)

Colonisation sites

Twenty-nine studies reported on colonisation sites for *C. auris* and their positivity rates based on predetermined sampling materials (Table 7). The studies were conducted in 11 different countries, most of them in the USA (N=12), in the period 2013 to 2023. Armstrong et al. and Escandon et al. reported on the same materials sampled from patients, but not from HCWs (31;54). The studies varied in designs and populations, and revealed diverse patterns, prevalence, and positive sites for the detection of *C. auris*, hence the findings vary considerably.

The axillae and groin regions were predominantly used for screening sites and emerged as the primary sites of colonisation. Positivity rates for screening sites in *C. auris* positive patients ranged from 36% to 100% for combined sampling of axilla and groin, 11.3% to 50% for axillae alone and 17.4% to 75% for groin separately (26;30;55). Colonisation of the nares was also observed, with positivity rates ranging from 17% to 64% (23;26;55-58). Adams et al., found that by combining axillae, groin and nares the positivity rates increased (23), while Rowlands et al. and Southwick et al. reported lower positivity rates when axillae, groin and nares were combined as screening site than axillae and groin alone (57;58). Piatti et al. used swab specimens from the skin of axilla, groin, auricular area and inframammary sulcus as screening sites and found a 27.3% (105/384) prevalence of skin colonisation of admission screenings in Italy (59). Additionally, positive cases were detected in other body sites such as rectum, oral cavity, respiratory tract, ear, urine, and wounds (55;60). Three studies reported separate results for the colonisation of *C. auris* on the hands of HCWs (30-32). Biswal et al. found that out of 145 screened HCWs, four (2.8%) tested positive. Whether the samples were reported as being taken bilaterally, in a composite swab, or individually varied between studies.

Studies employing screening methods where the pre-test probability of a positive screening test is higher (contact tracing, PPS) also consistently identified the axillae and groin as primary sites for *C. auris* colonisation. Southwick et al. found that among 1668 patients, 144 (7%) were positive for *C. auris* colonisation, and positive results were predominantly observed in composite samples from the axilla and groin (81%), followed by the nares (64%). Zhu et al. conducted an outbreak investigation in 2020 and included 11,035 samples of which 931 (8.4%) were positive for *C. auris*. The findings revealed that 80% (178/222) of positive samples were positive for *C. auris* from the axilla-groin (tested with a composite swab) and 58% (125/215) in the nares. They also found that if the nares are colonised, they harbour a relatively higher amount of *C. auris* than does the axilla or groin. Notably, when considering the combination of axillae-groin-nares, the positivity rate approached 100%.

In only three studies several different body sites in patients with confirmed *C. auris* infection were screened (54;55;59). Armstrong et al. included five positive *C. auris* patients and screened each patient 10-11 times at different sites. There was great variation in which of the body sites *C. auris* was detected in screening. Zhu et al. reported on 298 microbiological samples where individuals had an infection, but the results reporting positive body sites are presented in combination with results from a surveillance survey, precluding data extraction regarding positive patients alone. Piatti et al. conducted a study using skin and rectal swabs to screen for the presence of *C. auris* on all patients admitted to at-risk units. Upon analysing patients with confirmed *C. auris* infection, the prevalence of colonization in both skin and rectal areas was found to be nearly identical.

Discussion

In general, the studied populations and participant counts varied widely across the included studies. The body of literature on *C. auris* largely comprise single-centre studies with small sample sizes and descriptive statistics. These are often outbreak reports, summaries of clinical experiences with defined clusters, or studies summarizing data from laboratory findings over a certain period. Duration of *C. auris* colonisation among hospitalised patients varied from days to years, with colonisation for months and up to a year being common. However, most patients discharged to the community did not remain positive after 12 months. Several studies demonstrated that patients could have one or more negative screening results before obtaining a positive result. Overall, the risk of secondary cases varied both in studies where patients or HCWs had direct contact with a positive *C. auris* patient and in studies where the degree of exposure varied significantly. Regarding associated factors, most studies relied on multiple, simple statistical tests of differences or associations, which make inferences uncertain, particularly when combined with small sample sizes. However, we noted that most of the studies involve a patient population with critical illnesses and many comorbidities, who were often admitted to a critical care unit, like ICU. Some invasive medical devices, recent antimicrobial use, recent hospitalisation, and colonisation with other MDROs, seemed to be consistently associated with *C. auris* colonisation or infection. The axillae and groin regions were the most common sites of *C. auris* colonisation, but also the body sites from which samples were most frequently taken.

Duration of colonisation

The absence of predefined, standardised protocols for research into colonisation duration - including set time intervals and the number of tests to conduct - coupled with the lack of unified definitions for spontaneous decolonization, complicates the interpretation of how long individuals may harbour *C. auris*. Regarding recommendations for screening, as well as other infection control measures, the critical factor will be whether people who have once been diagnosed with *C. auris* should be considered permanent carriers or whether test results can determine if infection control measures should be implemented or can be discontinued if already implemented. Based on the included studies, it appears that persistent colonisation of *C. auris* is common for up to a year, even among patients discharged to the community. Colonised patients and residents may intermittently have negative results, which is followed by a positive result. Hence, negative test results for a colonised patient should be interpreted with caution when considering whether to discontinue appropriate infection prevention and control precautions in healthcare. Such a careful approach is supported by international guidelines - CDC does not recommend routine reassessments for *C. auris* colonisation (61). An expert meeting organized by the International Society for Antimicrobial Chemotherapy in 2019 recommended maintenance of infection control measures until discharge and to flag the patient chart for at least 1 year after the first negative screening culture (62).

Risk of secondary cases

To determine the transmissibility of *C. auris*, several factors are crucial, including the microbe's inherent virulence, the susceptibility of individuals, the type and duration of contact and persistence in the environment. The studies under consideration reported numerical results on secondary cases following either direct or indirect exposure, primarily involving patients. These results potentially offer insights into the microbe's capability of spreading, irrespective of the

presence or absence of infection control measures. Several outbreaks described in the included studies revealed a high risk of transmission of *C. auris* among patients and between hospitals, especially in acute care facilities, but the number of secondary cases varied widely between studies. We could not calculate the secondary attack rate since the studies had different screening strategies, follow-up periods, and number of defined primary cases. Some studies did not report how many persons who were screened. However, as the proportion of positive cases out of screened patients were >40% in some studies, a high risk of secondary cases has been documented in outbreak settings (25;31). The highest proportion of secondary cases was found among patients. Several studies showed that a high number of patients were already colonised shortly after the outbreak was recognised, but in some situations transmission was limited to a small number of patients, and the proportion of positive cases out of those screened were <2% (29;34-36). The reason for this may be multifactorial – i.e., transmission depend on the setting, the population, when the outbreak was detected, the amount of environmental contamination, and the infection control measures implemented.

For effective screening guideline formulations, it is vital to identify those at high risk of becoming colonised or infected. The included studies used different definitions of screening, and several studies presented results from contact tracing alongside the number of detections of *C. auris* in broad surveillance surveys or screening. One should exercise caution when directly incorporating these results into decisions regarding screening recommendations. Conversely, numerous studies have reported secondary cases from screening patients who either shared a room as a positive case or occupied the neighbouring bed. This could support that an individual with a high degree of exposure is likely to have a high risk of becoming infected and may warrant their inclusion in screening protocols. Moreover, occupying the same environment as a *C. auris* case can potentially lead to colonisation or infection with the yeast. This has been corroborated by various studies that have reported secondary cases during outbreaks without any documented person-to-person transmission.

Schelenz et al. conducted a root cause analysis and discovered that the minimum duration of contact with a positive case or a contaminated environment for acquiring *C. auris* was ≥ 4 hours. However, they were unable to identify a single specific source of transmission (33). ECDC recommends prompt and robust measures if *C. auris* is detected in healthcare facilities including screening of close contacts (63). This is supported by the other identified international guidelines. CDC recommends screening patients sharing the same room, unit, or other care areas with a patient with *C. auris*.

The role of HCWs in the transmission of *C. auris* is still unclear, although the risk seems to be low. The selected studies discovered minimal positive instances among HCWs, primarily featuring yeast present on their hands, even though extensive screenings were conducted during outbreaks. Several authors have postulated that HCWs could potentially contribute in transmission chains due to transient hand contamination. However, to affirm this as a prevalent route of transmission, additional research is required.

