UK Health Security Agency

The risk of infectious disease transmission posed by communal accommodation settings

A rapid review

Contents

Main messages

1. This review (search to 16 March 2023) identified and assessed the available evidence on the risk of infectious disease transmission posed by communal accommodation settings. Forty-one studies are included (1 to 41). Accommodation settings included private households (25 studies) (1 to 25), dormitories (8 studies) (26 to 33), vessels (barges, cruise ships, or ferries, 2 studies) (34, 35), and emergency shelters and hostels for those experiencing homelessness (6 studies) (36 to 41).
2. There was consistent evidence across 25 studies of private households that living in a crowded household was associated with increased risk of acute respiratory (14 studies) (1 to 13), tuberculosis (TB), (7 studies) (14 to 20), gastrointestinal (4 studies) (21 to 24), skin (2 studies) (13, 21), and meningococcal infections (one study) (25). There was a small to moderate association between living in crowded households and an increased risk of each infection, although the one study looking at meningococcal infection suggested a large positive association with household density (25). How household crowding was defined varied between studies and has been described individually for each study.
3. There was consistent evidence across 8 studies that staying in dormitories, particularly with those with greater numbers of people, was associated with increased risk of acute respiratory (5 studies) (26 to 30), TB (one study) (31), and skin infections (2 studies) (32, 33). In almost all studies, there was a moderate or large association between staying in a dormitory, or how many people were staying in a dormitory, and an increased risk of each infection relative to those living in dormitories of fewer people or those not living in dormitories.
4. The 2 studies looking at transmission of influenza on vessels reported potentially conflicting results on the association between occupancy rates and infection risk. One study (rated as high-quality) suggested the risk of influenza increased with occupancy rate (34), whilst the second study (rated as low-quality) suggested the risk of influenza decreased with occupancy rate (35). The inconsistency in results may be explained by the fact that the low-quality study only looked at individual variable correlations (35), compared to the high-quality study which included a regression model adjusted for age, sex and whether ship duties included passenger contact (35).
5. There was consistent evidence across 6 studies that staying in emergency shelters, or shelters or hostels for those experiencing homelessness, particularly crowded shelters, was associated with increased risk of acute respiratory infection (5 studies) (36 to 40) and methicillin resistant staphylococcus aureus (MRSA) nasal colonisation (one study) (41). In almost all studies, there was a moderate association between staying in an emergency shelter, particularly if crowded, and the risk of acute respiratory and skin infections.
6. There was a lot of variation between included studies, in terms of their populations, methods, outcomes, and how occupancy was measured (for example household crowding was defined in different studies as the number of people per room, the number

of people per bedroom, the number of people per household or the number of people bed sharing). The studies suggest an association between increased accommodation density with increased risk of various infections, but as the studies were observational, as well as heterogenous, the association may not be causal.

7. Risk of bias was assessed using the Quality Criteria Checklist (QCC) (42). Six of 41 studies were rated as high-quality (2, 17, 20, 24, 27, 34) with the remaining studies rated as low or medium quality.
8. There were many gaps in the evidence. Most studies compared infectious disease transmission between different conditions within the same accommodation type rather than between accommodation types, there were limited studies looking at vessels, only one study investigating dormitories housing adults (33) and relatively few studies looking at infections other than COVID-19.

Background

There are considerable differences between communities and groups in society both in terms of the risk of exposure to health hazards, but also their susceptibility to poor outcomes when exposed and resilience against these hazards. Inclusion health is an approach to addressing extreme health inequities experienced by socially excluded groups.

Examples of inclusion health populations are people experiencing homelessness, people who use drugs, people in contact with the criminal justice system, sex workers, gypsy, Roma and traveller populations, victims of trafficking and modern slavery, and vulnerable migrants including undocumented migrants, asylum seekers and refugees (43). There is a high degree of overlap between inclusion health populations, particularly people experiencing homelessness, people who use drugs, sex workers and people in contact with the criminal justice system. Inclusion health populations have extremely high rates of preventable disease, including a vastly disproportionate burden of infection (44).

Inclusion health populations often live in communal, overcrowded settings such as hostels or asylum seeker accommodation. The extent to which the accommodation type contributes to increased risk of infection is not well defined.

In addition, there are social inequities in the exposure of individuals and groups to crowded accommodation, including people living in the social rented sector who are more likely to be more socially deprived. The 2021 to 2022 English Housing Survey identified that 8% of people in the social rented sector lived in crowded households compared to 3% of the overall population (45).

The purpose of this rapid review was to identify and assess the available evidence on the risk of infectious disease transmission in high-density, communal or crowded accommodation settings which are shared by non-family members. Due to the lack of

evidence specific to these settings, the scope was widened to include all communal non-detained accommodation settings.

The review is intended to inform future provision of advice and guidance to communal accommodation settings including those which cater for inclusion health populations.

Methods

Full details on the methodology are provided in the protocol in Annexe A. The following deviations from and clarifications to the initial protocol were made:

- clarification on definition of ‘care homes’ as an exclusion criterion, to exclude nursing homes and care homes for vulnerable people
- all studies looking at private households and houses in multiple occupation (HMO) were included
- studies were only included if they were published after the year 2000 (no date limit was stated in the original protocol), as studies published after 2000 were considered to be more generalisable for informing current advice and guidance
- removal of studies (one study only) with historical data even where published after the year 2000
- genomic sequencing studies, modelling studies and outbreak reports were added to the study types that would be excluded
- clarification on inclusion of all forms of vessels

This review was conducted following streamlined systematic methodologies to accelerate the review process. It was conducted by members of the Health Equity and Inclusion Health Division at UKHSA, supported by Clinical and Public Health Response Evidence Review Team.

A literature search was undertaken to look for relevant primary studies, published (or available as preprint) up to 16 March 2023. Screening on title and abstract was undertaken in duplicate by 2 reviewers for 20% of the eligible studies, with the remainder completed by one reviewer. Screening on full text was undertaken by one reviewer and checked by a second.

Risk of bias assessment was conducted independently by 2 reviewers using the Quality Criteria Checklist (QCC) (42, 46), with each study rated as high, medium, or low-quality. Disagreements were resolved by discussion with a third reviewer. The QCC also classifies study designs according to a hierarchy of their ability to identify causal relations between exposure and outcome. Ecological studies were not classified by the QCC, so have been classified based on the category each study most closely resembled:

- class A: randomised and quasi-randomised controlled trials
- class B: cohort studies
- class C: non-randomised controlled or crossover trial, case-control, time series, diagnostic, validity, or reliability studies
- class D: non-controlled trial, case study or case series, other descriptive study, cross-sectional study, trend study, before and after study

The search was not restricted by population group. The following high-density, communal or crowded accommodation settings were included:

- vessels (including barges, cruise ships, military ships, and ferries)
- dormitories or student housing with shared utilities and communal spaces
- homeless shelters or hostels
- houses in multiple occupation
- temporary settlements such as tented accommodation, camps or marquees

Only studies which focused on identifying the risk of infectious disease transmission specifically within a communal environment were included. Studies which discussed measures intended to mitigate the risk of infectious disease outbreak were beyond the scope of this review and not included.

Ecological studies were included in this review as they provided some evidence to answer the review question. However, ecological studies compare averages in a population rather than individuals within that population. This means that the interpretation of these studies is not generalisable to individuals, as results that apply to a population may not apply to individuals within those populations.

Evidence

In total, 6,478 references were screened on title and abstract, and 296 were screened on full text, resulting in 41 studies included in this rapid review (1 to 41). Studies excluded on full text screening are available, with exclusion reasons, in Annexe B.

The exposures investigated through the studies included household density, household crowding and number of persons sharing a room, bed or bathroom. Settings investigated across the 41 studies included 25 studies looking at private households (1 to 25), 8 looking at dormitories (26 to 33), 2 looking at vessels (34, 35), and 6 looking at emergency shelters and hostels for those experiencing homelessness (36 to 41). Outcomes also varied between studies, with 25 studies investigating the risk of transmission of acute respiratory infections (ARIs) (1 to 13, 26 to 30, 34 to 40), 8 investigating tuberculosis (TB) (14 to 20, 31), 3 investigating gastrointestinal infections (22 to 24), 5 investigating skin infections (13, 21, 32,

33, 41) and one investigating meningococcal infection (25) (studies investigating multiple infections are referenced twice). Results are summarised below according to accommodation type, alongside the QCC risk of bias assessment for the studies.

Full data extraction tables can be found in Annexe C, including details of study design, methodology, and analysis, such as variables that were adjusted for or matched on, and results of the risk of bias assessment can be found in Annexe D.

Private households and houses in multiple occupation (HMOs)

Private households and HMOs were defined as residential properties used by families or by multiple individuals (not family members). It was not always possible to distinguish the type of household in the included studies, but where a study related specifically to family members, this was noted in the data extraction.

In total, 25 included studies investigated infectious disease transmission risk in overcrowded private households and HMOs (1 to 25). 13 investigated the risk of ARIs (including COVID-19 and influenzas) (1 to 13), 7 investigated the risk of TB (14 to 20), 4 investigated the risk of gastrointestinal infections (including Escherichia coli, shigellosis, rotavirus and norovirus) (21 to 24), 2 investigated the risk of skin infections (scabies and MRSA) (13, 21), and one investigated the risk of meningococcal infections (25). The dominant exposure measure within private households and HMOs related to household crowding and number of individuals per room. However, there was heterogeneity across studies relating to how household crowding was determined, and individual definitions have been provided in the study descriptions.

Full data extraction tables for studies of private households and HMOs can be found in Table C.1a.

Acute respiratory infections (ARIs)

Thirteen studies reported on ARIs, with 12 studies reporting on COVID-19 between January 2020 and April 2021 (2 rated as low-quality (5, 10), 9 rated as medium quality (1, 3, 4, 6 to 9, 11, 12), and one rated as high-quality (2)). One study reported on Group A streptococcal (GAS) pharyngitis between 2018 and 2019 (rated as medium quality (13)). Six studies were ecological (1, 4 to 6, 10, 12), 3 studies were cohorts (2, 3, 8), 2 studies were case-control (7, 13), and 2 studies were cross-sectional (9, 11). Two studies were conducted in the UK (2, 9), 6 in North America (1, 3, 4, 6, 10, 12), 2 in Europe (excluding the UK) (7, 8), one in Kenya (11), one in Nepal (5), and one in New Zealand (13).

COVID-19

Ahmad and others conducted an ecological study (rated as medium quality, study design class D) investigating the association between poor housing conditions (defined as overcrowding, high housing cost, incomplete kitchen facilities, or incomplete plumbing facilities) and COVID-19 incidence in an ecological study of 3,141 counties in April 2020 in the US (1). The results suggested there was an increased risk of COVID-19 infection as the proportion of poor housing conditions increased in each county (incidence rate ratio [IRR] for a 5% increase in household with poor housing condition per county = 1.59, 95% CI: 1.49 to 1.70).

Boukari and others conducted a retrospective cohort study (rated as high-quality, study design class B) investigating the association between household overcrowding and COVID-19 infection in 23,478 people in England and Wales between September 2020 and April 2021 (2). This study aimed to identify how much of the difference in the odds of COVID-19 infection between those born in the UK compared to those born overseas could be explained by household crowding. The results suggested that household crowding accounted for 32% of the difference in the odds of COVID-19 infection (indirect effect odds ratio [OR] = 1.07, 95% CI: 1.03 to 1.12), implying that some of the difference in COVID-19 infections was due to people born overseas being more likely to live in overcrowded housing compared to the UK born participants (10.2% versus 2.0%).

Cerami and others conducted a prospective cohort study (rated as medium quality, study design class B) investigating the association between high living density and COVID-19 infections in 91 index cases and 176 household contacts in the US between April and October 2020 (3). High living density was defined as more than 3 persons in fewer than 6 rooms. Household transmission was higher amongst those living in high-density households compared to those not living in high-density households (secondary attack rate 52% versus 24%, OR = 1.4, 95% CI: 0.4 to 4.6).

Dasgupta and others conducted an ecological study (rated as medium quality, study design class D) investigating the association between household density (median percentage of household with more persons than rooms) and COVID-19 incidence amongst 3,142 counties in the US in July 2020 (4). The results suggested that in counties with above the median percentage of households with more persons than rooms, the risk of COVID-19 infection was twice that of counties with below the median percentage of households with more persons than rooms (unadjusted relative risk [RR] = 2.0, 95% CI: 1.8 to 2.3).

Lamichhane and others conducted an ecological study (rated as low-quality, study design class D) investigating the association between overcrowding (defined as households with more than 3 persons per room) and COVID-19 infections in 73 districts (12,862 women and 4,063 men) in Nepal between January 2020 and January 2021 (5). The results suggested an increased COVID-19 infection risk with increased overcrowding in each district (unadjusted

RR for a percentage increase in overcrowding at the district level = 1.04, 95% CI: 1.01 to 1.06).

Lee and others conducted an ecological study (rated as medium quality, study design class D) investigating the association between overcrowding and COVID-19 infection across 91 counties in 3 states in the US between March and November 2020 (6). Overcrowding was defined as more than one person per room. The results suggested that overcrowding was associated with an increased incidence of COVID-19 (change per unadjusted interquartile increase in mix-max standardised percentage overcrowding = 1.52, 95% CI: 1.34 to 1.72).

Leite and others conducted a case-control study (rated as medium quality, study design class C) investigating the association between household crowding and COVID-19 transmission in 1,088 COVID-19 cases and 787 controls in Portugal between October and November 2020 (7). The results suggested that household crowding was associated with increased COVID-19 infection risk (when comparing one or more persons per room with less than one person per room OR = 1.47, 95% CI: 1.14 to 1.91, p=0.004).

Lopez and others conducted a retrospective cohort study (rated as medium quality, study design class B) investigating the association between household crowding and COVID-19 transmission in 89 COVID-19 cases and 229 household contacts in Spain between April and June 2020 (8). The results suggested that household crowding was associated with increased COVID-19 infection, but the results were imprecise (OR for COVID-19 infection per unit increase in the ratio of the number of household members and the number of bedrooms = 1.44, 95% CI: 0.82 to 2.55).