Associated factors

When evaluating factors associated with infection or colonisation that are relevant to screening, the crucial variables are those helping us differentiate between incoming hospital patients who are at risk of being colonised and those with minimal risk. Therefore, it is not particularly

relevant, in this aspect, that studies focus on distinguishing the microbe in patients who already have invasive infections. Comparing patients with *C. auris* to those with other candidaemias limits the applicability of the findings for our purpose.

The term “risk factors” is often used by the authors of the included studies. Risk factors can either be endogenous, pertaining to the host themselves, or exogenous, related to external influences. However, it is crucial not to confuse these with endogenous and exogenous infections that occur within the healthcare. Risk factors can be general for all colonisations and infections or specific to a particular microbe.

The specific, exogenous risk factor of being exposed to *C. auris* is likely to remain the most important risk factor for acquiring *C. auris*. Exposure to the microbe is necessary for colonisation to occur. However, there have been very few studies investigating such exposure specifically, even though existing guidelines may target persons assumed to be exposed for instance through contact with healthcare system in endemic regions (64;65). We have only found one case series and one study examining the risk associated with travel and contact with healthcare abroad. The prior study found that most patients with *C. auris* had been to a healthcare institution in an endemic region, while the latter study, which screened individuals who had travelled to the endemic region, did not identify any cases (52;53). Although the foundation for inferences is sparse, the other studies align with the findings of these two studies, highlighting high-risk healthcare settings, particularly ICUs, as common sites of acquisition.

In terms of endogenous factors, prior reviews have identified correlations between *C. auris* infection with certain general factors, such as male gender along with severe underlying conditions such as immunosuppression, diabetes, and chronic kidney disease (7;66). Additionally, the presence of invasive devices and procedures is consistently cited as a risk factor (7;66;67). These general factors may be explained by our finding that most studies were conducted in critical care unit settings, as these patients are often implicated in hospital outbreaks or contract severe (and resistant) healthcare-associated infections, regardless of the specific causative agent. Some endogenous risk factors, like prior antifungal exposure, might be more specific, but it remains uncertain whether this selects for *C. auris* specifically or de-selects for other yeasts (7;66). Broad-spectrum antibiotics may also play a role by eliminating competing microbiota, thereby facilitating *C. auris* colonisation (66;67). Colonisation with other MDROs could indicate shared risk factors between these multidrug-resistant pathogens (66). Past hospitalisation may also capture the statistical association of this shared risk set, and its inclusion in models should be carefully evaluated to first determine whether it acts as a mediator or confounder in the exposure-outcome relationship. The inclusion of these and other covariates without such a consideration may result in an attenuation of effect sizes, or even lead to incorrect conclusions.

The common methodological approach included bivariable screening to identify potential risk factors, followed by multivariable regression models using stepwise selection techniques. This methodological approach may limit the validity of the identified factors due to several well-documented issues such as the multiple comparisons problem and a lack of theoretical reasoning underpinning the modelling choices (68;69). When reviewing these studies, counting how many times a factor has been found statistically significant does not provide robust inferences about their relative importance.

Colonisation sites

A low number of the incorporated studies aimed to discern the body sites where *C. auris* resides by testing various areas on infected patients. Results from these studies showed significant variation in detection sites (54;55). Many studies screened patients in the context of outbreak follow-up, either as contact tracing or PPSs, or tested patients on admission to a healthcare institution, according to pre-defined screening protocols. The studies found that the axilla and groin were the most frequent sites of colonisation in *C. auris* positive patients, but also the sample material most often examined. ECDC recommends the axilla and groin as screening sites, as well as other sites (urine, wounds, catheter exit sites, throat etc.) if clinically relevant or indicated (63) and US CDC recommends bilateral screening of axillae and groin (70). Pan American Health Organization (PAHO) recommends screening the axilla, oropharynx, nostrils, groin, urine and rectum, but if it is not feasible to collect samples from all sites, they recommend at least pooled samples from the groin and axilla (71). A literature review by the United Kingdom Health Security Agency draws attention to the study by Adams et al. where the addition of a sample from the nostril increases the probability of detection (23). Nares also showed to be a site of colonisation in several of the included studies, and the combination of sample material from the axilla, groin, and nares increased the positivity rate in two studies, but lowered it in two other studies. In other words, sampling from the axilla and groin bilaterally of patients at risk, as well as the nares, may find justification. While it might be worthwhile to evaluate the cost-effectiveness of sampling from the nares, a higher detection probability might be desired considering the significant concern over the spread of *C. auris*.

A few of the included studies also tested wounds, tracheal secretions, and catheter urine and detected *C. auris*. Invasive devices have been found to be a factor associated with colonisation, although this may only apply to critically ill patients. Furthermore, some studies contain description of screening indwelling devices when present, but whether it was tested from these locations is uncertain, and no results are reported from this sample material (33;60;64). Findings in urine are likely associated with a clinical infection, as urine normally does not contain yeast, although there are different definitions in the literature regarding whether urine as a specimen should be considered colonisation or infection depending on clinical presentations/symptoms. The studies incorporated, which include description of urine samples, do not provide detailed descriptions. The same may apply to wounds, although Zhu et al. consider wounds as a source of colonisation (55).

Strengths and limitations of this review

Our review has several strengths. First, we employed a systematic and reproducible search with a comprehensive strategy, and a thorough review of included studies. We chose to do a broad search for all articles on *C. auris* and have likely been able to identify all literature relevant to our outcomes of interest. Furthermore, findings were presented in the context of all existing studies, providing the most up to date overview yet. Finally, our systematic approach avoids some of the pitfalls and biases of purely narrative reviews without systematic searches. While a narrowing of the inclusion criteria could have addressed some of the heterogeneity issues we revealed, such an approach would perhaps exclude a significant proportion of the current literature. We opted for a narrative summary of our findings to provide the most comprehensive overview of this broad research field, as the heterogeneous nature of the included studies precluded a meta-analysis or other quantitative synthesis. A formal quality assessment was not performed, though

this limitation is somewhat mitigated by the high variability in study designs and settings. The open nature of our research question, however, introduces a risk of creating a less focused review, which may not allow for a full assessment of the strength of specific evidence. Additionally, without a quantitative synthesis, the findings lack the weighted perspective that a meta-analysis could offer in highlighting patterns across studies.

Conclusion

In our systematic review, we were able to summarise several relevant findings regarding the associated factors of colonisation/infection, the duration of colonisation, the potential for secondary transmission, and possible colonisation sites of *C. auris*. However, our primary finding was that in screening for *C. auris*, several major knowledge gaps remain. Most of the studies we reviewed described circumstances or outbreaks that arose unexpectedly, and lacked pre-developed protocols and a clear study aim that could be effectively addressed with the selected methods. The publication bias introduced by such a circumstantial body of literature must be acknowledged. If targeted screening of high-risk populations is chosen as a strategy to prevent establishment of *C. auris*, it remains unclear who should be screened, and there is no robust evidence either for or against current practices. Identifying individuals likely to have been exposed to *C. auris* remains the most critical factor in such guidelines, as highlighted also by others (66). Screening should continue to be performed in the axillae and groin, but considering additional sites like the nares could increase sensitivity, although there is conflicting evidence. Furthermore, routine screening of HCWs appears unnecessary unless there is clear evidence of direct exposure to contaminated settings. Given the lack of evidence that spontaneous decolonisation is a common occurrence among patients, it might be prudent to view exposed patients as potentially persistently colonised as a precaution.

Moving forward, the knowledge gaps we have identified herein should be addressed. There is an urgent need for primary research that methodically outlines the efficiency of current screening programs, including their sensitivity and specificity. This research should include findings from different anatomical sites and comparisons with composite swabs. To determine colonisation duration, it is crucial to register positive patients and systematically monitor them at pre-set intervals over a specified period to delineate the natural timespan of *C. auris* colonisation. Furthermore, it is crucial to map how the hospital environments act as a vector in the transmission of *C. auris*. This not only includes the surfaces of the hospital, its ventilation, water and sanitation systems, but also the surrounding nature and animals. The emergence of *C. auris* fundamentally pertains to One Health, and this multidisciplinary approach should remain the predominant for addressing *C. auris* establishment in healthcare settings. Finally, the study of factors associated with *C. auris* colonisation should focus on identifying factors able to discriminate high-risk patients that should be screened in larger cohorts that are representative of all patients in healthcare settings. In addition to factors that may be coded from the medical charts, history of travel and contact with healthcare in endemic regions should be included in such studies. It is crucial to acknowledge that the most significant "risk factor" for contracting *C. auris* is exposure to the microbe itself. Such research initiatives as mentioned here could greatly bolster our comprehension, thus aiding the formulation of more effective screening guidelines and infection control measures for *C. auris*. In the absence of these research initiatives, however, the success of *C. auris* screening is more likely if it is grounded on medical theory, current knowledge of yeast microbiology, and existing literature on screening against other similar microbes.

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Tables and figures

Table 1. Inclusion and exclusion criteria.

Inclusion criteria	Exclusion criteria
<ul style="list-style-type: none"> - Individuals tested/screened for <i>C. auris</i> - Studies reporting duration of <i>C. auris</i> colonisation - Studies reporting number of secondary cases in relation to a positive <i>C. auris</i> case - Studies reporting factors associated with <i>C. auris</i> infection or colonisation - Studies with reported screening results by body site - Systematic reviews with systematic literature search and pre-defined inclusion criteria - RCT and observational studies with total participants ≤ 5 - No limitations on year of publication - No filter on country/context for reviews and trials - Studies in English, Norwegian, Swedish, or Danish 	<ul style="list-style-type: none"> - Studies on treatment of <i>C. auris</i> - Studies on management of <i>C. auris</i> cases - Studies on laboratory methods (including sampling methods) for detecting <i>C. auris</i> - Studies investigating drug resistance in <i>C. auris</i> - Studies related to the genetics or cell biology of <i>C. auris</i> - Studies exclusively focused on environmental screening or environmental sampling during outbreaks - Studies investigating preventive measures, including screening, against postoperative wound infections - Cross-sectional studies featuring aggregated data (considered for studies on colonisation sites) - Case reports with $n \leq 5$ <i>C. auris</i> positive cases - Letters to the editor, abstracts/posters, non-peer-reviewed studies, correspondences, short communications, and comments - Studies where outcomes are not specifically reported for <i>C. auris</i>

Table 2. Definitions used in the narrative synthesis and discussion.

Term	Definition
Screening of <i>C. auris</i>	Performing a test to identify individuals at risk of <i>C. auris</i> to warrant direct preventive action.
Prevention-based screening for colonisation	Colonisation screening that is planned and conducted independently of the detection of a case in a facility, e.g. prevention-driven PPS or admission screening.
Response-based screening for colonisation	Colonisation screening that is conducted in response to detection of a case (or cases) in a facility, e.g. contact investigation (case-finding) or response-driven PPS (72;73).
Colonisation with <i>C. auris</i>	The presence of <i>C. auris</i> on or in the body of an individual without causing signs or symptoms of infection (asymptomatic). Individuals who are colonised can be a source of spread to the environment and other patients and can develop infections with the colonizing organism (73). In this review, we include intermittent carriage in our definition of colonisation.
Secondary case	A person who is diagnosed with <i>C. auris</i> after being in direct or indirect contact with a <i>C. auris</i> colonised or infected person.
Risk of secondary cases	Proportion of secondary cases (new cases among those exposed).
Positivity rate (colonisation sites)	Number of people with one or more positive screening sites divided by the total number of positive people.

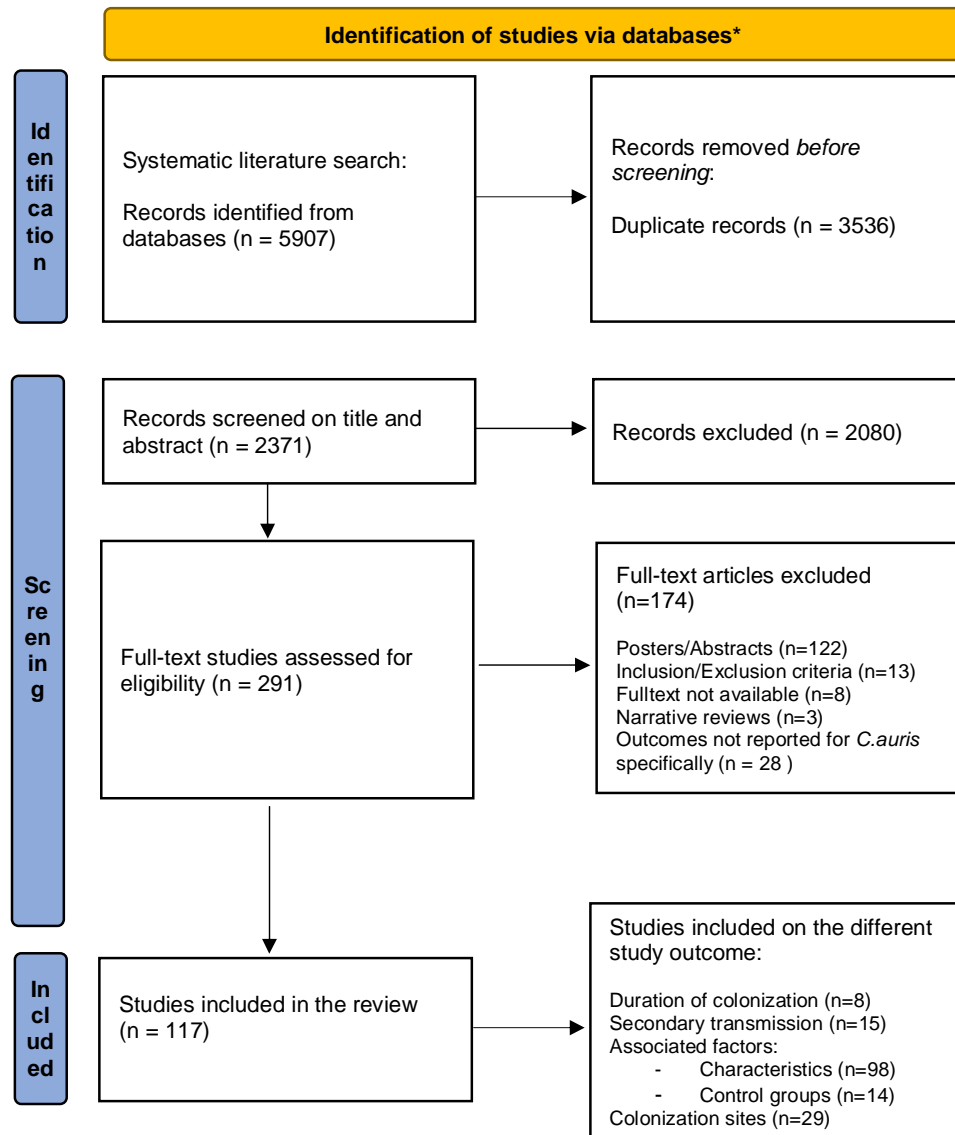


Figure 1: Flow diagram of search strategy and study inclusion. Adapted from (1). Databases include Ovid Medline® and Epub Ahead of Print, Embase, Cochrane Database of Systematic Reviews, Cochrane Central Register of Controlled Trials, Web of Science and Epistemonikos.

Table 3. Overview of included studies.