Martin and others conducted a cross-sectional study (rated as medium quality, study design class D) investigating the association between household size, and shared spaces with other households, and COVID-19 infection in 10,772 healthcare workers in the UK between December 2020 and March 2021 (9). The results suggested no association between household size and COVID-19 infection odds (OR presumed by the authors of this report to represent a per unit increase in household size = 1.02, 95% CI: 0.98 to 1.06, p=0.34) or between shared spaces with other households and COVID-19 infection odds (OR for COVID-19 infection comparing shared spaces and no shared spaces = 0.93, 95% CI: 0.81 to 1.06, p=0.28).

Mendez and others conducted an ecological study (rated as low-quality, study design class D) investigating the association between overcrowding and risk of COVID-19 infection in 183 Latin American families in the US between May and September 2020 (10). The results suggested that there was an association between household size and increased COVID-19 incidence (OR for a unit increase in household size = 1.58, 95% CI: 1.12 to 2.23, p<0.01), but there did not appear to be an association between persons per bedroom (OR for a unit increase in number of persons per bedroom = 1.05, 95% CI: 0.66 to 1.68, p=0.82) or number

of people eating together daily (OR for a unit increase in number of people eating together daily = 1.06, 95% CI: 0.73 to 1.56, p=0.75) and COVID-19 incidence.

Munywoki and others conducted a cross-sectional study (rated as medium quality, study design class D) investigating the association between household size and COVID-19 infection in 175 households in urban informal settlements in Kenya between November and December 2020 (11). After testing the seroprevalence of COVID-19 amongst individuals randomly selected from an existing population level survey, results suggested that there was no clear trend between household size and COVID-19 seroprevalence. Compared to household sizes of 3 to 4 people, both smaller and larger household sizes were associated with higher risk of COVID-19 seropositivity (household sizes of 1 to 2 people, OR = 2.31, 95% CI: 0.93 to 5.74, p=0.072 and for 5 to 6 people OR = 1.98, 95% CI: 1.17 to 3.34, p=0.011).

Van Ingen and others conducted an ecological study (rated as medium quality, study design class D) investigating the association between household size and COVID-19 infection in 28,808 people in Canada in July 2020 (12). The results suggested an association between increased housing size and higher COVID-19 incidence (RR comparing the 90th percentile and 10th percentile in average housing size = 1.9, 95% CI: 1.7 to 2.1), and between unsuitably crowded housing, as defined by the Canadian National Occupancy Standard, and higher COVID-19 incidence (RR comparing the 90th percentile and 10th percentile in those living in unsuitably crowded housing = 2.1, 95% CI: 2.0 to 2.3).

Group A streptococcal (GAS) pharyngitis

Bennett and others conducted a case-control study (rated as medium quality, study design class C) investigating the association between household crowding and bed sharing with the risk of GAS pharyngitis infection in 733 children in households in New Zealand between 2018 and 2019 (13). Householding crowding (OR comparing more than one person per room and one person per room or less = 1.5, 95% CI: 0.9 to 2.4) and bed sharing (OR comparing bed sharing with no bed sharing = 1.3, 95% CI: 0.8 to 2.3) were both positively associated with increased odds of GAS pharyngitis infection in children.

Tuberculosis

Seven studies investigated the association between overcrowding and the risk of TB infection (2 studies rated as low-quality (15, 18), 3 studies rated as medium quality (14, 16, 19), 2 studies rated as high-quality (17, 20)). Three studies were ecological (14,16,19), 2 were case-control studies (17, 20), and 2 were cross-sectional studies (15, 18). Three studies were conducted in Africa (15, 19, 20), 2 in Asia (17, 18), one in New Zealand (14), and one in Brazil (16). All studies reporting the study period were conducted between 1999 and 2019 (14, 16, 19, 20), although 3 studies did not report the study period (15, 17, 18).

Baker and others conducted an ecological study (rated as medium quality, study design class D) investigating the association between household crowding (defined as a bedroom deficit of one or more) and TB infection (1,898 cases) across New Zealand (3,737,277 residents) between 2000 and 2004 (14). The results suggested a small association between household crowding and TB infection across the population (incidence rate ratio [IRR] for a percentage increase in household crowding in each census area unit = 1.05, 95% CI 1.02 to 1.08).

Bigwan and others conducted a cross-sectional study (rated as low-quality, study design class D) investigating the association between number of people staying in the same room and active TB infection in people who gave 303 sputum samples in Nigeria (study period not stated) (15). The results showed that having more people staying in the same room was associated with an increased risk of TB infection (one person sharing = 2 of 29 [6.9%], 2 people = 1 of 41 [2.4%], 3 people = 6 of 48 [12.5%], 4 people and above = 20 of 185 [10.8%], $p<0.05$ for trend).

Harling and others conducted an ecological study (rated as medium quality, study design class C) investigating the association between household crowding (defined as more than 2 household members per bedroom) and TB infection in 5,565 municipalities in Brazil between 2002 and 2009 (16). The results suggested that municipalities with a higher percentage of overcrowded households experienced greater risk of TB infection compared to municipalities with a lower percentage of overcrowded households (IRR for a standard deviation [SD] (11.4 percentage points) increase in household crowding in municipalities = 1.17, 95% CI: 1.13 to 1.21.

Irfan and others conducted a case-control study (rated as high-quality, study design class C) investigating the association between household crowding (defined as more than 2 family members per room) and TB infection in 178 cases and 179 controls in Bangladesh (study period not stated) (17). The result suggested that household overcrowding was associated with increased risk of TB infection (OR comparing overcrowding with no overcrowding = 3.49, 95% CI: 2.08 to 5.93, $p<0.001$).

Kapoor and others conducted a cross-sectional study (rated as low-quality, study design class D) investigating the association between the number of people per room and TB infection in India (study period not stated) (18). The results suggested that households with 3 to 5 people per room were more likely to have TB than households with less than 3 people per room (unadjusted OR = 3.31, 95% CI: 2.49 to 4.41), but that households with 6 to 7 people per room (unadjusted OR = 1.01, 95% CI: 0.67 to 1.52) and households with more than 8 people per room (unadjusted OR = 0.54, 95% CI: 0.25 to 1.19) were not more likely to have TB than households with less than 3 people per room. The presented results are, however, limited by the low numbers of people within the analysis of 6 to 7 and 8 or more persons per room groups.

Kapwata and others conducted an ecological study (rated as low-quality, study design class D) investigating the association between overcrowding (defined as more than 2 people per room) and TB infections (12,053 TB cases in 7,769 households) in South Africa between 2014 to 2019 (19). The results suggested that overcrowding was associated with increased risk of TB infection (OR comparing overcrowding with not overcrowding = 2.15, 95% CI: 1.66 to 2.78, p=0.001).

Lienhardt and others conducted a case-control study (rated as high-quality, study design class C) investigating the association between household size, and household density, and TB infection in 822 cases, 687 household controls and 816 community controls in The Gambia, Guinée Conakry, and Guinea Bissau between 1999 and 2001 (20). The results suggested that having both 6 to 10 (OR = 1.37, 95% CI: 1.03 to 1.82) and more than 10 (OR = 2.80, 95% CI: 1.71 to 4.57) adults in the household was associated with an increased risk of TB infection compared with having one to 5 adults in the household. The results also suggested that having one to 2 people per room (OR = 1.07, 95% CI: 0.64 to 1.82) or more than 2 people per room (OR = 1.26, 95% CI: 0.73 to 2.16) was associated with only a small increased risk of TB infection compared with having less than one person per room, and the results are imprecise.

Gastrointestinal infections

Four studies investigated the association between household density and the risk of gastrointestinal infections, including E. coli, shigellosis, rotavirus and norovirus (3 studies rated as medium quality (21 to 23), one study rated as high-quality (24)). Two studies were ecological (21, 22), one was a prospective cohort study (23), and one was a case-control study (24). One study was conducted in New Zealand (21), one in the US (22), one in Vietnam (24), and one in 8 nations across Africa and Asia (23). The studies were conducted between 2004 and 2014.

Blakiston and others conducted an ecological study (rated as medium quality, study design class D) investigating the association between crowded housing (defined using the Canadian National Occupancy Standard) and E. coli infections in 18 regions of New Zealand in 2013 (21). The results suggested an association between crowded housing and increased risk of E. coli infections (unadjusted correlation coefficient = 0.77, 95% CI: 0.34 to 0.60, p=0.50).

Libby and others conducted an ecological study (rated as medium quality, study design class D) investigating the association between household crowding (defined as more than one person per room) and shigellosis infections (21,246 cases) in 7 US States under the Foodborne Diseases Active Surveillance Network (Connecticut, Georgia, Maryland, Minnesota, New Mexico, Oregon, and Tennessee and selected counties in California, Colorado, and New York) between 2004 to 2014 (22). Census tract crowding level was determined by the percentage of households in the Census tract with more than one person per room, The results suggested an association between household crowding and increased

incidence of shigellosis infections (IRR comparing more than 5% with less than 1% Census tract crowding = 1.8, 95% CI: 1.7 to 1.9).

Mohan and others conducted a prospective cohort study (rated as medium quality, study design class B) investigating the association between overcrowding in the family (defined as more than 2 people per room) and rotavirus infections amongst 1,737 children across Bangladesh, Brazil, India, Nepal, Peru, Pakistan, South Africa and Tanzania between 2009 and 2014 (23). The results suggested overcrowding was associated with increased incidence of rotavirus diarrhoea (IRR comparing overcrowding with no overcrowding = 1.40, 95% CI: 1.07 to 1.83, p=0.014) and rotavirus infection (IRR comparing overcrowding with no overcrowding = 1.17, 95% CI: 0.98 to 1.40, p= 0.077).

My and others conducted a case-control study (rated as high-quality, study design class D) investigating the association between the number of children per household and norovirus infection amongst children (n=1,419 cases with acute diarrhoea, n=609 controls with no gastroenteritis) in Vietnam between 2009 and 2010 (24). The results suggested an association between a higher number of children per household and an increased risk of norovirus infections (OR comparing households of 3 or more children with households of less than 3 children = 1.7, 95% CI: 1.0 to 2.9, p=0.052).

Skin infections

Two studies (both rated as medium quality) investigated the association between household density and transmission of skin infections, including MRSA and GAS skin infection (13, 21). Both studies were conducted in New Zealand, one in 2013 (21), and one between 2018 and 2019 (13).

Bennett and others conducted a case-control study (rated as medium quality, study design class C) investigating the association between household crowding (defined as more than one person per room) and GAS skin infection in 733 children in New Zealand between 2018 and 2019 (13). The results suggested that household crowding (OR comparing crowded with not crowded = 1.9, 95% CI: 1.0 to 3.4) and bed sharing (OR comparing bed sharing with not bed sharing = 1.4, 95% CI: 0.8 to 2.6) were both associated with an increased risk of GAS skin infection, although the results were imprecise.

Blakiston and others conducted an ecological study (rated as medium quality, study design class D) investigating the association between household crowding (based on the Canadian National Occupancy Standard) and MRSA infection in 18 regions of New Zealand in 2013 (21). The results suggested that household crowding was associated with an increased risk of MRSA infections (unadjusted correlation coefficient = 0.90, 95% CI: 0.74 to 0.96, p<0.01).

Meningococcal disease

Baker and others conducted a case-control study (rated as medium quality, study design class C) investigating the association between household density, defined as the number of adolescents or adults per room within a household, and risk of meningococcal disease. The study included 202 children with meningococcal disease and 313 children without meningococcal disease in New Zealand between 1997 to 1999 (25). The results suggested that household density was associated with a large increased risk of meningococcal disease (OR for a unit increase in the number of adult and adolescent household members per room = 10.7, 95% CI: 3.9 to 29.5, p<0.0001).

Summary

Overall, there was consistent evidence across studies of private households and HMOs that crowding was associated with increased risks of ARIs (13 studies), TB (7 studies), gastrointestinal (4 studies), skin (2 studies), and meningococcal (one study) infections although the quality of the studies varied from low to high-quality and many of the results were imprecise. The studies were heterogeneous in terms of their populations, pathogens studied, study methods, and outcomes, but also in how household crowding was measured, such as number of people (or adults or children) per room, bedroom, or household, the Canadian National Occupancy Standard, and bed sharing. Because of this heterogeneity, it is not possible to directly compare the effect sizes between studies. In almost all studies however, there was a small to moderate size of association between household crowding and an increased risk of each infection, and one study looking at meningococcal disease suggested a large positive association with household density (25).

Dormitories

Dormitories are defined as group living environments used by institutions such as schools, universities, or the military. Seven of the 8 included dormitory studies were set in schools or university halls of residence (26 to 32), and one study investigated dormitories used by the Pakistani military (33). Five studies investigated the risk of ARIs (26 to 30), one investigated the risk of TB infections (31), and 2 investigated the risk of skin infections (32, 33).

Full data extraction tables for studies of dormitories can be found in Table C.1b.

Acute respiratory infections

Five studies investigated the association between staying in a dormitory and the risk of ARIs, including COVID-19 (26, 27), influenza (28, 30), and the common cold (29, 30) (4 studies rated as medium quality (26, 28 to 30), and one study rated as high-quality (27)). Four studies were cross-sectional (26, 27, 29, 30), and one was a retrospective cohort study (28).

Four studies were conducted in Asia (26, 28 to 30), and one in the US (27). The studies were conducted between 2006 and 2020.

Akaishi and others conducted a cross-sectional study (rated as medium quality, study design class D) investigating the association between group living environments, including school dormitories, and COVID-19 infections in 4,550 people who attended a COVID-19 drive through test centre in Japan between 2020 and 2021 (26). The results suggested that people who had close contact with someone with COVID-19 in a dormitory (unadjusted RR = 2.43, 95% CI: 1.74 to 3.40, p<0.0001), or a dormitory with no infection control measures (unadjusted RR = 5.12, 95% CI: 3.87 to 6.77, p<0.0001), were at higher risk of COVID-19 infection than people who had close contact with someone with COVID-19 outside of their residence, but not people who had close contact with someone at a dormitory with appropriate infection control measures (unadjusted RR = 0.10, 95% CI: 0.01 to 1.52, p=0.10). Infection control measures included wearing face masks in shared spaces, disinfection of commonly touched surfaces, and location of alcohol disinfection pumps on each floor and in shared spaces. Analysis looking specifically at student populations suggested those who lived in a dormitory were more at risk of COVID-19 infection than students who lived at home (unadjusted RR = 6.14, 95% CI: 3.83 to 9.84).