Author (Year)	Title	Country	Outcome reported
Systematic reviews			
Osei Sekyere J (2018) (7)	Candida auris: A systematic review and meta-analysis of current updates on an emerging multidrug-resistant pathogen		Associated factors (characteristics)
Vaseghi N (2022) (18)	Global prevalence and subgroup analyses of coronavirus disease (COVID-19) associated Candida auris infections (CACA): A systematic review and meta-analysis		Associated factors (characteristics)
Vinayagamoorthy K (2022) (19)	Prevalence, risk factors, treatment and outcome of multidrug resistance Candida auris infections in Coronavirus disease (COVID-19) patients: A systematic review	Most cases from USA, Mexico, India	Associated factors (characteristics)
Observational studies			
Adam RD (2019) (39)	Analysis of Candida auris fungemia at a single facility in Kenya	Kenya	Associated factors (control group)
Adams E (2018) (23)	Candida auris in Healthcare Facilities, New York, USA, 2013-2017	USA	Duration of colonisation, risk of secondary cases, colonisation site, associated factors (characteristics)
Ahmad S (2020) (74)	Candida auris in various hospitals across Kuwait and their susceptibility and molecular basis of resistance to antifungal drugs	Kuwait	Associated factors (characteristics)
Al Maani A (2019) (75)	Ongoing Challenges with Healthcare-Associated Candida auris Outbreaks in Oman	Oman	Associated factors (characteristics)
Alfouzan W (2020) (76)	Molecular Epidemiology of Candida Auris Outbreak in a Major Secondary-Care Hospital in Kuwait	Kuwait	Associated factors (characteristics)
Allaw F (2022) (40)	COVID-19 and C. auris: A Case-Control Study from a Tertiary Care Center in Lebanon	Lebanon	Associated factors (control group)
Allaw F (2021) (77)	First Candida auris Outbreak during a COVID-19 Pandemic in a Tertiary-Care Center in Lebanon	Lebanon	Associated factors (characteristics)
Almaghrabi RS (2020) (78)	Molecular characterisation and clinical outcomes of Candida auris infection: Single-centre experience in Saudi Arabia	Saudi Arabia	Associated factors (characteristics)
Al-Rashdi A (2021) (79)	Characteristics, Risk Factors, and Survival Analysis of Candida auris Cases: Results of One-Year National Surveillance Data from Oman	Oman	Associated factors (characteristics)
Alshahrani FS (2023) (60)	Description of Candida auris Occurrence in a Tertiary Health Institution in Riyadh, Saudi Arabia	Saudi Arabia	Colonisation site, associated factors (characteristics)
Alshamrani MM (2021) (34)	Management of Candida auris outbreak in a tertiary-care setting in Saudi Arabia	Saudi Arabia	Risk of secondary cases, associated factors (characteristics)
Alvarado-Socarras JL (2021) (80)	A Cluster of Neonatal Infections Caused by Candida auris at a Large Referral Center in Colombia	Colombia	Associated factors (characteristics)
Alvarez-Moreno CA (2023) (41)	The Mortality Attributable to Candidemia in C. auris Is Higher than That in Other Candida Species: Myth or Reality?	Colombia	Associated factors (control group)
Amer HA (2023) (81)	Characteristics and Mitigation Measures of Candida auris Infection: Descriptive Analysis from a Quaternary Care Hospital in Saudi Arabia, 2021-2022	Saudi Arabia	Associated factors (characteristics)
Arauz AB (2018) (82)	Isolation of Candida auris from 9 patients in Central America: Importance of accurate diagnosis and susceptibility testing	Panama	Associated factors (characteristics)
Arenas SP (2023) (24)	Persistent colonization of Candida auris among inpatients rescreened as part of a weekly surveillance program	USA	Duration of colonisation, associated factors (characteristics)
Arensman K (2020) (83)	Clinical Outcomes of Patients Treated for Candida auris Infections in a Multisite Health System, Illinois, USA	USA	Associated factors (characteristics)
Armstrong PA (2019) (54)	Hospital-Associated Multicenter Outbreak of Emerging Fungus Candida auris, Colombia, 2016	Colombia	Colonisation site, associated factors (characteristics)
Asadzadeh M (2022) (84)	Molecular characterisation of Candida auris isolates from immunocompromised patients in a tertiary-care hospital in Kuwait reveals a novel mutation in FKS1 conferring reduced susceptibility to echinocandins	Kuwait	Associated factors (characteristics)

Barantsevich NE (2019) (85)	Emergence of Candida auris in Russia	Russia	Associated factors (characteristics)
Barantsevich NE (2020) (86)	Candida auris Bloodstream Infections in Russia	Russia	Associated factors (characteristics)
Benedict K (2023) (87)	Candida auris-Associated Hospitalizations, United States, 2017-2022	USA	Associated factors (characteristics)
Bergeron G (2021) (20)	Candida auris Colonization After Discharge to a Community Setting: New York City, 2017-2019	USA	Duration of colonisation, associated factors (characteristics)
Berrio I (2021) (88)	Bloodstream Infections with Candida auris Among Children in Colombia: Clinical Characteristics and Outcomes of 34 Cases	Colombia	Associated factors (characteristics)
Bing J (2024) (89)	Candida auris-associated hospitalizations and outbreaks, China, 2018-2023	China	Associated factors (characteristics)
Biran R (2023) (90)	Nationwide Outbreak of Candida auris Infections Driven by COVID-19 Hospitalizations, Israel, 2021-2022	Israel	Associated factors (characteristics)
Biswal M (2017) (30)	Controlling a possible outbreak of Candida auris infection: lessons learnt from multiple interventions	India	Risk of secondary cases, colonisation site
Briano F (2022) (91)	Candida auris Candidemia in Critically Ill, Colonized Patients: Cumulative Incidence and Risk Factors	Italy	Colonisation site, associated factors (characteristics)
Caceres DH (2020) (42)	Case-Case Comparison of Candida auris Versus Other Candida Species Bloodstream Infections: Results of an Outbreak Investigation in Colombia	Colombia	Associated factors (control group)
Calvo B (2016) (92)	First report of Candida auris in America: Clinical and microbiological aspects of 18 episodes of candidemia	Venezuela	Associated factors (characteristics)
Chakrabarti A (2020) (93)	Characteristics, outcome and risk factors for mortality of paediatric patients with ICU-acquired candidemia in India: A multicentre prospective study	India	Associated factors (characteristics)
Chandramati J (2020) (94)	Neonatal Candida auris infection: Management and prevention strategies - A single centre experience	India	Associated factors (characteristics)
Chibabhai V (2022) (95)	Incidence of candidemia and prevalence of azole-resistant candidemia at a tertiary South African hospital - A retrospective laboratory analysis 2016-2020	South Africa	Associated factors (characteristics)
Chow NA (2018) (96)	Multiple introductions and subsequent transmission of multidrug-resistant Candida auris in the USA: a molecular epidemiological survey	USA	Colonisation site, associated factors (characteristics)
Chowdhary A (2020) (97)	Multidrug-Resistant Candida auris Infections in Critically Ill Coronavirus Disease Patients, India, April-July 2020	India	Associated factors (characteristics)
Corcione S (2022) (98)	First Cases of Candida auris in a Referral Intensive Care Unit in Piedmont Region, Italy	Italy	Colonisation site, associated factors (characteristics)
de Melo CC (2023) (99)	Colonized patients by Candida auris: Third and largest outbreak in Brazil and impact of biofilm formation	Brazil	Colonisation site, associated factors (characteristics)
de St Maurice A (2023) (100)	Clinical, microbiological, and genomic characteristics of clade-III Candida auris colonization and infection in southern California, 2019-2022	USA	Associated factors (characteristics)
Di Pilato V (2021) (101)	Molecular Epidemiological Investigation of a Nosocomial Cluster of C. auris: Evidence of Recent Emergence in Italy and Ease of Transmission during the COVID-19 Pandemic	Italy	Risk of secondary cases
Eckbo EJ (2021) (35)	First reported outbreak of the emerging pathogen Candida auris in Canada	Canada	Risk of secondary cases, associated factors (characteristics)
Escandon P (2018) (102)	Notes from the Field: Surveillance for Candida auris - Colombia, September 2016-May 2017	Colombia	Colonisation site, associated factors (characteristics)
Escandon P (2022) (103)	Laboratory-based surveillance of Candida auris in Colombia, 2016-2020	Colombia	Associated factors (characteristics)
Escandon P (2019) (31)	Molecular Epidemiology of Candida auris in Colombia Reveals a Highly Related, Countrywide Colonization with Regional Patterns in Amphotericin B Resistance	Colombia	Risk of secondary cases, associated factors (characteristics)
Eyre DW (2018) (14)	A Candida auris Outbreak and Its Control in an Intensive Care Setting	UK	Duration of colonisation, risk of secondary cases, colonisation site, associated factors (characteristics)
Farooqi JQ (2020) (43)	Outbreak investigation of Candida auris at a tertiary care hospital in Karachi, Pakistan	Pakistan	Associated factors (control group)
Garcia-Bustos V (2020) (104)	A clinical predictive model of candidaemia by Candida auris in previously colonized critically ill patients	Spain	Colonisation site, associated factors (characteristics)
Garcia-Jeldes HF (2020) (105)	Prevalence of Candida auris in Canadian acute care hospitals among at-risk patients, 2018	Canada	Associated factors (characteristics)

Gómez CF (2021) (106)	Analysis of Candida auris candidemia cases in an Intensive Care Unit of a tertiary hospital	Spain	Associated factors (characteristics)
Goulart MA (2023) (107)	Identification and infection control response to Candida auris at an academic level I trauma center	USA	Colonisation site, associated factors (characteristics)
Govender NP (2018) (108)	Candida auris in South Africa, 2012-2016	South Africa	Associated factors (characteristics)
Hamprecht A (2019) (53)	Candida auris in Germany and Previous Exposure to Foreign Healthcare	Germany	Associated factors (characteristics)
Hanson BM (2021) (109)	Candida auris Invasive Infections during a COVID-19 Case Surge	USA	Associated factors (characteristics)
Jung J (2020) (22)	Candida auris colonization or infection of the ear: A single-center study in South Korea from 2016 to 2018	South Korea	Duration of colonisation, associated factors (characteristics)
Kaki R (2023) (110)	Risk factors and mortality of the newly emerging Candida auris in a university hospital in Saudi Arabia	Saudi Arabia	Associated factors (characteristics)
Kekana D (2023) (111)	Candida auris Clinical Isolates Associated with Outbreak in Neonatal Unit of Tertiary Academic Hospital, South Africa	South Africa	Associated factors (characteristics)
Khan Z (2018) (112)	Invasive Candida auris infections in Kuwait hospitals: epidemiology, antifungal treatment and outcome	Kuwait	Associated factors (characteristics)
Koleri J (2023) (113)	Candida auris Blood stream infection- a descriptive study from Qatar	Qatar	Associated factors (characteristics)
Lee EH (2024) (32)	Intrahospital transmission and infection control of Candida auris originating from a severely infected COVID-19 patient transferred abroad	South Korea	Risk of secondary cases, colonisation site, associated factors (characteristics)
Leonhard SE (2024) (64)	Proposal for a screening protocol for Candida auris colonization	Netherlands	Colonisation site, associated factors (characteristics)
Lockhart SR (2017) (114)	Simultaneous Emergence of Multidrug-Resistant Candida auris on 3 Continents Confirmed by Whole-Genome Sequencing and Epidemiological Analyses	Pakistan, India, Venezuela, South Africa	Associated factors (characteristics)
Magnasco L (2021) (115)	Spread of Carbapenem-Resistant Gram-Negatives and Candida auris during the COVID-19 Pandemic in Critically Ill Patients: One Step Back in Antimicrobial Stewardship?	Italy	Associated factors (characteristics)
Magnasco L (2023) (116)	Frequency of Detection of Candida auris Colonization Outside a Highly Endemic Setting: What Is the Optimal Strategy for Screening of Carriage?	Italy	Associated factors (characteristics)
Magobo R (2020) (117)	Multilocus sequence typing of azole-resistant Candida auris strains, South Africa	South Africa	Associated factors (characteristics)
McDougal AN (2023) (38)	A cluster investigation of Candida auris among hospitalized incarcerated patients	USA	Risk of secondary cases, colonisation site, associated factors (characteristics)
McPherson TD (2020) (118)	Notes from the Field: Candida auris and Carbapenemase-Producing Organism Prevalence in a Pediatric Hospital Providing Long-Term Transitional Care - Chicago, Illinois, 2019	USA	Colonisation site, Risk factors (characteristics)
Mohsin J (2020) (119)	A Cluster of Candida auris Blood Stream Infections in a Tertiary Care Hospital in Oman from 2016 to 2019	Oman	Associated factors (characteristics)
Moin S (2021) (44)	C. auris and non-C. auris candidemia in hospitalized adult and pediatric COVID-19 patients; single center data from Pakistan	Pakistan	Associated factors (control group)
Morales-Lopez SE (2017) (120)	Invasive Infections with Multidrug-Resistant Yeast Candida auris, Colombia	Colombia	Associated factors (characteristics)
Mulet Bayona JV (2023) (121)	Candida auris from colonisation to candidemia: A four-year study	Spain	Associated factors (characteristics)
Mulet Bayona JV (2020) (122)	Characteristics and Management of Candidaemia Episodes in an Established Candida auris Outbreak	Spain	Colonisation site, associated factors (characteristics)
Munshi A (2024) (123)	Risk factors, antifungal susceptibility, complications, and outcome of Candida auris bloodstream infection in a tertiary care center in the western region of Saudi Arabia	Saudi Arabia	Associated factors (characteristics)
Nobrega de Almeida J (2021) (124)	Axillary Digital Thermometers uplifted a multidrug-susceptible Candida auris outbreak among COVID-19 patients in Brazil	Brazil	Associated factors (characteristics)
Ortiz-Roa C (2023) (125)	Mortality Caused by Candida auris Bloodstream Infections in Comparison with Other Candida Species, a Multicentre Retrospective Cohort	Colombia	Associated factors (characteristics)
Pacilli M (2020) (25)	Regional Emergence of Candida auris in Chicago and Lessons Learned From Intensive Follow-up at 1 Ventilator-Capable Skilled Nursing Facility	USA	Duration of colonisation, transmission, associated factors (characteristics)
Pandya N (2021) (126)	International Multicentre Study of Candida auris Infections	India, Oman, Turkey,	Associated factors (characteristics)

		USA, Pakistan	
Parak A (2022) (45)	Clinical and laboratory features of patients with Candida auris cultures, compared to other Candida, at a South African Hospital	South Africa	Associated factors (control group)
Park JY (2019) (127)	Management of Patients with Candida auris Fungemia at Community Hospital, Brooklyn, New York, USA, 2016-2018 ¹	USA	Associated factors (characteristics)
Peng Y (2024) (128)	First report of Candida auris in Guangdong, China: clinical and microbiological characteristics of 7 episodes of candidemia	China	Associated factors (characteristics)
Piatti G (2022) (59)	Colonization by Candida auris in critically ill patients: role of cutaneous and rectal localization during an outbreak	Italy	Colonisation site, associated factors (characteristics)
Prestel C (2021) (129)	Candida auris Outbreak in a COVID-19 Specialty Care Unit - Florida, July-August 2020	USA	Associated factors (characteristics)
Proctor DM (2021) (56)	Integrated genomic, epidemiologic investigation of Candida auris skin colonization in a skilled nursing facility	USA	Colonisation site, associated factors (characteristics)
Rosow J (2021) (27)	Factors Associated with Candida auris Colonization and Transmission in Skilled Nursing Facilities With Ventilator Units, New York, 2016-2018	USA	Risk of secondary cases, associated factors (control group)
Rowlands J (2023) (57)	Candida auris admission screening pilot in select units of New York City health care facilities, 2017-2019	USA	Colonisation site, associated factors (characteristics)
Ruiz-Gaitan A (2019) (46)	Detection and treatment of Candida auris in an outbreak situation: risk factors for developing colonization and candidemia by this new species in critically ill patients	Spain	Associated factors (control group)
Ruiz-Gaitan A (2018) (37)	An outbreak due to Candida auris with prolonged colonisation and candidaemia in a tertiary care European hospital	Spain	Colonisation site, secondary transmission, associated factors (characteristics)
Sathyapalan DT (2021) (130)	Evaluating the measures taken to contain a Candida auris outbreak in a tertiary care hospital in South India: an outbreak investigational study	India	Associated factors (characteristics)
Sayeed MA (2019) (131)	Clinical spectrum and factors impacting outcome of Candida auris: a single center study from Pakistan	Pakistan	Associated factors (characteristics)
Sayeed MA (2020) (47)	Comparison of risk factors and outcomes of Candida auris candidemia with non-Candida auris candidemia: A retrospective study from Pakistan	Pakistan	Associated factors (control group)
Schelenz S (2016) (33)	First hospital outbreak of the globally emerging Candida auris in a European hospital	UK	Risk of secondary cases, colonisation site
Sharp A (2021) (132)	Screening for Candida auris in patients admitted to eight intensive care units in England, 2017 to 2018	UK	Colonisation site
Shastri PS (2020) (48)	Candida auris candidaemia in an intensive care unit - Prospective observational study to evaluate epidemiology, risk factors, and outcome	India	Associated factors (control group)
Shaukat A (2021) (133)	Experience of treating Candida auris cases at a general hospital in the state of Qatar	Qatar	Associated factors (characteristics)
Simon SP (2023) (49)	Comparative Outcomes of Candida auris Bloodstream Infections: A Multicenter Retrospective Case-Control Study	USA	Associated factors (control group)
Southwick K (2022) (58)	A description of the first Candida auris-colonized individuals in New York State, 2016-2017	USA	Colonisation site, associated factors (characteristics)
Stanciu (2023) (134)	First report of Candida auris in Romania: clinical and molecular aspects	Romania	Associated factors (characteristics)
Sticchi C (2023) (135)	Increasing Number of Cases Due to Candida auris in North Italy, July 2019-December 2022	Italy	Associated factors (characteristics)
Taori SK (2019) (50)	Candida auris outbreak: Mortality, interventions and cost of sustaining control	UK	Associated factors (control group)
Taori SK (2022) (136)	First experience of implementing Candida auris real-time PCR for surveillance in the UK: detection of multiple introductions with two international clades and improved patient outcomes	UK	Associated factors (characteristics)
Thomsen J (2023) (137)	Emergence of highly resistant Candida auris in the United Arab Emirates: a retrospective analysis of evolving national trends	United Arab Emirates	Associated factors (characteristics)
Tian S (2018) (138)	First cases and risk factors of super yeast Candida auris infection or colonization from Shenyang, China	China	Associated factors (characteristics)
Townsend JO (2021) (29)	Identification of Candida auris in a foreign repatriated patient to Ontario, Canada and infection control strategies to prevent transmission	Canada	Secondary transmission, colonisation site