Bigouette and others conducted a cross-sectional study (rated as high-quality, study design class D) investigating the association between living in university dormitories and COVID-19 in 2,187 university students in the US in 2020 (27). The results suggested both that sharing a bedroom (OR = 1.52, 95% CI: 1.15 to 2.03) and sharing living space, defined as sharing a bedroom or sharing a bathroom, common area, or kitchen (OR = 1.80, 95% CI: 1.28 to 2.55), were associated with an increased risk of COVID-19 infection.

Li and others conducted a retrospective cohort study (rated as medium quality, study design class B) investigating the association between sharing a dormitory of 6 to 13 students and influenza H1N1 infection in a boarding school of 1,570 students in China in 2009 (28). The results suggested that students sharing a dormitory with someone with a fever were more at risk of influenza infection than students not sharing a dormitory with someone with a fever (OR = 2.05, 95% CI: 1.57 to 2.68, p<0.01).

Sun and others conducted a cross-sectional study (rated as medium quality, study design class D) investigating the association between crowded dormitories and self-reported common cold infections in 3,712 students in China between 2006 and 2007 (29). The results suggested that there was an association between increasing numbers of students sharing rooms and an increased risk of common cold (OR comparing 4 people per room to 3 per room = 1.55, 95% CI: 0.74 to 3.32; OR comparing 6 to 3 people per room = 2.58, 95% CI: 1.07 to 6.26, p=0.002 for association between number of persons per room and incidence of common colds).

Yang and others conducted a cross-sectional study (rated as medium quality, study design class D) investigating the association between crowded dormitories and common cold and influenza infections in 2,952 students in China between 2015 and 2016 (30). The results suggested that students in higher occupancy dormitories may be more likely to have a self-reported common cold or influenza infection compared to those in less occupied rooms. The percentage of students reporting a common cold more than 10 times a year was highest in the most occupied rooms (3 or fewer students per room: 3.4%, 4 students per room: 1.6%, 5 or more students per room: 7.1%, unadjusted $p<0.05$ for trend). The percentage of students reporting influenza infection more than 6 times a year was also highest in the most occupied rooms, 3 or fewer students per room: 3.3%, 4 students per room: 2.1%, 5 or more students per room: 5.1%, unadjusted $p<0.05$ for trend). The trend, however, was not consistent, with 4 persons per room having a lower prevalence of both common-cold and influenza compared to those in rooms of 3 or less.

Tuberculosis

Maina and others conducted a cross-sectional study (rated as medium quality, study design class D) investigating the association between overcrowded university accommodation and TB infection in 51 students with TB and 156 student contacts (of which 5 were diagnosed with TB) in Kenya between 2016 and 2017 (31). The results suggested that sharing a bed with someone with TB was associated with an increased risk of TB infection, although the results were extremely imprecise, as only 5 people who contracted TB were included in the analysis (RR = 22.2, 95% CI: 2.45 to 202, $p=0.008$).

Skin infection

Two studies (both rated as medium quality) investigated the association between living in a dormitory and transmission of skin infections, including dermatophytosis and scabies infections (32, 33). One study was conducted in Turkey (study date not reported (32)), and one study in Pakistan in 2006 (33).

Metintas and others conducted a cross-sectional study (rated as medium quality, study design class D) investigating the association between living in a school dormitory and dermatophytosis infections in 2,384 students in a rural area of Turkey (study period not reported) (32). The results suggested that living in a school dormitory was associated with an increased risk of dermatophytosis compared to living at home (OR = 2.94, 95% CI: 1.72 to 5.05, $p<0.0001$).

Raza and others conducted a case-control study (rated as medium quality, study design class C) investigating the association between bed sharing and scabies infections in 200 male soldier cases and 200 matched male soldier controls housed in a dormitory in Pakistan in 2006 (33). The results suggested sharing a dormitory was associated with an increased risk of scabies infections (cases: 41.5% prevalence, controls: 27% prevalence, OR = 4.44, 95% CI: 2.19 to 9.1).

Summary

Overall, there was consistent evidence across studies that staying in dormitories, particularly with more people, was associated with increased risks of ARIs (5 studies), TB infection (one study), and skin infections (2 studies). Similar to the studies in private households, the results from these studies were mostly imprecise, and there was variation between studies in terms of their populations, study methods, outcomes, and comparator (for example comparing living in dormitories to not living in dormitories, how many people were staying in a room within the dormitories, or bed sharing). As such, it is not possible to directly compare the effect sizes between studies. However, in almost all studies, there was a moderate to large association suggested between staying in a dormitory, or increased number of people staying in a dormitory, with an increased risk of infection.

Vessels

Vessels were defined as ships and boats including barges, cruise ships, ferries, and military ships. Two studies investigated the risk of infectious disease transmission on vessels, both of which investigated influenza infections (34, 35). One study was a case-control study conducted on a cruise ship near Brazil in 2012 (34), and the other study was a cross-sectional study conducted on a US aircraft carrier in 2009 (35). Full data extraction tables for studies of vessels can be found in Table C.1c.

Fernandes and others conducted a case-control study (rated as high-quality, study design class C) investigating the association between housing deck level and the incidence of influenza like illness in 104 acute respiratory illness cases affecting passenger and crew onboard a cruise ship sailing off the coast of Brazil during February 2012 (34). The lower decks (decks 2 to 3) were composed of cabins with poor ventilation, no windows and 2 to 4 persons per room, while the upper decks (decks 4 to 7) were composed of cabins with windows and private rooms. The results suggested that being housed on a lower deck was associated with a higher risk of influenza like illness when compared to those housed on upper decks (OR = 2.39, 95% CI: 1.09 to 5.25).

Harwood and others conducted a cross-sectional study (rated as low-quality, study design class D) investigating the association between the size of berthing areas and influenza infection in 4,596 vaccinated sailors onboard a US aircraft carrier during an influenza outbreak in July 2009 (35). The results suggested only a small association between the square feet of living space per person and the attack rate of influenza (unadjusted correlation coefficient = 0.13, one-tailed p = 0.29), but a negative association between occupancy rate and the attack rate of influenza (unadjusted correlation coefficient = -0.56, one-tailed p = 0.005).

Summary

Overall, the 2 studies looking at transmission of influenza on vessels had conflicting evidence for the association between occupancy rates and infection risk, with one study suggesting the risk of influenza increased with occupancy rate (34), and the other suggesting the risk of influenza decreased with occupancy rate (35).

Emergency shelters, and shelters and hostels for those experiencing homelessness

Six studies investigated infectious disease transmission risk associated with being housed in emergency shelters such as evacuation shelters or storm shelters and shelters or hostels for those experiencing homelessness (one study rated as low-quality (40), 5 studies rated as medium quality (36 to 39, 41)). Five of these studies investigated the risk of ARIs within shelter settings (36 to 40), and one study investigated MRSA nasal colonisation (41). There were 3 cohort studies (38, 39, 41), and 3 cross-sectional studies (36, 37, 40). Three studies were conducted in Europe (36, 39, 40), 2 in the US (37, 41), and one in Japan (38). The studies were all conducted between 2011 and 2021.

Full data extraction tables for studies of emergency shelters, and shelters and hostels for those experiencing homelessness can be found in Table C.1d.

Acute respiratory infections (including COVID-19)

Four studies investigated the transmission risk of ARIs, including COVID-19 specifically (36, 37, 39, 40), and ARIs generally (38).

Alvarez-Fischer and others conducted a cross-sectional study (rated as medium quality, study design class D) comparing the risk of COVID-19 in refugee shelter accommodation and the risk of COVID-19 infections in 97 asylum seekers in Germany to a control group drawn from a prospective, longitudinal population-based cohort study of the local population at 2 different time points; between November and December 2020, and in February 2021 (36). Between November and December 2020, the incidence of COVID-19 was higher amongst those living in refugee shelters (reverse transcriptase polymerase chain reaction [RT-PCR] positivity = 2.1%, 95% CI: 0.4% to 6.3%) than the local population (RT-PCR positivity = 0.1%, 95% CI: 0% to 0.3%, p<0.001), as was the seroprevalence (seropositivity in refugees = 4.1%, 95% CI: 1.4% to 9.2%; seropositivity in local population = 0.5%, 95% CI: 0.3% to 0.8%, p<0.001). The results were similar in February 2021, as both the incidence (RT-PCR positivity in refugees = 3%, 95% CI: 0.5% to 9.1%; RT-PCR positivity in local population = 0.1%, 95% CI: 0% to 0.3%, p<0.001) and seroprevalence (seropositivity in refugees = 37.3%, 95% CI: 27.4% to 48.1%; seropositivity in local population = 1.6%, 95% CI: 1.2% to 2.1%, p<0.001) of COVID-19 were higher in refugees than in the local population.

Ghinai and others conducted a cross-sectional study (rated as medium quality, study design class D) investigating the association between sharing a room and COVID-19 infections in 1,435 residents of a homeless shelter in the US between March and May 2020 (37). The results suggested that sharing a room with increasing numbers of people was associated with an increased prevalence of COVID-19 infection. Sharing with 2 to 4 people (prevalence ratio = 1.35, 95% CI: 0.87 to 2.11, p=0.19), 5 to 8 people (prevalence ratio = 1.59, 95% CI: 1.00 to 2.53, p=0.05), 9 to 20 people (prevalence ratio = 1.64, 95% CI: 1.00 to 2.70 p=0.05), and above 20 people (prevalence ratio = 1.76, 95% CI: 1.11 to 2.80, p = 0.02) all led to a higher prevalence of COVID-19 than in people not sharing a room.

Kawano and others conducted a retrospective cohort study (rated as medium quality, study design class B) investigating the association between crowding (defined as having less than 5.5 m^2 mean floor space per person) and the risk of all ARIs in 7,439 evacuees living in emergency shelters in Japan following the tsunami in March 2011 (38). The results suggested that crowding was associated with an increased cumulative incidence of ARIs, with the crowded shelters having more cases per day than non-crowded shelters (difference = 19.1 cases per 10,000 person-days, 95% CI: 5.9 to 32.4 cases per 10,000 person-days).

Mosnier and others conducted a prospective cohort study (rated as medium quality, study design class B) investigating the association between time spent in homeless shelters and COVID-19 incidence in 1,241 homeless adults in France in 2020 (39). The results suggested that increased time in homeless shelters was associated with an increased risk of COVID-19 infection, with homeless adults spending between 33% and 66% of their time (HR = 1.70, 95% CI: 1.11 to 2.62), and more than 66% of their time (HR = 1.93, 95% CI: 1.18 to 3.15), having higher risks of COVID-19 infection than those who spent less than 33% of their time in shelters.

Roederer and others conducted a cross-sectional study (rated as low-quality, study design class D) investigating the association between living in an emergency shelter, and crowding (defined using a cumulative crowding indicator that considers number of persons per room, sanitary facility, and kitchen as well as number of close contacts per day), and the risk of COVID-19 seropositivity in 818 people experiencing homelessness in France between June and July 2023 (40). The results suggested that living in an emergency shelter was associated with an increased risk of COVID-19 infection when compared to living in other rough sleeping settings, such as food distribution sites (OR = 1.7, 95% CI: 1.1 to 2.7, p=0.025). The results also suggested that people living in high crowding residences (OR = 3.4, 95% CI: 1.7 to 6.9, p<0.0001) and medium crowding residences (OR = 2.7, 95% CI: 1.5 to 5.1, p=0.002) were more at risk of COVID-19 infection than people living in low crowding residences.

Skin infections

Leibler and others conducted a cohort study nested within a randomised controlled trial (rated as medium quality, study design class B) investigating the association between sleeping in a homeless shelter over the past 3 months, and sharing bedding with other people, and the incidence of MRSA nasal colonisation in 78 injecting drug users in the US between October and April 2018 (41). The results suggested that sleeping in a homeless shelter was associated with an increased risk of MRSA nasal colonisation (unadjusted OR = 3.0, 95% CI: 1.2 to 7.6, p=0.02), as was sharing bedding with other people (unadjusted OR = 2.2, 95% CI: 1.0 to 4.7, p=0.05).

Summary

There was consistent evidence across studies that staying in emergency shelters, or shelters or hostels for those experiencing homelessness, particularly crowded shelters, was associated with increased risk of ARIs (5 studies (36 to 40)) and MRSA nasal colonisation (one study (41)). Four studies compared either presence in a shelter or time spent in a shelter as an exposure (36, 39 to 41) suggesting that staying in a shelter compared to not staying in a shelter, particularly for longer amounts of time, were both associated with increased transmission of ARIs and MRSA. Three studies investigated crowding as an exposure (37, 38, 40) and also suggested an association between crowding and increased transmission risk of ARIs. As with studies in other settings, the studies for shelters were heterogeneous, in terms of their populations, study methods, and outcomes, but also whether the studies were measuring staying in a shelter, time spent in a shelter, or crowding within shelters. As such, it is not possible to directly compare the effect sizes between studies. However, in almost all studies, there was a moderate association between staying in an emergency shelter, particularly if crowded, and the risk of ARIs or skin infections.

Inequalities

This review describes the available evidence on the risk of infectious disease transmission posed by non-detained accommodation settings including high-density, communal or crowded settings. These types of accommodation settings are more frequently inhabited by populations that experience social exclusion and poor health outcomes (47).

The increased burden of infection observed in inclusion health groups is likely due to many different contributing factors including a higher background prevalence of infection, low vaccine uptake and poor access to healthcare (44, 48). This review provides evidence to support the contribution of crowded and shared accommodation settings to the observed increased infection risk.

Some of the findings are relevant to specific groups who experience extreme health inequities. For example, studies focusing on homeless shelters identified an increased risk of

transmission of ARIs and MRSA nasal colonisation for individuals living in these settings. One study identified an increased risk of COVID-19 incidence for asylum seekers living in a shelter (36).