Tsay S (2017) (139)	Notes from the Field: Ongoing Transmission of Candida auris in Health Care Facilities - United States, June 2016-May 2017	USA	Colonisation site, associated factors (characteristics)
Turbett IS (2022) (52)	Evaluation of Candida auris acquisition in US international travellers using a culture-based screening protocol 1	Africa, Asia, USA, Europe	Colonisation site, associated factors (characteristics)
Umamaheshwari S (2021) (140)	Clinical profile, antifungal susceptibility, and molecular characterization of Candida auris isolated from patients in a South Indian surgical ICU	India	Risk factors (characteristics)
Vallabhaneni S (2016) (21)	Investigation of the First Seven Reported Cases of Candida auris, a Globally Emerging Invasive, Multidrug-Resistant Fungus-United States, May 2013-August 2016	USA	Duration of colonisation, colonisation site, associated factors (characteristics)
van Schalkwyk E (2019) (51)	Epidemiologic Shift in Candidemia Driven by Candida auris, South Africa, 2016-2017	South Africa	Associated factors (control group)
Villanueva-Lozano H (2021) (141)	Outbreak of Candida auris infection in a COVID-19 hospital in Mexico	Mexico	Associated factors (characteristics)
Vu CA (2022) (142)	Challenges and opportunities in stewardship among solid organ transplant recipients with Candida auris bloodstream infections	USA	Associated factors (characteristics)
Walits E (2023) (143)	Outcome of Candida auris contact investigations conducted in a 6 month period at a New York City hospital	USA	Associated factors (characteristics)
Waters A (2023) (144)	Investigation of a Candida auris outbreak in a skilled nursing facility - Virginia, United States, October 2020-June 2021	USA	Associated factors (characteristics)
Worth L J (2020) (36)	Candida auris in an Australian health care facility: importance of screening high risk patients	Australia	Secondary transmission, associated factors (characteristics)
Yadav A (2021) (26)	Colonisation and Transmission Dynamics of Candida auris among Chronic Respiratory Diseases Patients Hospitalised in a Chest Hospital, Delhi, India: A Comparative Analysis of Whole Genome Sequencing and Microsatellite Typing	India	Duration of colonisation, colonisation site, associated factors (characteristics)
Zerrouki H (2022) (145)	Emergence of Candida auris in intensive care units in Algeria	Algeria	Associated factors (characteristics)
Zhu Y (2020) (55)	Laboratory Analysis of an Outbreak of Candida auris in New York from 2016 to 2018: Impact and Lessons Learned	USA	Colonisation site, associated factors (characteristics)

Table 4. Overview of characteristics and findings from studies on the duration of *C. auris*-colonisation.

Author (Year)	Country	Study period	Setting	Follow up cohort (N)	Loss to follow up (N)	Age of cohort Median years (IQR)	Follow up time ^a	Screening site	Screening interval	Clearance defined	Duration of colonisation
Adams (2018)	USA	2013 - 2017	Hospitals	38	2	72 (21 – 96)	0 - >250 days	A, G, N, R, U, W	No standardized interval	2 negative cultures taken >1 week apart	Days – >200 days
Arenas (2023)	USA	2021 - 2022	Hospital	50	–	68 (61 – 78)	2 – 33 weeks	A, G	Twice weekly	Not defined	Few days – 33 weeks
Bergeron (2021)	USA	2017 - 2019	Community	75	30	63 (51 – 70.5)	0 – 20+ months	A, G	Every three months ^b	2 negative PCR/fungal cultures taken >1 week apart	Days – 12 months ^c
Eyre (2018)	UK	2015 - 2017	Hospitals	70	10	52 (42 – 64)	6 months	A, G, N, U, W, other	Weekly and on discharge	2 – 3 negative screening	2 – 3 months ^d
Jung (2020)	South-Korea	2016 - 2018	Hospitals	24	17	56 (43 – 65)	1 – 16 months	E	No standardized interval	Not defined	1 – 11 months ^e
Pacilli (2020)	USA	2016 - 2018	Acute/long-term facilities	51	–	63 (18 – 94)	1 – 10 months	A, I	Median 35 days (28 – 84 days)	Not defined	Up to 10 months
Vallabhaneni (2016)	USA	2013 - 2016	Hospitals	3	–	Not defined	Not defined	A, G, N, R	No standardized interval	Not defined	1 – 3 months
Yadav (2021)	India	2019 - 2020	Hospital	12	–	51	10 – 150 days	A, G, N, E	Every week	Not defined	10 – 60 days

A, axilla; G, groin; N, nasal; R, rectum; U, urine; W, wound, I, inguinal; Other, tracheostomy; E, ear; IQR, Interquartile range.

^aFrom first positive test; ^bVaried by patients; ^cMedian time for patients to be serial negative was 8.6 months (IQR: 5.7 – 10.8). Approx. two thirds (62%) of patients colonised with *C. auris* and discharged to a community setting no longer have detectable *C. auris* colonisation; ^dMedian duration of colonisation among patients was 61 days when two consecutive negative screening results were used to define clearance of colonisation and 82 days when three consecutive negative results were used; ^eSeven patients had follow-up culture results. Two patients had positive culture at 8 months after first isolation and one patient at 11 months.

Table 5. Overview of characteristics and findings of studies on secondary transmission of *C. auris*.