The review identified a lack of evidence for transmission risk for some accommodation types including asylum seeker accommodation. In addition, there was little evidence available to explore variations or inequities across populations and subgroups. For example, the review was not able to explore differences in infection transmission within high-density accommodation by ethnicity or deprivation, or across different inclusion health populations.

Limitations

The sources of evidence in this review included articles from published and preprint servers; an extensive search of other sources, such as grey literature, was not conducted. As with all reviews, the evidence identified may be subject to publication bias, whereby null or negative results are less likely to have been published by the authors. This review followed a streamlined methodology and studies were limited to English language and publication from the year 2000 meaning relevant studies or information within studies may have been missed.

The included studies were highly heterogeneous, both in terms of their populations, study methods (including ecological, case-control, cohort, and cross-sectional studies, but no experimental study designs), and outcomes, but also in which exposures the studies measured and how they measured them, such as the number of people, or adults or children, per room, bedroom, or household, or bed sharing, or comparing staying in a specific type of accommodation or somewhere else. The relationships between people sharing accommodation, such as family members or unrelated house shares, were not reported in the majority of studies. The measurement of exposures was also often self-reported. The pathogens included are heterogeneous in their transmission routes and levels of infectiousness and it is likely that the impact of overcrowding varies depending on a range of pathogen-specific factors. As such, it was not possible to directly compare the effect sizes between studies, even those looking at the same outcomes in the same settings. The diversity of the studies also means generalisability to any particular setting is difficult, although notably there was relative consistency of results between studies despite the heterogeneity. Most of the included studies focussed on ARIs, especially COVID-19, with few studies looking at other infections.

It is not possible to directly infer causality from the included studies. Although there are plausible mechanisms for understanding why increasing housing density could increase the risk of transmission of different infections, and the evidence included in this review is broadly supportive of this, all studies were observational with varying approaches to accounting for other factors that might bias the results (confounding variables). The studies suggest an association between increased housing density and increased risk of various infections, but

there may be other explanations for this association. Additionally, housing stock, infrastructure, and architecture may be potential confounding variables, with the possibility that those living in crowded settings may be more likely to live in low-quality, poorly ventilated and poor insulated accommodation. Particular caution with interpretation is needed for the ecological study designs, which compare averages in a population, rather than individuals within that population. This means that the interpretation of these studies may not be generalisable to an individual, as population-level results may not apply to individuals within those populations.

Overall, most identified studies were rated as low or medium quality, with 6 of 41 studies rated as high-quality. This indicates that the majority of included studies are at a higher risk of bias, and many studies had imprecise results. It should be noted that it is generally more difficult to infer causality from study designs lower down the hierarchy (A to D), independent of their quality rating.

Evidence gaps

This rapid review revealed several clear gaps within existing evidence surrounding the risk of infectious disease transmission in shared accommodation sites.

The primary gap identified in this review is the lack of high-quality evidence for risk of infectious disease transmission in all communal accommodation settings. The health inequalities section sets out why this review is likely to be of particular relevance for inclusion health populations. The studies in inclusion health settings were very limited with a small number of studies in homeless hostel studies and one study in an asylum seeker setting outside of the UK. Studies that did include inclusion health settings primarily focused on ARIs, meaning that the transmission risk of infections of particular importance in inclusion health populations (TB, blood-borne viruses and STIs) is not captured.

Most studies compared infectious disease transmission between different exposures within the same accommodation type, such as the density of people in an accommodation setting, rather than comparing risk between different accommodation types, such as the risk of infection between vessels and dormitories. This makes it difficult to directly compare the risk of infection transmission between different accommodation types.

Additionally, there were no studies providing evidence for infection transmission in other commonly used forms of communal accommodation, such as tents, only one study looking at dormitories housing adults, and only 2 studies looking at vessels, which provided inconsistent results. It is therefore difficult to make firm conclusions about infection transmission in these settings.

The limitations section outlines why causality cannot be inferred from the studies identified and the relatively low number of high-quality studies. There is a need for further, high-quality research, with appropriate adjustment for potential confounding variables, to be able to determine the casual relationship between accommodation type and risk of infection transmission. This is needed to inform infection prevention and control advice and strategies to mitigate risk for commissioners and providers of communal accommodation. In addition, this review highlights a specific gap relating to inclusion health populations who are often under-represented in research. Further work is needed to ensure consideration of inclusion health groups within planned research programmes.

Conclusion

Overall, the evidence suggested that being housed in shared or overcrowded accommodation settings, including private housing and HMO settings, dormitories, and shelters, was associated with an increased risk in the transmission of infectious diseases, including ARIs, TB, gastrointestinal, skin, and meningococcal infections. For private households and HMOs, the associations were typically small to moderate in magnitude, whilst the associations were larger for dormitories and shelters. Results were inconsistent for vessels, noting there were only 2 studies included that focused on vessels.

The included studies were highly heterogeneous, in terms of their populations, study methods (including ecological, case-control, cohort, and cross-sectional studies, but no experimental study designs), and outcomes, but also in which exposures the studies measured and how they measured them. This means it was not possible to directly compare the effect sizes between studies, even those looking at the same outcomes in the same settings.

As all studies were observational, with varying approaches to accounting for confounding variables, it is not possible to infer causality from the evidence. Rather, the studies show an association between increased housing density and housing type with increased risk of various infections, but not necessarily that increased housing density or housing type causes an increase in the risk of various infections. Some lower quality studies did not account for important confounding variables and the identified associations may be explained by factors other than those stated in the results.

There were also large evidence gaps including limited studies looking at vessels, only one study looking at dormitories housing adults, relatively few studies looking at infections other than COVID-19, particularly in inclusion health groups.

Acknowledgment

We would like to thank colleagues within the Health Equity division and Clinical and Public Health Response division who either reviewed or input into aspects of the review.

Disclaimer

UKHSA's rapid reviews aim to provide the best available evidence to decision makers in a timely and accessible way, based on published peer-reviewed scientific papers, unpublished reports and papers on preprint servers. Please note that the reviews:

- use accelerated methods and may not be representative of the whole body of evidence publicly available
- have undergone an internal, but not independent, peer review
- are only valid as of the date stated on the review

In the event that this review is shared externally, please note additionally, to the greatest extent possible under any applicable law, that UKHSA accepts no liability for any claim, loss or damage arising out of, or connected with the use of, this review by the recipient or any third party including that arising or resulting from any reliance placed on, or any conclusions drawn from, the review.

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Annexe A: Protocol

Review question

The review question for this rapid scoping review is:

1. What is the risk of infectious disease transmission posed by communal accommodation settings potentially used for housing asylum seekers?

Of particular interest for this review will be capturing infection transmission risk in high-density or over-crowded accommodations shared by non-family members who would not have previously come into contact. Over-crowding is defined as at least 2 people living in less than 18 m^2 per person (49). The definition of high-density is less stringent but often refers to high-rise buildings with facilities shared by large numbers of people (stairs, lifts, bathrooms, communal areas or kitchens) or a high ratio of people dwelling to limited number of living spaces, for example 3 people sharing 6 living rooms (50, 51).

A search for primary evidence to answer these review questions will be conducted up to 16 March 2023.

This work is conducted to support the provision of health protection advice on future accommodation provision for asylum seekers, to ascertain if there is an increased risk of infection transmission in this group compared to the general population. However, due to the lack of evidence specific to these settings, it was agreed to widen the scope to include communal accommodation settings which could conceivably be used as housing for asylum seekers, including:

- disused vessels (barges, cruise ships or ferries) converted to temporary housing
- dormitories or student housing with shared utilities and communal spaces
- homeless shelters or hostels
- houses in multiple occupation (HMO)
- places of detention or detainment, for example immigration removal centres
- temporary settlements such as tented accommodation, camps or marquees

Infectious diseases of interest include (but are not limited to):

- coronavirus (COVID-19)
- diphtheria
- gastrointestinal infections, for example norovirus, shigella or e-coli
- group a streptococcus (GAS), methicillin-resistant staphylococcus aureus (MRSA) or methicillin-sensitive staphylococcus aureus (MSSA)
- influenza

- measles
- tuberculosis
- varicella
- hepatitis A
- hepatitis B or C

Only studies which focus on identifying the risk of infectious disease transmission specific to communal environments will be included. Studies pertaining to other environments which may result in increased risk of infection in asylum seekers will be excluded, such as potential disease outbreak which may occur when travelling to the accommodation sites, transitory locations, or prevalence of infectious diseases in countries of origin. Additionally, studies which discuss measures intended to mitigate the risk of infectious disease outbreak are beyond the scope of this review and will not be included.

Eligibility criteria

	Included	**Excluded**
Population	Any population housed in the settings of interest	Animals
Settings	Communal accommodations: • disused vessels (barges, cruise ships or ferries) converted to temporary housing • dormitories or student housing with shared utilities and communal spaces • homeless shelters or hostels • houses in multiple occupation (HMO) • places of detention or detainment • temporary settlements such as tented accommodation, camps or marquees	• prisons • care homes
Context	Accommodation provision for asylum seekers, but other relevant contexts will be included if they provide evidence	
Intervention or exposure	High-density or over-crowded accommodation when shared by non-family members	High-density or over-crowded accommodation when shared by family members
Outcomes	Risk of transmission or increased risk of outbreak of infectious diseases in	• infection risk arising from travel

	communal accommodations, including: • COVID-19 • diphtheria • gastrointestinal infections • group a streptococcus (GAS), methicillin-resistant staphylococcus aureus (MRSA) or methicillin-sensitive staphylococcus aureus (MSSA) • influenza • measles • tuberculosis • varicella • hepatitis A • hepatitis B or C	• disease outbreaks in the context of countries travelled through or from • studies reporting on mitigations or interventions to reduce infection transmission in these settings
Language	English	
Date of publication	Articles published before 16 March 2023	
Study design	• primary studies	• prevalence based studies • systematic or narrative reviews • guidelines • opinion pieces • genomic sequencing • modelling studies • outbreak reports
Publication type	Published and preprint	

Identification of studies

We will search OVID Medline, OVID Embase, and preprint servers (medRxiv, bioRxiv, aRxiv, and Research Square, via COVID-19 portfolio and preprints via Europe PMC) for studies published prior to 16 March 2023.

Screening

Screening on title and abstract will be undertaken in duplicate by 2 reviewers for at least 10% of the eligible studies, with the remainder completed by one reviewer. Disagreement will be resolved by discussion.

Screening on full text will be undertaken by one reviewer and excludes will be checked by a second.

Data extraction

Summary information for each study will be extracted and reported in tabular form. Information will include infection type, accommodation type, country, study period, study design, participants, results, and any relevant contextual data. This will be undertaken by one reviewer and checked by a second reviewer.

Risk of bias assessment

Risk of bias assessment will be undertaken using the Quality Criteria Checklist by one reviewer and checked by a second reviewer.

Synthesis

A narrative synthesis may be written to describe the results from this review. Note, this will not be performed by CPHR UKHSA evidence team.

Search strategy

Search strategy Ovid Medline

Database: Ovid MEDLINEI ALL (1946 to 15 March 2023)

1 exp Communicable Disease Control/ (409310)
2 (infectio* adj7 (prevent* or control*)).tw,kf. (166495)
3 (disease* adj7 (prevent* or control*)).tw,kf. (327261)
4 (outbreak* adj7 (prevent* or control*)).tw,kf. (13577)
5 ((stop* or Prevent* or reduc* or mitigat*) adj5 spread*).tw,kf. (21614)
6 ((stop* or prevent* or reduc* or mitigat*) adj5 transmi*).tw,kf. (44681)
7 ((stop* or prevent* or reduc* or mitigat*) adj5 risk*).tw,kf. (265062)
8 (risk* adj5 (spread* or transmi* or infecti* or contagi* or outbreak*)).tw,kf. (146028)
9 risk*.ti,kf. (687842)
10 outbreak*.ti,kf. (45149)
11 transmi*.ti,kf. (132175)

12 (Risk/ or Protective Factors/ or Risk Factors/) and (Disease Transmission, Infectious/ or exp Disease Outbreaks/) (13927)
13 (Transmi* adj5 (route* or mode* or method*)).tw,kf. (42464)
14 or/1-13 (1926537)
15 vaccine preventable disease*.tw,kf. (3594)
16 Vaccine-Preventable Diseases/ (227)
17 exp Communicable Diseases/ (562727)
18 (communicable disease* or infectious disease*).tw,kf. (134725)
19 Streptococcus pyogenes/ (14265)
20 S* pyogenes.tw,kf. (9983)
21 Streptococcal Infections/ or Impetigo/ or Scarlet Fever/ (37890)
22 group A strep*.tw,kf. (8266)
23 (strep* A or strep* group A).tw,kf. (2209)
24 scarlet fever.tw,kf. (2576)
25 impetigo.tw,kf. (1793)
26 exp Staphylococcus aureus/ (87815)
27 S* aureus.tw,kf. (132742)
28 (MRSA or MSSA).tw,kf. (29282)
29 Respiratory Tract Infections/ (42438)
30 (respiratory adj5 (infect* or pathogen* or illness* or disease* or contagi* or virus* or viral* or bacteri*)).tw,kf. (162234)
31 exp Tuberculosis/ (205069)
32 tuberculos#s.tw,kf. (234123)
33 Influenza, Human/ (57115)
34 influenza.tw,kf. (113131)
35 exp SARS-CoV-2/ (149731)
36 exp COVID-19/ (213870)
37 (corona* adj1 (virus* or viral*)).tw,kw,kf. (6034)
38 (CoV not (Coefficien* or "co-efficien*" or covalent* or Covington* or covariant* or covarianc* or "cut-off value*" or "cutoff value*" or "cut-off volume*" or "cutoff volume*" or "combined optimi?ation value*" or "central vessel trunk*" or CoVR or CoVS)).tw,kw,kf. (115607)
39 (coronavirus* or 2019nCoV* or 19nCoV* or "2019 novel*" or Ncov* or "n-cov" or "SARS-CoV-2*" or "SARSCoV-2*" or SARSCoV2* or "SARS-CoV2*" or "severe acute respiratory syndrome*" or COVID*2).tw,kw,kf. (351954)
40 Norovirus/ (4870)
41 Rotavirus Infections/ or Rotavirus/ (12605)
42 norovirus.tw,kf. (6558)
43 rotavirus.tw,kf. (15837)
44 Gastrointestinal Diseases/ (41693)
45 (gastrointestinal* adj5 (infect* or pathogen* or illness* or disease* or contagi* or virus* or viral* or bacteri*)).tw,kf. (38992)

46 (gastro-intestinal* adj5 (infect* or pathogen* or illness* or disease* or contagi* or virus* or viral* or bacteri*)).tw,kf. (1115)
47 Skin Diseases, Infectious/ (5729)
48 (skin adj5 (infect* or pathogen* or illness* or disease* or contagi* or virus* or viral* or bacteri*)).tw,kf. (78971)
49 Measles/ (14768)
50 measles.tw,kf. (26065)
51 Diphtheria/ (6938)
52 (diphtheri* or diptheri*).tw,kf. (19625)
53 exp Shigella/ (12275)
54 shigella.tw,kf. (15996)
55 exp Escherichia coli/ (302064)
56 e* coli.tw,kf. (350873)
57 Chickenpox/ (7903)
58 (chicken pox or chickenpox or varicella).tw,kf. (17960)
59 Hepatitis A/ or exp Hepatitis B/ or exp Hepatitis C/ (140888)
60 (hepatitis A or hepatitis B or hepatitis C).tw,kf. (170051)
61 or/15-60 (2341633)
62 Refugee Camps/ (287)
63 Emergency Shelter/ (302)
64 Group Homes/ (1021)
65 ("Transients and Migrants"/ or Refugees/ or (migrant* or asylum seeker* or refugee*).tw,kf.) and (residence* or residential* or home* or hous* or accommodation* or dwelling* or shelter*).tw,kf. (7317)
66 ((asylum* or refugee*) adj3 (camp or camps or camping or campsite*)).tw,kf. (1586)
67 ((homeless* or emergenc* or crisis or evacuation* or evacuee* or large* or mass) adj5 (camp or camps or camping or campsite*)).tw,kf. (779)
68 ((homeless* or emergenc* or crisis or evacuation* or evacuee* or large* or asylum* or refugee*) adj5 shelter*).tw,kf. (1953)
69 ((homeless* or emergenc* or crisis or evacuation* or evacuee* or large* or asylum* or refugee*) adj5 hostel*).tw,kf. (127)
70 (dormitories or dormitory).tw,kf. (926)
71 hotel*.tw,kf. (5135)
72 (large* adj5 (residence* or residential* or home* or hous* or accommodation* or dwelling* or shelter*)).tw,kf. (9158)
73 housing facilit*.tw,kf. (414)
74 (residential facilit* or residential setting*).tw,kf. (2385)
75 ((refugee* or asylum*) adj3 settlement*).tw,kf. (209)
76 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 home*).tw,kf. (13360)
77 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 hous*).tw,kf. (10215)

78 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 dwelling*).tw,kf. (972)
79 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 shelter*).tw,kf. (395)
80 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 accommodation*).tw,kf. (549)
81 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 (residential* or residence*)).tw,kf. (2813)
82 (high-density adj5 (residence* or residential* or home* or hous* or accommodation* or dwelling* or shelter*)).tw,kf. (379)
83 ((overcrowd* or crowd*) adj5 (residence* or residential* or home* or hous* or accommodation* or dwelling* or shelter*)).tw,kf. (1664)
84 marquee*.tw,kf. (306)
85 (tent or tents).tw,kf. (2198)
86 ((immigrant* or migrant* or immigration* or refugee* or asylum*) adj5 (detain* or detention* or incarcerat* or secure setting* or secure accommodation*)).tw,kf. (465)
87 ((immigrant* or migrant* or immigration* or refugee* or asylum*) adj5 (removal* or removing or remove*)).tw,kf. (85)
88 (vessel* and (marine or sea* or cruise* or river* or refugee* or asylum* or migrant* or immigrant*)).tw,kf. (10756)
89 (boat or boats or barge* or ship or ships or ferries or ferry).tw,kf. (15755)
90 Ships/ (7156)
91 ((Diamond or Grand or Regal or Golden or Pacific or Caribbean or Royal or Ruby) adj1 princess).tw,kf. (163)
92 or/62-91 (89473)
93 14 and 61 and 92 (4269)

Search strategy Ovid Embase

Database: Embase (1974 to 16 March 2023)

1 exp communicable disease control/ (159955)
2 (infectio* adj7 (prevent* or control*)).tw,kf. (214865)
3 (disease* adj7 (prevent* or control*)).tw,kf. (449936)
4 (outbreak* adj7 (prevent* or control*)).tw,kf. (15817)
5 ((stop* or Prevent* or reduc* or mitigat*) adj5 spread*).tw,kf. (25103)
6 ((stop* or prevent* or reduc* or mitigat*) adj5 transmi*).tw,kf. (54819)
7 ((stop* or prevent* or reduc* or mitigat*) adj5 risk*).tw,kf. (386789)
8 (risk* adj5 (spread* or transmi* or infecti* or contagi* or outbreak*)).tw,kf. (201940)
9 risk*.ti,kf. (1000188)
10 outbreak*.ti,kf. (48434)
11 transmi*.ti,kf. (151394)
12 infection risk/ (102387)

13 (risk factor/ or risk/ or exp environmental risk/) and (exp disease transmission/ or exp epidemic/) (39282)
14 (Transmi* adj5 (route* or mode* or method*)).tw,kf. (53282)
15 or/1-14 (2333073)
16 vaccine preventable disease*.tw,kf. (4293)
17 vaccine preventable disease/ (719)
18 communicable disease/ (38620)
19 (communicable disease* or infectious disease*).tw,kf. (179828)
20 Streptococcus pyogenes/ or exp group A streptococcal infection/ or streptococcus group a/ (34956)
21 S* pyogenes.tw,kf. (12191)
22 Streptococcal Infections/ or Impetigo/ or Scarlet Fever/ (13766)
23 group A strep*.tw,kf. (9483)
24 (strep* A or strep* group A).tw,kf. (2421)
25 scarlet fever.tw,kf. (1148)
26 impetigo.tw,kf. (2299)
27 exp Staphylococcus aureus/ (208839)
28 S* aureus.tw,kf. (171124)
29 (MRSA or MSSA).tw,kf. (43957)
30 respiratory tract infection/ (67521)
31 (respiratory adj5 (infect* or pathogen* or illness* or disease* or contagi* or virus* or viral* or bacteri*)).tw,kf. (221193)
32 exp tuberculosis/ (221034)
33 tuberculos#s.tw,kf. (213129)
34 exp influenza/ (106099)
35 influenza.tw,kf. (129994)
36 exp severe acute respiratory syndrome coronavirus 2/ (95279)
37 coronavirus disease 2019/ or experimental coronavirus disease 2019/ (337971)
38 (corona* adj1 (virus* or viral*)).tw,kw,kf. (7490)
39 (CoV not (Coefficien* or "co-efficien*" or covalent* or Covington* or covariant* or covarianc* or "cut-off value*" or "cutoff value*" or "cut-off volume*" or "cutoff volume*" or "combined optimi?ation value*" or "central vessel trunk*" or CoVR or CoVS)).tw,kw,kf. (143215)
40 (coronavirus* or 2019nCoV* or 19nCoV* or "2019 novel*" or Ncov* or "n-cov" or "SARS-CoV-2*" or "SARSCoV-2*" or SARSCoV2* or "SARS-CoV2*" or "severe acute respiratory syndrome*" or COVID*2).tw,kw,kf. (429341)
41 exp Norovirus/ or norovirus infection/ (8824)
42 rotavirus/ or human rotavirus/ or Rotavirus infection/ (18379)
43 norovirus.tw,kf. (8020)
44 rotavirus.tw,kf. (19020)
45 gastrointestinal disease/ (99102)
46 (gastrointestinal* adj5 (infect* or pathogen* or illness* or disease* or contagi* or virus* or viral* or bacteri*)).tw,kf. (52217)

47 (gastro-intestinal* adj5 (infect* or pathogen* or illness* or disease* or contagi* or virus* or viral* or bacteri*)).tw,kf. (1552)
48 exp skin infection/ (186081)
49 (skin adj5 (infect* or pathogen* or illness* or disease* or contagi* or virus* or viral* or bacteri*)).tw,kf. (107146)
50 exp measles/ (22670)
51 measles.tw,kf. (26850)
52 diphtheria/ (9774)
53 (diphtheri* or diptheri*).tw,kf. (16778)
54 exp Shigella/ (19709)
55 shigella.tw,kf. (16043)
56 exp Escherichia coli/ (423131)
57 e* coli.tw,kf. (381945)
58 chickenpox/ (12787)
59 (chicken pox or chickenpox or varicella).tw,kf. (22752)
60 exp hepatitis a/ or exp hepatitis b/ or exp hepatitis c/ (232172)
61 (hepatitis A or hepatitis B or hepatitis C).tw,kf. (249870)
62 or/16-61 (2575159)
63 refugee camp/ (1077)
64 emergency shelter/ (617)
65 (exp migrant/ or (migrant* or asylum seeker* or refugee*).tw,kf.) and (residence* or residential* or home* or hous* or accommodation* or dwelling* or shelter*).tw,kf. (9683)
66 ((asylum* or refugee*) adj3 (camp or camps or camping or campsite*)).tw,kf. (1718)
67 ((homeless* or emergenc* or crisis or evacuation* or evacuee* or large* or mass) adj5 (camp or camps or camping or campsite*)).tw,kf. (934)
68 ((homeless* or emergenc* or crisis or evacuation* or evacuee* or large* or asylum* or refugee*) adj5 shelter*).tw,kf. (2346)
69 ((homeless* or emergenc* or crisis or evacuation* or evacuee* or large* or asylum* or refugee*) adj5 hostel*).tw,kf. (202)
70 (dormitories or dormitory).tw,kf. (1177)
71 hotel*.tw,kf. (6117)
72 (large* adj5 (residence* or residential* or home* or hous* or accommodation* or dwelling* or shelter*)).tw,kf. (11298)
73 housing facilit*.tw,kf. (514)
74 (residential facilit* or residential setting*).tw,kf. (3041)
75 ((refugee* or asylum*) adj3 settlement*).tw,kf. (202)
76 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 home*).tw,kf. (18475)
77 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 hous*).tw,kf. (13008)
78 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 dwelling*).tw,kf. (1248)

79 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 shelter*).tw,kf. (454)
80 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 accommodation*).tw,kf. (956)
81 ((share* or sharing or group* or communal* or collectiv* or multiple occup* or congregat* or centrali#ed or mass) adj5 (residential* or residence*)).tw,kf. (3549)
82 (high-density adj5 (residence* or residential* or home* or hous* or accommodation* or dwelling* or shelter*)).tw,kf. (449)
83 ((overcrowd* or crowd*) adj5 (residence* or residential* or home* or hous* or accommodation* or dwelling* or shelter*)).tw,kf. (1938)
84 marquee*.tw,kf. (160)
85 (tent or tents).tw,kf. (2893)
86 ((immigrant* or migrant* or immigration* or refugee* or asylum*) adj5 (detain* or detention* or incarcerat* or secure setting* or secure accommodation*)).tw,kf. (537)
87 ((immigrant* or migrant* or immigration* or refugee* or asylum*) adj5 (removal* or removing or remove*)).tw,kf. (79)
88 (vessel* and (marine or sea* or cruise* or river* or refugee* or asylum* or migrant* or immigrant*)).tw,kf. (16321)
89 (boat or boats or barge* or ship or ships or ferries or ferry).tw,kf. (17745)
90 ship/ (6146)
91 ((Diamond or Grand or Regal or Golden or Pacific or Caribbean or Royal or Ruby) adj1 princess).tw,kf. (248)
92 or/63-91 (112466)
93 15 and 62 and 92 (4689)

Europe PMC

(SRC:"PPR") (TITLE:transmi* OR TITLE:”outbreak*” OR TITLE:”infectious disease*” OR TITLE:”disease spread*” OR TITLE:”contagious disease*” OR TITLE:“infection risk*” OR TITLE:“outbreak risk*” OR TITLE:“contagion risk*” OR TITLE:“disease* risk*”) AND (TITLE:shared OR TITLE:communal* OR TITLE:”multiple occup*” OR TITLE:refugee* OR TITLE:asylum* OR TITLE:migrant* OR TITLE:immigrant*) AND (TITLE:accommodation OR TITLE:housing OR TITLE:home* OR TITLE:house* OR TITLE:camp OR TITLE:camps OR TITLE:campsite* OR TITLE:dormitory* OR TITLE:ship OR TITLE:ships OR TITLE:”high densit*”) - 8 results
(SRC:"PPR") (TITLE:measles OR TITLE:hepatitis OR TITLE:streptococcus OR TITLE:staphylococcus OR TITLE:MRSA OR TITLE:MSSA OR TITLE:tuberculosis OR TITLE:influenza OR TITLE:Covid OR TITLE:sars-cov-2 OR TITLE:varicella OR TITLE:”chicken pox” OR TITLE:diphtheria OR TITLE:shigella OR TITLE:e*coli) AND (TITLE:shared OR TITLE:communal* OR TITLE:”multiple occup*” OR TITLE:refugee* OR TITLE:asylum* OR TITLE:migrant* OR TITLE:immigrant*) AND (TITLE:accommodation OR TITLE:housing OR TITLE:home* OR TITLE:house* OR TITLE:camp OR TITLE:camps OR