Author (Year)	Country	Study period	Setting	Index cases (N) ¹	Type of screening	Screened (N)	Persons screened	Secondary cases (N)	Description secondary cases (N)	WGS	Description of screening/PPS
Adams (2018)	USA	2013 - 2017	Hospitals, LTCF	51	CT, PPS*	580	Patients (572), HCW (4), F (4)	62	Patients (61) F (1)	No	Screening of patients in the same room as positive case in the 90 days before the diagnosis. PPS of facility contacts.
Alshamrani (2021)	Saudi-Arabia	2018 - 2019	Hospital	23	CT	960	Patients (253), HCW (707)	11	Patients	No	Screening of HCW with direct contact with positive case or patients sharing the ward/unit.
Biswal (2017)	India	2017	Hospital (ICU)	3	PPS*	792	Patients (647), HCW (145)	140	Patients (136) HCW (4)	No	Several PPS of patients/HCW admitted/working in the same ICUs as primary cases.
Di Pilato (2021)	Italy	2019 - 2020	Hospital (ICU)	1	N/A ²	N/A	N/A	8	Patients	Yes	WGS on clinical cases; the 9 cases belonged to the same cluster.
Eckbo (2021)	Canada	2018	Hospital (ICU)	1	CT	180	Patients	3	Patients	Yes	CT of patients with overlapping ICU stay with positive case. Weekly swabs for 3 weeks. All cases clustered on WGS.
Escandon (2019)	Colombia	2015 - 2016	Hospitals	51	CT*	17	Patients (7), HWC (6), V/F (4)	7	Patients (5) HCW (2)	Yes	Screening in 4 hospitals with recent outbreaks. WGS showed a cluster in 1 hospital.
Byre (2018)	UK	2015 - 2017	Hospital (ICU)	9	PPS*	900	Patients	62	Patients	Yes	Screening on ICU admission, weekly and discharge. WGS showed a single genetic cluster.
Lee (2024)	South-Korea	2022 - 2023	Hospitals (ICU)	1	CT, PPS*	718	Patients (111), HCW (194)	54	Patients (53) HCW (1)	No	Screening of patients staying in the bed next to a positive case. PPS included HCW and other patients in the unit.
McDougal (2023)	USA	2022	Hospital ³ (ICU)	1	CT, PPS*	344	216 inpatients, 128 outpatients	8	Patients	Yes	Screening of out- and inpatients sharing rooms with a positive case since admission. WGS showed that isolates clustered together.
Pacilli (2020)	USA	2017	vSNFs	1	PPS*	114	Patients	66	Patients	No	7 PPS were performed over a 10-month period.
Rossow (2021)	USA	2016 - 2018	vSNFs	1	PPS	N/A	Patients	60	Patients	No	Screening of patients on 6 facilities were positive case resided or had resided in the 90 days before diagnosis. No denominator for screened patients.
Ruiz- Gaitan (2018)	Spain	2016- 2017	Hospital (ICU, SICU)	2	PPS*	? 101	Patients HCW	140 0	Patients HCW	No	3 surveillance sampling (weekly) until discharge on wards where a positive case had been admitted.
Schelenz (2016)	UK	2015 - 2016	Hospital (ICU)	50	CT, surveillance* [*]	? 258	Patients HCW	1	HCW	Yes	Prospective surveillance of clinical cases/screening of direct contacts/HCWs. No denominator for screened patients. Genotyping showed clustered strains, indicating a single introduction.
Townsend (2021)	Canada	2019 - 2020	Hospital	1	Surveillance* [*]	600	Patients	0	N/A	No	Screening of patients who were present on the unit with the index case. Screened on day 0, 7, and 21 following transfer/discharge.
Worth (2020)	Australia	2018 - 2019	Hospital	1	CT	73	Patients	1	Patients	No	Screening of ward contacts.

A, axilla; G, groin; O, oral; H, hands; R, rectum; W, wound; CV, central venous site; N, nares; U, urine; E, ear; PPS, Point-prevalence survey; ICU, intensive care unit; vSNFs, ventilator-capable skilled nursing facilities; SICU, surgical unit; CT, contact tracing; WGS, Whole genome sequencing; LTCF, long-term healthcare facility; N/A, not applicable; HCW, healthcare worker; V, visitor; F, family-member

*Environmental samples taken

¹Patients ²Molecular investigation ³Prison hospital

Table 6. Overview of characteristics and findings of studies on associated factors (control group) for *C. auris* infection or colonisation.

First author (year)	Country	Study period	Outcome type	Exposure group	Control group	Exposed (n)	Control (n)	Risk factors (authors' conclusions)
Adam (2019)	Kenya	2010-2016	Candidaemia	<i>C. auris</i> candidaemia	Other candidaemia	77	124	Carbapenem use, critical care unit, presence of CVC
Allaw (2022)	Lebanon	2020-2021	Infection (bloodstream, deep tracheal aspiration, urine, wound)	<i>C. auris</i> positive with or without severe covid-19	<i>C. auris</i> negative with or without severe covid-19	56	130	qSOFA, length of stay in hospital
Alvarez-Moreno (2023)	Colombia	2016-2017	Mortality (crude 30 and 90 day)	<i>C. auris</i> candidaemia	Other candidaemia	22	52	Previous use of fluconazole, HIV
Caceres (2020)	Colombia	2015-2016	Candidaemia	<i>C. auris</i> candidaemia	Other candidaemia	40	50	BSI: ≥ 15 days of pre-infection ICU stay, evidence of severe sepsis, and diabetes mellitus
Farooqi (2020)	Pakistan	2015-2016	Colonisation or infection, confirmed or suspected	<i>C. auris</i> confirmed or suspected	Other admitted patients matched on age and sex	30	62	History of surgery 90 days before diagnosis, admission through the ED and having chronic kidney disease
Moin (2021)	Pakistan	2020	Candidaemia	<i>C. auris</i>	Other candidaemia	4	22	Prior antifungal exposure
Parak (2022)	South Africa	2015-2018	Candida spp. Isolated	<i>C. auris</i>	<i>C. albicans</i> and <i>C. glabrata</i>	45	90	Indwelling devices and previous antibiotic exposure
Rossow (2021)	USA	2016-2018	Colonisation	<i>C. auris</i>	Controls from the same facility without <i>C. auris</i>	60	218	Specific invasive medical devices, recent antimicrobial use, recent hospitalization, and colonisation with other MDROs
Ruiz-Gaitan (2019)	Spain	2016-2017	Colonisation or candidaemia	<i>C. auris</i>	Concurrent controls without <i>C. auris</i>	114	114	The presence of CVC, parenteral nutrition and mechanical ventilation
Sayeed (2020)	Pakistan	2014-2017	Candidaemia	<i>C. auris</i>	Other candidaemia	37	101	Prior history of surgery, prior antifungal exposure, and MDR bacteria isolation
Shastri (2020)	India	2016-2017	Candidaemia	<i>C. auris</i>	Other candidaemia	42	66	Underlying respiratory or neurological diseases. Presence and use of CVC for long period, prolonged ICU stay prior to candidaemia, invasive ventilation, and broad-spectrum antibiotic usage
Simon (2023)	USA	2016-2020	Candidaemia	<i>C. auris</i>	Other candidaemia	83	113	Admission from nursing homes, prior colonisation with <i>C. auris</i> /multidrug-resistant bacterial organisms, extensive use of antimicrobials concomitant bacterial infections with gram-negative and multidrug-resistant organisms.
Taori (2019)	UK	2016-2017	Clinical infection	<i>C. auris</i> infection	<i>C. auris</i> colonisation	8	6	ICU stay, long hospital stays, presence of CVC, haemodialysis, and prior antifungal therapy
van Schalkwyk (2019)	South Africa	2016-2017	Candidaemia	<i>C. auris</i>	Other candidaemia	794	5875	Prior systemic antifungal drug therapy, presence of a CVC, admission to a private-sector facility, older age, longer hospitalization before the first positive blood culture, prior hospitalization within the past year, admission to an ICU during the current hospital stay, and HIV seropositivity.

Table 7. Overview of characteristics and findings of studies on colonisation sites for *C. auris*