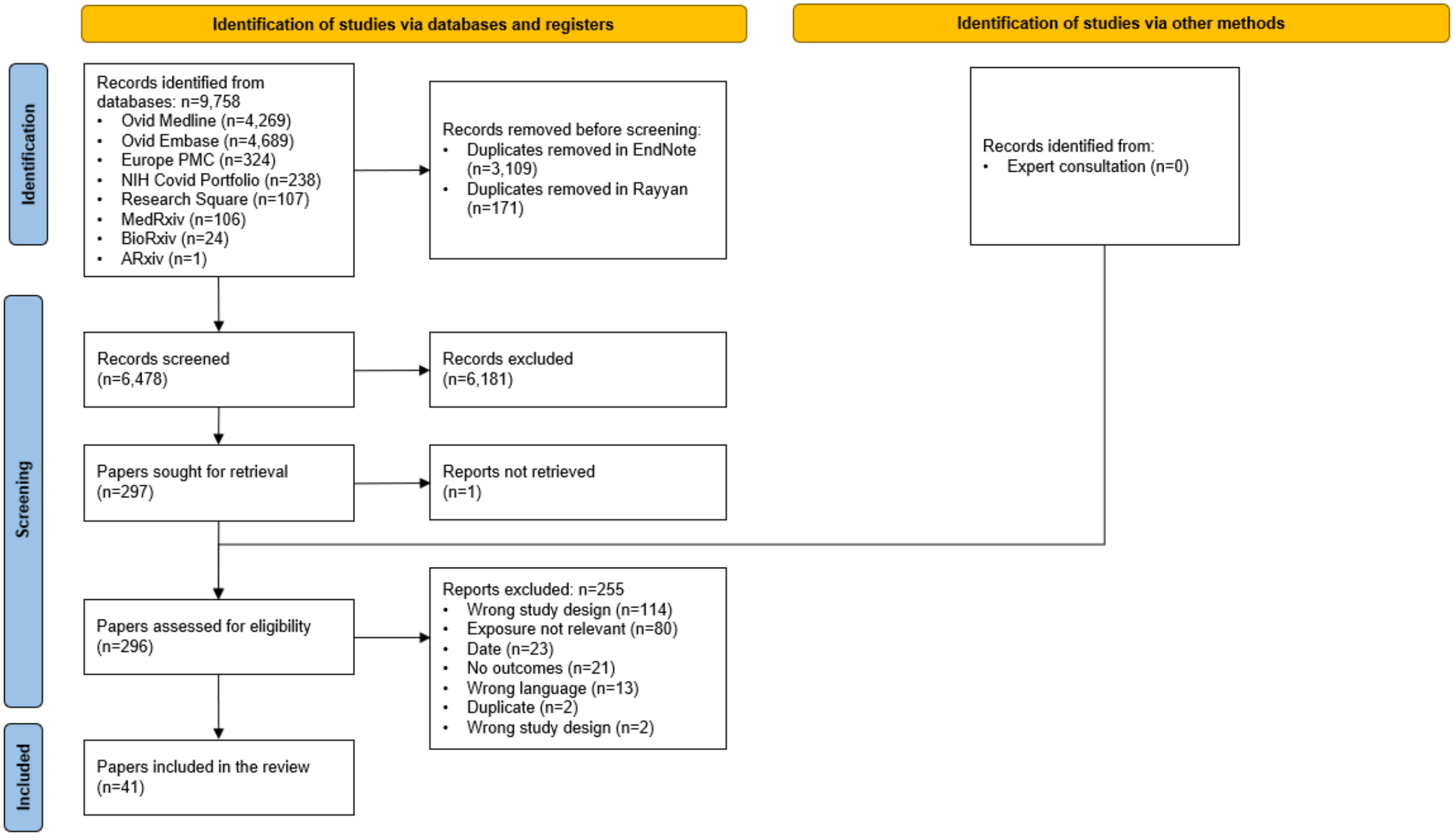
TITLE:campsite* OR TITLE:dormitory* OR TITLE:ship OR TITLE:ships OR TITLE:”high densit*”) - 31 results
(SRC:"PPR") (ABSTRACT:transmi* OR ABSTRACT:”disease outbreak*” OR ABSTRACT:”infectious disease*” OR ABSTRACT:”disease spread*” OR ABSTRACT:”contagious disease*” OR ABSTRACT:“infection risk*” OR ABSTRACT:“outbreak risk*” OR ABSTRACT:“contagion risk*” OR ABSTRACT:“disease* risk*”) AND (ABSTRACT:shared OR ABSTRACT:communal* OR ABSTRACT:”multiple occup*” OR ABSTRACT:refugee* OR ABSTRACT:asylum* OR ABSTRACT:migrant* OR ABSTRACT:immigrant*) AND (ABSTRACT:accommodation OR ABSTRACT:housing OR ABSTRACT:home* OR ABSTRACT:house* OR ABSTRACT:camp OR ABSTRACT:camps OR ABSTRACT:campsite* OR ABSTRACT:dormitor* OR ABSTRACT:ship OR ABSTRACT:ships OR ABSTRACT:”high densit*”) – 143 results
(SRC:"PPR") (ABSTRACT:measles OR ABSTRACT:hepatitis OR ABSTRACT:streptococcus OR ABSTRACT:staphylococcus OR ABSTRACT:MRSA OR ABSTRACT:MSSA OR ABSTRACT:tuberculosis OR ABSTRACT:influenza OR ABSTRACT:Covid OR ABSTRACT:sars-cov-2 OR ABSTRACT:varicella OR ABSTRACT:”chicken pox” OR ABSTRACT:diphtheria OR ABSTRACT:shigella OR ABSTRACT:e*coli) AND (ABSTRACT:shared OR ABSTRACT:communal* OR ABSTRACT:”multiple occup*” OR ABSTRACT:refugee* OR ABSTRACT:asylum* OR ABSTRACT:migrant* OR ABSTRACT:immigrant*) AND (ABSTRACT:accommodation OR ABSTRACT:housing OR ABSTRACT:home* OR ABSTRACT:house* OR ABSTRACT:camp OR ABSTRACT:camps OR ABSTRACT:campsite* OR ABSTRACT:dormitor* OR ABSTRACT:ship OR ABSTRACT:ships OR ABSTRACT:”high densit*”) - 324 results

NIH Covid portfolio
(transmi* OR ”disease outbreak*” OR ”infectious disease*” OR ”disease spread*” OR ”contagious disease*” OR “infection risk*” OR “outbreak risk*” OR “contagion risk*” OR “disease* risk*”) AND (shared OR communal* OR ”multiple occup*” OR refugee* OR asylum* OR migrant* OR immigrant*) AND (accommodation OR housing OR home* OR house* OR camp OR camps OR campsite* OR dormitor* OR ship OR ships OR high densit*)

MedRxiv – 106 results
BioRxiv – 24 results
Arxiv – 1 result
Research Square – 107 results

PRISMA diagram

Figure A.1. PRISMA diagram



Text version of Figure A.1. PRISMA diagram

A PRISMA diagram showing the flow of studies through this review, ultimately including 41 studies concerning infectious disease transmission posed by communal accommodation settings.

From identification of studies via databases for the studies, n=9,758 records were identified from the databases:

- Ovid Medline (n=4,269)
- Ovid Embase (n=4,689)
- Europe PMC (n=324)
- NIH Covid Portfolio (n=238)
- Research Square (n=107)
- MedRxiv (n=106)
- BioRxiv (n=24)
- Arxiv (n=1)

From these, records removed before screening:

- duplicates removed in EndNote (n=3,109)
- duplicates removed in Rayyan (n=171)

n=6,478 records screened, of which n=6,181 were excluded, leaving n=297 papers sought for retrieval, of which n=296 were retrieved (n=1 not retrieved).

Of the n=296 papers assessed for eligibility, n=255 reports were excluded:

- wrong study design (n=114)
- exposure not relevant (n=80)
- date (n=23)
- no outcomes (n=21)
- wrong language (n=13)
- duplicate (n=2)
- wrong study design (n=2)

From identification of studies via other methods, n=0 studies were identified from expert consultation, and n=0 studies were identified from previous reviews.

Overall, n=41 papers included concerning infectious disease transmission posed by communal accommodation settings.

Annexe B: Excluded full texts

Reasons for exclusion of studies at full text screening (n=255)

Exclusion reason = wrong study design (n=114)

Accorsi EK and others. 'Sleeping Within Six Feet: Challenging Oregon's Labor Housing COVID-19 Guidelines' Journal of Agromedicine 2020: volume 25, issue 4, pages 413-6

Acevedo F and others. 'Varicella at sea: a two-year study on cruise ships' International Maritime Health 2011: volume 62, issue 4, pages 254-61

Acevedo-Garcia D. 'Residential segregation and the epidemiology of infectious diseases' Social Science and Medicine 2000: volume 51, issue 8, pages 1143-61

Adams B. 'Household demographic determinants of Ebola epidemic risk' Journal of Theoretical Biology 2016: volume 392, pages 99-106

Adiga A and others. 'Disparities in spread and control of influenza in slums of Delhi: findings from an agent-based modelling study' BMJ Open 2018: volume 8, issue 1, pages e017353

Adrami O and others. 'Health interventions in Refugee camps' Tropical Medicine and International Health 2009: volume 2, pages 244

Ahmed S and others. 'Mathematical model of transmission dynamics and optimal control strategies for 2017-2018 diphtheria outbreak in Rohingya refugee camp in Bangladesh' International Journal of Infectious Diseases 2020: volume 101, pages 211

Aiello AE and others. 'Design and methods of a social network isolation study for reducing respiratory infection transmission: The Ex-FLU cluster randomized trial' Epidemics 2016: volume 15, pages 38-55

Al-Abdullah N. 'A measles outbreak in a refugee community in Jeddah City, Saudi Arabia' Journal of Hospital Infection 2018: volume 100, issue 4, pages e264-e5

Alahakoon P and others. 'How effective was maritime quarantine in Australia during the influenza pandemic of 1918-19?' 41. 2023: volume 18

Alvarez GG and others. 'Molecular epidemiology of Mycobacterium tuberculosis to describe the transmission dynamics among Inuit residing in Iqaluit Nunavut using whole genome

sequencing' Clinical infectious diseases: an official publication of the Infectious Diseases Society of America. 2020: volume 13

Anonymous. 'From the Centers for Disease Control and Prevention. Outbreaks of gastroenteritis associated with noroviruses on cruise ships–United States, 2002' JAMA 2003: volume 289, issue 2, pages 167-9

Anonymous. 'Outbreak of 2009 pandemic influenza A (H1N1) on a Peruvian Navy ship – June-July 2009'. MMWR – Morbidity and Mortality Weekly Report 2010: volume 59, issue 6, pages 162-5

Anonymous. 'Outbreaks of gastroenteritis associated with noroviruses on cruise ships–United States, 2002'. MMWR – Morbidity and Mortality Weekly Report 2002: volume 51, issue 49, pages 1112-5

Anonymous. 'Public health dispatch: tuberculosis outbreak in a homeless population–Portland, Maine, 2002-2003'. MMWR – Morbidity and Mortality Weekly Report 2003: volume 52, issue 48, pages 1184

Attal-Juncqua A and others. Health services in long-term refugee camps: Implications for integration with national surveillance systems. American Journal of Tropical Medicine and Hygiene; (Attal-Juncqua, Reddy, Sorrell, Standley) Georgetown University, Washington, DC, United States A. Attal-Juncqua, Georgetown University, Washington, DC, United States2019. P. 223.

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Annexe C: Data extraction table

Table C.1a: Private households and houses in multiple occupation
Abbreviations: CI = confidence interval, GAS = Group A Streptococcal, IQR = interquartile range, MRSA = Methicillin-resistant Staphylococcus aureus, PCR = polymerase chain reaction, QCC = Quality Criteria Checklist, UK = United Kingdom, US = United States

Reference	Study design	Methods	Key findings	Risk of bias
Ahmed and others, 2020 (1) Association of poor housing conditions with COVID-19 incidence and mortality across US counties	Study design: Ecological Population: US counties (n=3,141) Country: United States Study period: 21 April 2020	Exposure: Poor housing conditions (including overcrowding, high housing cost, incomplete kitchen facilities, or incomplete plumbing facilities). Outcome measurement: COVID-19 infection and mortality (publicly available data collected from the Centers for Disease Control, US census Bureau and John Hopkins Coronavirus Resource Center). Statistical analysis Multivariable regression including the variables population density and test density, demographics, socioeconomic status, respiratory exposure, prevalence of comorbidities, medicare hospitalization rates, access to healthcare.	County COVID-19 incidence as of 21 April 2020 related to percent households with poor housing conditions: Incidence rate ratio: 1.59 (95% CI: 1.49 to 1.70)	Risk of bias: Confounding: ecological bias QCC rating: medium Study design class: D
Baker and others, 2000 (25) Household crowding a major risk factor for epidemic meningococcal disease in Auckland children	Study design: Case-control Participants: • n=202 cases of confirmed and probable meningococcal disease in children younger than 8 years old. • n=313 controls cluster sample matched with age and ethnicity to cases (recruited door-to-door).	Exposure: Questionnaire of demographic and environmental features including number of adults per room (the number of rooms included the kitchen, dining room, living room/s, bedrooms and sleeping areas in camper vans, sheds, and garage). This was measured as a continuous variable. Bed sharing was also an exposure. Outcome measurement: Meningococcal disease through laboratory testing and symptom identification.	Cases of meningococcal disease relating to number of persons per room: • cases = median reported incidence of disease: 0.60 • controls = median reported incidence of disease: 0.43 • odds ratio for risk of meningococcal disease = 10.7 (95% CI: 3.9 to 29.5, p<0.0001) Cases of meningococcal disease relating to bed sharing: • cases = frequency of reported incidence of disease: 72%	Risk of bias: • selection bias: cases and controls recruited differently • exposure measures were self-reported (potential recall bias) QCC rating: medium Study design class: C

Reference	Study design	Methods	Key findings	Risk of bias
	Age: • 0 to 1 years = 55 (27%) cases and 65 (21%) controls • 1 to 2 years = 63 (31%) cases and 85 (27%) controls • 3 to 4 years = 46 (23%) cases and 83 (26%) controls • 5 to 7 years = 38 (19%) cases and 80 (26%) controls Gender: • male = 114 (56%) cases and 167 (53%) controls • female = 88 (44%) cases and 146 (47%) controls Country: New Zealand Study Period: May 1997 to March 1999	Statistical analysis: Multivariable regression including the variables age, ethnicity, possession of community service card, education level and other confounding variables including analgesic use by child, number of smokers in usual household, sharing an item of food, drink or pacifier, number of days of attendance at substantial social gatherings, symptoms of respiratory infection in a household member, symptoms of respiratory infection in child.	• controls = frequency of reported incidence of disease: 49% • odds ratio for risk of meningococcal disease = 1.5 (95% CI 0.9 to 2.5, p=0.11)	
Baker and others, 2008 (14) Tuberculosis associated with household crowding in a developed country	Study design: Ecological Population: N=1860 census area units in New Zealand (non-administrative geographical areas) Country: New Zealand	Exposure Proportion of household crowding (a bedroom deficit of one or more), proportion of population who are migrants born in high-tuberculosis-incidence countries, median household income, and deprivation level. Outcome measurement: Incidence of tuberculosis cases in the total population in each census area units, as well as the subgroups of local-born population (sub-group: less than 40 years old, equal to or more than 40 years old) and migrant population. The number of tuberculosis cases by	Relationship between tuberculosis and crowding (total population): Incidence rate ratio = 1.05 (95% CI: 1.02 to 1.08, p=0.001) New Zealand born people aged less than 40 years: Incidence rate ratio = 1.08 (95% CI:1.04 to 1.12, p<0.001)	Risk of bias: Confounding: ecological bias QCC rating: medium Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
	Study period: Notified tuberculosis cases for the 2000 to 2004 period	census area units was determined from tuberculosis surveillance data from the Institute of Environmental Science and Research Limited (ESR). Statistical analysis: Multivariable analysis including crowding, migrants born in high tuberculosis incidence countries, socioeconomic status, proportion of people less than 40 years and the incidence of tuberculosis cases in total population in previous 5-year period in the full model of the total population. The model of the New Zealand population only included crowding, migrants born in in high tuberculosis incidence countries, median income for households with at least one New Zealand born person, proportion of people under 40 years, incidence of tuberculosis cases in total population in previous 5-year period and incidence of tuberculosis cases in New Zealand born population in previous 5-year period.		
Bennett and others, 2022 (13) Risk factors for group A streptococcal pharyngitis and skin infections: A case-control study.	Study design: Case-control Participants: • n=733 children: n=543 cases and n=190 controls cases breakdown: • n=210 pharyngitis cases • n=182 seronegative carriers • n=151 skin infections • mean age: 9.2 years (range 5 to 14 years) • sex: n=41.2 (56%) male, n=321 (44%) female • ethnicity: n=244 (33%) Maori, n=278 (38%) Pacific, n=86	Exposure: Bed sharing and household crowding, with household crowding measured using the American Crowding Index: • crowding: more than one person per room (excluding bathrooms, balconies, porches, foyers, hallways and half-rooms) • severe crowding: more than 1.5 persons per room Outcome measurement: Group A Streptococcal pharyngitis (GAS), seronegative carrier and Group A Streptococcal skin infection confirmed through swab and blood samples Statistical analysis: Multivariable logistic regression adjusting for age, sex, ethnicity, and socioeconomic deprivation.	GAS pharyngitis infection by household crowding: • crowded: n=110 (52.9%) • not crowded: n=98 (47.1%) • odds ratio: 1.5 (95% CI: 0.9 to 2.4) GAS carrier status by household crowding: • crowded: n=92 (50.8%) • not crowded: n=89 (49.2%) • odds ratio: 1.6 (95% CI: 1.0 to 2.8) GAS positive skin infections by household crowding: • crowded: n=100 (66.2%) • not crowded: n=51 (33.8%) • odds ratio: 1.9 (95% CI: 1.0 to 3.4) GAS pharyngitis infection by number of people bed sharing:	Risk of bias: Exposure measurement: self-reported QCC rating: medium Study design class: C

Reference	Study design	Methods	Key findings	Risk of bias
	(12%) Asian, n-125 (17%) NZ European Country: New Zealand Study period: March 2018 to October 2019		• sharing with more than one person: n=81 (38.6%) • sharing with no one: n=129 (61.4%) • odds ratio: 1.3 (95% CI: 0.8 to 2.3) GAS carrier status by number of people bed sharing: • sharing with more than one person: n=70 (38.7%) • sharing with no one: n=111 (61.3%) • odds ratio: 1.3 (95% CI: 0.8 to 2.2) GAS positive skin infections by number of people bed sharing: • sharing with more than one person: n=61 (40.4%) • sharing a bed with no one: n=90 (59.6%) • odds ratio: 1.4 (95% CI: 0.8 to 2.6)	
Bigwan and others, 2014 (15) Some risk factors associated with Acid-alcohol-fast bacilli in patients with suspected pulmonary tuberculosis in Jos, central Nigeria	Study design: Cross-sectional Participants: • n=303 sputum samples of suspected tuberculosis patients • age: 15 years and older Country: Nigeria Study Period: Not stated	Exposure: Structured questionnaire on number of people staying together in the same household and number of persons sharing the same room Outcome measurement: Smear positive for acid-alcohol-fast bacilli through sputum samples using Ziehl Neelson method Statistical analysis: Descriptive statistics and chi-square test.	Number of positive smears by number of people staying together: • 1 person = 2 out of 29 (6.89%) • 2 persons = 1 out of 41 (2.44%) • 3 persons = 6 out of 48 (12.50%) • more than 4 persons = 20 out of 185 (10.81%) p<0.05 The prevalence of smear-positive increased with increase in number of persons sharing the same room and number of persons staying in a household.	Risk of bias: • selection bias: lack of information on recruitment and baseline demographics • confounding: no assessment of basic confounders (age, sex, and some measure of socioeconomic deprivation) • measurement of exposure is self-reported QCC rating: low Study design class: D
Blakiston and others, 2020 (21) Population-level exposures associated	Study design Ecological	Exposure: Household crowding based on Canadian National Occupancy Standard. Collected from 2013 Census data.	Association between living in crowded housing and MRSA infection: Spearman's correlation coefficient = 0.90 (95% CI: 0.74 to 0.96, p<0.01)	Risk of bias: Confounding: ecological bias and no adjustment for basic variables (age, sex or some measure of socioeconomic deprivation)

Reference	Study design	Methods	Key findings	Risk of bias
with MRSA and ESBL-E. coli infection across district health boards in Aotearoa New Zealand: an ecological study	Population: N=18 geographically distinct districts. Country: New Zealand Study period: 2013	Outcome measurement: Incidence rate of Methicillin-resistant Staphylococcus aureus (MRSA) and Escherichia-coli obtained from national survey of all public and private laboratories. Statistical analysis Spearman's correlation coefficient test for association.	Association between living in crowded housing and Escherichia-coli infection: Spearman's correlation coefficient = 0.77 (95% CI: 0.34 to 0.60, p=0.50)	QCC: medium Study design class: D
Boukari and others, 2022 (2) SARS-CoV-2 infections in migrants and the role of household overcrowding: A causal mediation analysis of Virus Watch data	Study design: Retrospective cohort Participants • n=23,478 adults (n=21,416 UK born and n=2062 migrants) • mean age: 59 years (SD: 15 years) • gender: 12810 females (54.6%), 10276 males (43.8%), and 392 (1.7%) unknown. • ethnicity: n=20456 (87.1%) White British, 2544 (10.8%) Minority ethnic and 478 (2.0%) missing Country: England and Wales Study period: 1 September 2020 to 30 April 2021	Exposure: Persons per room, excluding kitchens and bathrooms. Overcrowding was defined as greater than one person per room. Outcome measurement: COVID-19 infection confirmed by self-report test results and monthly antibody screening. Statistical analysis: Buis' logistic decomposition regression with bootstrapped standard errors was used to estimate the total and direct effects of migration status on infection, and the indirect effects mediated through household overcrowding, adjusting for age, sex at birth, ethnicity, clinical vulnerability baseline total household income, occupation and whether the household included children. Confounders were identified using a directed acyclic graph.	10.9% of migrants lived in overcrowded housing compared with 2.0% of the UK-born group. COVID-19 infection for migrants versus UK born individuals: • direct odds ratio = 1.22 (95% CI: 1.01 to 1.47, p=0.04) COVID-19 infection with household crowding as mediator: • indirect odds ratio = 1.07 (95% CI: 1.03 to 1.12, p=0.002) Household crowding accounted for 32% of the effect in the difference in odds of COVID-19 infection between migrants and UK-born individuals.	Risk of bias: None identified QCC rating: high Study design class: B
Cerami and others, 2022 (3)	Study design: Prospective cohort	Exposure: High household density (defined as having more than 3 persons in fewer than 6 rooms).	Secondary household attack rate: • high living density: 52% (95% CI: 27 to 75)	

Reference	Study design	Methods	Key findings	Risk of bias
Household Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 in the United States: Living Density, Viral Load, and Disproportionate Impact on Communities of Colour	Participants: • n=91 index cases (earliest onset of infection within a household) and N= 176 household contacts • median age (index cases): 37 years (IQR: 4 to 7 years) • age range (household contacts): 2 to 77 years • gender: n=130 (49%) male, n=137 (51%) female • race: n=148 (55%) White or non-Hispanic, n=116 (43%) non white, n=3 (2%) unknown Country: United States Study period: Recruitment occurred between April 2020 to October 2020 and the study follow up period was 28 days	Outcome measurement: Severe Acute Respiratory Syndrome Coronavirus 2 infection confirmed with PCR testing from nasal swabs and blood samples taken for serology (days 1, 7, 14 and 21). Index cases completed daily questionnaires until they reported no symptoms for 2 days. Household contacts completed daily questionnaires for 21 days. Participants all received serological testing from blood samples on day 28 (final visit). Statistical analysis Secondary household attack rate with 96% Cis (risk of incident infection among household contacts) calculated as the proportion of contacts who were PCR negative at baseline and developed infection during the study follow up. Multivariable logistic regression, including the variables non-white, white, non-Hispanic, higher index nasopharyngeal viral load, high living density, not high living density.	• not high living density: 24% (95% CI: 15 to 37) Infection risk in those living in high-density households versus those not: Odds ratio: 1.4 (95% CI 0.4 to 4.6)	Risk of bias: Confounding: no adjustment for basic variables age and sex QCC rating: medium Study design class: B
Dasgupta and others, 2020 (4) Association Between Social Vulnerability and a County's Risk for Becoming a COVID-19 Hotspot –	Study design: Ecological Population level: US counties (n=3142) Country: United States	Exposure: Social vulnerability measures including overall social vulnerability score, socioeconomic status, household composition and distribution, racial and ethnic minority, housing type and transportation and percentage of households with more persons than rooms.	Percentage of housing structures with more than or equal to 10 units (median = 2.9%) Risk ratio of being a COVID-19 hot spot in counties that had equal to or above the median percentage of housing structures with more than or equal to 10 units compared to countries with less than the median percentage = 3.1 (95% CI: 2.7 to 3.6)	Risk of bias: • selection bias: county level age, sex or other baseline demographic distributions not assessed • confounding: ecological bias and no adjustment for basic variables (age, sex

Reference	Study design	Methods	Key findings	Risk of bias
United States, June 1-July 25, 2020	Study period: 1 June to 25 July 2020, linked with CDC social vulnerability data from 2018.	Outcome measurement: Daily country level COVID-19 case counts were obtained through USAFacts and hotspots were identified from March 8 2020 onwards. Hotspots were defined as countries which met the following 4 center for disease control standard criteria: • more than 100 new COVID-19 cases in the most recent 7 days • higher COVID-19 incidence in the most recent 7 days incidence compared with the preceding 7 days • a decrease of less than 60% or an increase in the most recent 3 day COVID-19 incidence over the preceding 3 day incidence • the ratio of 7 day incidence to 30-day incidence exceeds 0.31 Additionally, hotspots must have either more than a 60% change in the most recent 3 day COVID-19 incidence or more than a 60% change in the most recent 7 day incidence. Statistical analysis: Risk ratios with 95% confidence Intervals were calculated using bivariate log-binomial models.	Percentage of households with more persons than rooms (median = 1.9%) Risk ratio of being a COVID-19 hotspot in countries that had the median or had above the median percentage of households with more persons than rooms compared to those with less than the median percentage = 2.0 (95% CI: 1.8 to 2.3)	and some measure of socioeconomic deprivation) QCC rating: medium Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
Harling and others, 2014 (16) A spatial analysis of social and economic determinants of tuberculosis in Brazil	Study design: Ecological Population: Brazilian municipalities (26 states and one federal district divided into 5565 municipalities) Country: Brazil Study period: 2002 to 2009	Exposure: Households with more than 2 members per bedroom and household crowding (persons per bedroom) Outcome measurements Tuberculosis infection (notified cases stored in the Brazil Information System for Notifiable Diseases (Sistema de Informação de Agravos de Notificação). Statistical analysis Bivariate analysis adjusted for age and sex. Multivariable spatial regression model including the variables households in extreme poverty, individuals living in an urban area, population density, race, health facilities per capita, doctors per capita, acquired immunodeficiency disorder syndrome cases per capita, tuberculosis cure rate percentage.	Bivariate analysis: Incident rate ratio of tuberculosis in households with more than 2 members per bedroom = 1.37 (95% CI: 1.35 to 1.39) Multivariate spatial regression model: Incident rate ratio of household crowding = 1.17 (95% CI: 1.13 to 1.21)	Risk of bias: Confounding: ecological bias QCC rating: medium Study design class: D
Irfan and others, 2017 (17) Socio-demographic determinants of adult tuberculosis: A matched case-control study in Bangladesh	Study design: Case-control study Participants: • n=178 tuberculosis patients and n=179 controls Mean age: • cases = 28.3 years • controls = 27.6 years Sex: • cases = 101 (57%) males and 77 (43%) females • controls = 101 (56%) males and 78 (43.5%) females Country: Bangladesh Study Period: Not stated	Exposure: crowding intensity levels, refers to the average number of people living per room (family size divided by the number of rooms). Outcome measurement: Tuberculosis infection determined through hospital diagnosis. Statistical analysis: Patients were matched for age and sex to controls. Multivariate logistic regression to adjust for confounding variables such as education, crowding, monthly income and contact with tuberculosis patients.	Crowding: Less than or equal to 2 family members per room: • cases = 67 (33%) • controls = 134 (66%) More than 2 family members per room: • cases = 111 (70%) • controls = 45 (30%) Risk of TB infection in more than 2 family members per room compared to less than 2 family members per room: odds ratio = 3.492 (95% CI 2.08 to 5.93, p<0.001)	Risk of bias: None identified QCC rating: high Study design class: C