First author (Year)	Study period	Country	Setting	Population	Type of screening	Number of screened persons (or samples)	Screening sites	Total positive N (%)	Positive body site
Adams (2018)	2017 - 2017	USA	Hospital, LTCF, vSNF	Patients, HCW and family members	CT and PPS	346 patients	A, G, N	36	A-G 13/36 (36%), N 9/36 (25%), A-G-N 14/36 (39%)
Alshahrani (2023)	2020 – 2022	Saudi Arabia	Hospital	Patients	On admission, CT	N/A	A, G, N (W, IDS, U, etc)	46	A 6 (11.3%), U 16 (30.2%) *
Armstrong (2019)	2015-2016	Colombia	Acute care hospitals,	Adult and pediatric patients	Different body sites of positive <i>C. auris</i> patients	7 patients	A, G, bilateral N, E, O, R	5	P1 (BSI): 1/11 R, P2 (BSI): 0/10, P3 (BSI): 7/11 E, A, N, R, fecal material, P4 (UVI): 1/10 G, P5 (sputum): 1/11 G
Biswal (2017)	2017	India	Hospital	Patients, HCW	On admission, HCW	647 patient samples 145 HCW samples	A, G, O, R + H (HCW)	136 (4)	A 72/196 (36.7%), G 36/206 (17.4%), R 18/118 (15.2%), O 10/95 (10.5%), HCW hands 4/145 (2.8%)
Briano (2022)	2020-2021	Italy	Hospital	ICU patients	On admission, weekly and on discharge	N/A	Combined A-G	157	S 146/157 (93%), U 38/157 (24%), RT 77/157 (49%), multisite 48/157 (50%)
Chow (2018)	2013-2017	USA	Acute care facility	Patients	CT, PPS	N/A	A, G (some N, W)	60	Mixed infection and colonisations
Corcione (2022)	2021-2022	Italy	Hospital	ICU patients	CT, PPS	N/A	A, G, N, T	8	S 5/8 (%), U 2/8 (%), RT 1/8 (%)
De Melo (2023)	2021-2022	Brazil	Hospital	Patients	CT	N/A	A, G	7	7/7 A-G
Escandon (2019)	2015-2016	Colombia	1 acute care hospital, 2 adult hospital, 1 pediatric hospital	Adult and pediatric patients	Different body sites of positive or suspected <i>C. auris</i> patients and HCW	17	A, G, bilateral N, E, O, R + HCW hands	5 patients 2 HCW	H 2/2 HCW G 1/2 HCW
Eyre (2018)	2015-2017	UK	Hospital	Neuroscience ICU patients	On admission, weekly and on discharge	900 patients	A, G, N, U (W, T)	60	A 22/60 (37%), G-U 21/60 (35%), multisite 17/60 (28%)
Goulart (2023)	2021 – 2023	USA	Trauma center	Patients	PPS	91 patients	A, G	5	Not specified which site
Lee (2024)	2022	South Korea	Hospital	ICU/CCU Patients and HCW	CT, PPS, HCW	111 patients 194 HCW	Bilateral A, bilateral G	53 patients and 1 HCW	Results mixed for patients with infection and colonisation. HCW positive hands/pockets
Leonhard (2024)	2023	Netherlands	University medical center	Patients	On admission	199 patients	A, G (IDS, U etc)	1	A-G 1/1 (100%)

McDougal (2023)	Not specified	USA	Prison hospital	Patients in prison health care	CT, PPS	344 patients	Combined bilateral A-G	8	A-G 8/8 (100%)
McPherson (2020)	2019	USA	Hospital (long term transitional care)	Pediatric patients	PPS	25 patients	Combined bilateral A-G	0	
Mulet Bayona (2020)	2017	Spain	Hospital	ICU patients	On admission, follow-up, PPS	N/A	N/A	35	9 A-R-P, 24 A-R and 2 P
Piatti (2022)	2021	Italy	Hospital	ICU patients	On admission, on discharge	384 patients	A, G, E, IS, R (some)		S 105/384 (27.3%), R 50/86 58.1%), 69/77 (89.6%)
Proctor (2021)	2019	USA	Skilled nursing facility		PPS	N/A	A, G, N, E, PS, TW, PF, B, TO, T	49	N 42.9%, foot 35.7%, PF 40.4%
Rowlands (2023)	2017-2019	USA	2 ventilator units nursing homes and 1 hospital (ventilator/pulmonary unit, ICU and cardiac care unit)	Patients	On admission	2062 patients	Combined bilateral A-G, bilateral N	188	A-G 93/188 (49.5%), N 32/188 (17.0%), A-G-N 61/188 (32.4%)
Ruiz-Gaitan (2018)	2016 – 2017	Spain	Tertiary care hospital	Patients and HCW	PPS	N/A	S, TH, R, H (HCW), E	140	Results mixed for patients with infection and colonisation
Schelenz (2016)	2015 – 2016	UK	Hospital Trust	ICU patients and HCW	CT	N/A	A, G, N, R, W, U, IDS	50	Results mixed for patients with infection and colonisation. N (HCW) 1/258
Sharp (2021)	2017 – 2018	UK	8 adult ICUs in different hospitals	ICU patients	On admission	921	A, G, N, TH, PS, R, CU	0	
Southwick (2022)	2016 – 2017	USA	Different Health care facilities	Patients	CT and PPS	1668 patients	Combined A-G, N	114	A-G 92/114 (81%), N 73/114 (64%), A-G-N 68/114 (60%)
Townsend (2021)	2019 – 2020	Canada	Acute care community hospital	Patients	On admission	N/A	Bilateral A, G, N	1	
Tsay (2017)	2016 – 2017	USA	Healthcare facilities	Patients	CT	390 patients	Combined A-G, N (some)	45	A-G 45/45 (100%)
Turbett (2022)	2019 – 2020	USA	Travel to Africa, Asia, USA, Europe	Travellers	Before and after travel	94 travellers	Bilateral A, bilateral G	0	
Vallabhaneni (2017)	2013 – 2016	USA	Hospitals	HCW	HCW hands	52 samples	Hands	0	
Yadav (2021)	2019 – 2020	India	Chest hospital	Patients	On admission ^a	32 patients	A, G, N, E	12	G 9/12 (75%), N 5/12 (45%), E 4/12 (33%)

Zhu (2020)	2016 – 2018	USA	Hospitals, nursing homes, hospice, LTACH	Patients	1) Surveillance and 2) different body sites of positive <i>C. auris</i> patients	11035 samples	A, G, N (R, other)	1) 931 samples (350 patients) 2) 298	A-G bilateral 178/222 (80%), N bilateral 125/215 (58%), A-G-N bilateral 106/103 (100%), A unilateral 10/20 (50%), G unilateral 10/20 (50%), N unilateral 6/14 (43%), W 4/11 36%, R 4/7 (57%), E 4/6 (67%), S 1/1 (100%)
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PPS, Point- prevalence survey; CT, contact tracing; LTCH, long-term healthcare facility; vSNF: ventilator Skilled nursing facility; N/A, not applicable; HCW, healthcare worker; A, axilla; B, buccal mucosa; CU, catheter urine; CV, central venous site; E, ear; G, groin; H, hands; IDS:

Indwelling device site; IS: Inframammary sulcus; N, nares; O, oral; P, pharyngeal; PF: palm and fingertips; PS: perianal skin; R, rectum; RT, respiratory tract; TH; throat; TO: tongue; TW: toe web; U: Urine; W, wound

* Additionally, patients were positive in the thigh (n=5), anus (n=5), arm (n=4), penis (n=3), hip (n=3), buttock (n=2), leg (n=2), neck (n=1), tissue (n=1) wound (n=1) nail (n=1), foot (n=1) area.

Appendix 1: search strategies

CANDIDA AURIS

Contact person: Mari Molvik
Search: Ragnhild Agathe Ternes
Duplicate control in EndNote: Before duplicate control: 5907
After duplicate control: 2386

Database: Ovid MEDLINE(R) and Epub Ahead of Print, In-Process, In-Data-Review & Other Non-Indexed Citations, Daily and Versions <1946 to February 01, 2024>
Date: 2 February, 2024
Number of hits: 1480

1	Candida auris/	302
2	("candida auris" or "c auri?" or txid498019).tw,kf.	1480
3	1 or 2	1480

Database: Embase <1974 to 2024 February 01>
Date: 2 February, 2024
Number of hits: 40 systematic reviews, 120 primary studies

1	Candida auris/	1716
2	("candida auris" or "c auri?" or txid498019).tw,kf.	1748
3	1 or 2	2047
4	limit 3 to (conference abstracts or embase or "preprints (unpublished, non-peer reviewed)")	1898

Database: Cochrane Database of Systematic Reviews
Issue 2 of 12, February 2024
Cochrane Central Register of Controlled Trials
Issue 2 of 12, February 2024
Date: 2 February, 2024
Number of hits: 3

#1	[mh ^"Candida auris"]	0
#2	("candida auris" or (c NEXT auri?) or txid498019):ti,ab	3
#3	#1 or #2	3

Database: Web of Science Core Collection:

**Science Citation Index Expanded
(SCI-EXPANDED)--1987-present
Social Sciences Citation Index
(SSCI)--1987-present
Arts & Humanities Citation Index
(AHCI)--1987-present
Emerging Sources Citation Index
(ESCI)--2018-present**

Date: 2 February, 2024
Number of hits: 1633

1	TS=("Candida auris" or "c auri\$" or txid498019)	exact search	1633
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Database: Epistemonikos
Date: 2 February, 2024
Number of hits: 257

Title/abstract: ("candida auris" OR "c auri" or "c auris" or txid498019)
257 hits