Reference	Study design	Methods	Key findings	Risk of bias
Kapoor and others, 2016 (18) Pattern of socio-economic and health aspects among TB patients and controls	Study design: Cross-sectional Participants: • n=983 tuberculosis cases, n=333 community controls • age range: 15 to 80 years • sex: cases= 57% males and 43% females and controls= 52% males and 48% females Country: India	Exposure: Home ownership, individuals per room, family type defined as joint or extended. Outcome measurement: Tuberculosis infection. Cases defined as those prescribed tuberculosis medication. Statistical analysis: Cases and controls matched for age. Univariate analysis conducted. No multivariable analysis or adjustment for confounding conducted. Crude odds ratios with 95% confidence intervals presented.	Individuals per room: Less than 3 (reference group) • cases= 250 (25.4%) • controls= 146 (43.8%) Between 3 and 5: • cases= 635 (64.6%) • controls= 112 (33.6%) • odds ratio for TB infection = 3.31 (95% CI 2.49 to 4.41) Between 6 and 7: • cases= 83 (8.4%) • controls 48 (14.4%) • odds ratio = 1.01 (95% CI 0.67 to 1.52) More than 8: • cases= 13 (1.3%) • controls= 14 (4.2%) • odds ratio = 0.54 (95% CI 0.25 to 1.19) Family type: Joint family: • cases= 297 (30.2%) • controls= 73 (21.9%) Nuclear family: • cases= 686 (69.8%) • controls= 248 (74.5%) • odds ratio = 0.68 (95% CI 0.51 to 0.91)	Risk of bias: • selection bias: unclear how the controls were recruited • unclear how exposure was measured • confounding: no adjustment for basic variables (age, sex and some measure of socioeconomic deprivation) QCC rating: low Study design class: D
Kapwata and others, 2022 (19) Demographic and socio-economic risk factors associated with self-reported TB	Study design: Ecological Population: A number of sites implementing community-oriented primary care (COPC) in the Gauteng Province of the country (no further detail provided)	Exposure: Overcrowding using United Nations Definition of more than 2 people per room. Outcome measurement: Household tuberculosis (self-reported) Statistical analysis Multivariable logistic regression model including sex, demographic, and socio-economic variables. Model did not include age of households.	Overcrowding: More than 2 people per room compared to less than 2 people per room: • odds ratio for TB infection = 2.15 (95% CI 1.66 to 2.78), p<0.001	Risk of bias: • selection bias: no information on population and demographic distributions • confounding: no adjustment for age or some measure of deprivation. • reporting bias: self-reported tuberculosis diagnosis susceptible to reporting bias, possibly resulting in an inaccurate

Reference	Study design	Methods	Key findings	Risk of bias
	Country: South Africa Study period: 2014 to 2019			measure of tuberculosis infection levels QCC rating: low Study design class: D
Lamichhane and others 2022 (5) District-Level Risk Factors for COVID-19 Incidence and Mortality in Nepal	Study design: Ecological Population: n=12,862 women and n=4,063 men, aged 15 to 49 years who were permanent residents of selected households in n=73 districts. Country: Nepal Study period: 23 January 2020 to 22 January 2021	Exposure Household crowding: percentage of households in a district who lived in homes with more than 3 people per room for sleeping (Collected from Demographic Health Survey) Outcome measurement COVID-19 incidence (data collected from national database of COVID-19 cases) Statistical analysis Negative binominal regression model used to estimate risk ratio for population density, household crowding, obesity prevalence in women, smoking in men, no access to handwashing facilities, adult literacy, percentage aged 60 or over.	Risk of COVID 19 infection with household crowding: Risk ratio compared to no household crowding = 1.04 (95% CI 1.01 to 1.06), p<0.01	Risk of bias: • selection bias: no information on patient demographics at individual level • confounding: no adjustment for basic variables (age, sex, and some measure of deprivation) • measurement of exposure and outcome: exposure data and outcome data collected 3 years apart (possible districts would have changed during this time) QCC: low Study design class: D
Lee and others 2021 Urban environments and COVID-19 in 3 Eastern states of the United States	Study design: Ecological Population: Data analysed from 91 counties in 3 states (New York, New Jersey and Connecticut) Country: United States	Exposure measurements: Six urban environment indicators including percentage of households that are overcrowded (defined as more than one person per room, room type not specified). Outcome measurements: COVID-19 incidence (counts of confirmed cases per 100,000 persons), daily reproduction number (average number of new infections caused by a single infected individual), and COVID-19 mortality (deaths per 100,000 persons).	Percentage of households that are overcrowded: The incidence of COVID-19 increased as the percentage of overcrowding in counties (defined as more than one person per room) increased (change per interquartile increase in min-max standardised percentage overcrowding: 1.52, 95% CI [estimated empirically]: 1.34 to 1.72)	Risk of bias: Confounding: ecological bias and no adjustment for minimal relevant variables (age, sex, or any measure of deprivation) QCC rating: medium Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
	Study period: March to November 2020	Statistical analysis: Regression analysis to estimate association with environment indicators and COVID-19 outcomes. Environmental indicators were minimum maximum standardised between 0 and 1 due to differences in the individual variable scales, with change in outcomes measured by interquartile increase to compare magnitude of the associations. Confidence intervals were estimated empirically for change in interquartile range.		
Leite and others, 2021 (7) A Case-Control Study of Contextual Factors for SARS-CoV-2 Transmission	Study design: Case-control Participants: • n=1,088 COVID-19 cases identified through the national surveillance system. • n=787 community controls recruited through random digital dialling (mobile and landline) • mean age of cases: 44 years (SD: 16 years) • mean age of controls: 53 years (SD: 16 years) • sex of cases: n=637 (59%) female, n=450 (41%) male • sex of controls: n=490 (62%) female and n=297 (38%) male Country: Portugal	Exposure: Household density assessed by the number of individuals per room (more than 4m2, excluding bathrooms, vestibules, and storage rooms): • not crowded: less than one person per room • overcrowded: one or more persons per room Outcome measurement: COVID-19 infection cases were identified by positive PCR test results submitted to the National System of Epidemiological Surveillance. Statistical analysis: Multivariable logistic regression model of risk factors associated with COVID-19 infection adjusted for sex, age, education level and citizenship status. Cases and controls were also matched for sex, age (within 10 year bands) and municipality.	COVID-19 infection risk for those living in a house with one or more persons per room versus those with less than one person per room: odds ratio: 1.47 (95% CI: 1.14 to 1.91, p= 0.004)	Risk of bias: • selection bias: cases recruited differently to controls (cases recruited via national system of epidemiological surveillance, controls recruited by random digital dialling) • measurement of outcome: Controls self-reported if they had COVID-19 whereas cases had a PCR test QCC rating: medium Study design class: C

Reference	Study design	Methods	Key findings	Risk of bias
	Study period: 2 October 2020 to 6 November 2020			
Libby and others, 2020 (22) Disparities in shigellosis incidence by census tract poverty, crowding, and race/ethnicity in the United States, FoodNet, 2004-2014	Study design: Ecological Population: N=21,246 cases linked to census data, categorised into 4 poverty and 4 crowding strata Country: United States Study period: 2004 to 2014	Exposure: Foodborne Disease Active Surveillance Network data was linked to data from the American Community Survey and measures of household crowding and poverty were assessed. Crowding was rated on a 4-point scale based on the percentage of households in the Census tract with >1 person per room (<1%, 1% to <3%, 3% to <5%, ≥5%). Outcome measurement: Positive Shigellosis infections recorded in FoodNet 2004-2014 survey confirmed by laboratory testing. Statistical analysis: Incident rates per 100,000 population was calculated for Foodborne Disease Active Surveillance Network data sites (states of Connecticut, Georgia, Maryland, Minnesota, New Mexico, Oregon, and Tennessee and selected counties in California, Colorado, and New York), sex, age and race/ethnicity. Age and socioeconomic position were adjusted for, and results were stratified by sex and ethnicity. 95% confidence intervals and p values were recorded. Adjusted shigellosis incident rate ratios were also estimated using a multivariate regression model which included sex, age group, race/ethnicity, Foodborne Disease Active Surveillance Network data sites, poverty and crowding.	Incidence of Shigellosis infections comparing more than 5% with less than 1% census tract crowding: incident rate ratio = 1.8 (95% CI: 1.7 to 1.9)	Risk of bias: Confounding: ecological bias QCC: medium Study design class: D
Lienhardt and others, 2005 (20) Investigation of the risk factors for tuberculosis: a case-control study in 3	Study design: Case-control Participants: N = 822 cases N= 687 household controls and 816 community controls	Exposure: Questionnaire on a range of demographic and environmental factors including number of persons per room, number of adults per household and total number of occupants. Outcome measurement: Smear Positive tuberculosis patients	Number of adults in household: Between 1 and 5: • cases = 389 (57%) • controls = 463 (67%) Between 6 and 10: • cases = 216 (31%) • controls = 191 (28%)	Risk of bias: None identified QCC rating: high Study design class: C

Reference	Study design	Methods	Key findings	Risk of bias
countries in West Africa	Mean age: • Gambia= 31.3 years (SD 11.5 years) • Conakry= 29.1 years (SD 10.2) • Bissau= 34.6 years (SD 12.0) Sex: • Gambia= 560 males and 378 females • Conakry= 419 males and 358 females • Bissau= 323 males and 287 females Countries: The Gambia, Guinée Conakry, and Guinea Bissau Study period: January 1999 to March 2001	Statistical analysis: Multivariable analysis of associated environmental and host-related risk factors including sex, HIV infection status, smoking, history of asthma, marital status, family history of TB, number of adults in household and status of home ownership.	• odds ratio compared to between 1 and 5 = 1.37 (95% CI 1.03 to 1.82), p<0.001 More than 10: • cases= 83 (12%) • controls= 34 (5%) • odds ratio compared to between 1 and 5 = 2.80 (95% CI 1.71 to 4.57) Number of people per room: Less than 1: • cases= 31 (4%) • controls= 35 (5%) 1 to 2: • cases= 345 (46%) • controls= 367 (49%) • odds ratio compared to less than one = 1.07 (95% CI 0.64 to 1.82) More than 2: • cases= 370 (50%) • controls= 344 (46%) • odds ratio compared to less than one = 1.26 (95% CI 0.73 to 2.16), p=0.4	
Lopez and others, 2021 (8) Impact of isolating COVID-19 patients in a supervised community facility on transmission reduction among household members	Study design: Dynamic cohort Participants: • n=89 index patients who were either isolating in a hotel (n=44, 49%) or in their homes (n=45, 50%). The mean age of index patients was 53.6 years (SD: 16.9 years) and n=57 (64%) was female. • index patients reported information	Exposure: Household crowding defined by dividing the number of persons living in a house by the number of bedrooms. Outcome measurement: COVID-19 infection in any of the household members of index patients, assessed by interviews (reported symptoms compatible with COVID-19 or reported a positive PCR test). Statistical analysis: Multivariable logistic regression adjusting for age (15 to 44 years, 45 to 65 years, and more than 65 years), isolation at home and overcrowding	COVID-19 infection for those experiencing household crowding: • odds ratio for a unit increase in the ratio of the number of household members and the number of bedrooms 1.44 (95% CI computed from graph: 0.82 to 2.55)	Risk of bias: • confounding: no adjustment for sex or some measure of deprivation • measurement of outcome: Potential information bias as index cases provided information on the household contacts outcomes QCC rating: medium Study design class: B

Reference	Study design	Methods	Key findings	Risk of bias
	on n=229 household contacts, of which n=90 were household contacts of home isolating index cases and n=139 were household contacts of hotel isolating index cases. Country: Spain Study period: April to June 2020			
Martin and others, 2022 (9) Risk factors associated with SARS-CoV-2 infection in a multiethnic cohort of United Kingdom healthcare workers (UK-REACH): A cross-sectional analysis	Study design: Cross-sectional Participants: • n=10,772 healthcare workers, of which n=2,496 were positive COVID-19 cases. • median age: 45 years (IQR 35 to 54 years), 54 (0.5%) missing • sex: n=2660 (24.7%) males, n=8089 (75.1%) females and n=23 (0.2%) missing • ethnicity: n=7583 (70.4%) white, n=2057 (19.1%) Asian, n=462 (4.3%) black, n=446 (4.1%) mixed, n=224 (2.1%) other	Exposure: Shared areas with other households and household size. Outcome measurement: COVID-19 Infection by self-reported PCR or serology Statistical analysis: Multivariable regression model adjusted for demographic factors (age, sex, ethnicity) and home and work factors during lockdown	Household size: odds ratio for OCVID-19 infection per unit increase in household size = 1.02 (95% CI 0.98 to 1.06, p=0.34) Shared spaces with other households: odds ratio for COVID-19 infection amongst those with shared spaces versus not = 0.93 (95% CI, 0.81 to 1.06, p=0.28)	Risk of bias: • selection bias: participants were self-recruited QCC rating: medium Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
	Country: United Kingdom Study period: December 2020 to March 2021			
Mendez and others, 2021 (10) Overcrowding and exposure to secondhand smoke increase risk for COVID-19 infection among Latinx families in the greater San Francisco Bay Area	Study design: Ecological Population: N=383 households, (consisting of n=1875 people) recruited from 3 longitudinal cohort studies of Latinx families (the Hispanic Eating and Nutrition Study, The Latinx Eating and Diabetes Study, and the Telomeres at Birth Study). Country: United States Study period: May to September 2020	Exposure: Fifteen minute interview in which participants were asked about household size, number sharing bedroom, number sharing bathroom, number eating together, number of children. Outcome measurement: COVID-19 infection within a household, (determined by self-reported PCR test) or the presence of symptoms including loss of taste or smell. The household was deemed to be positive if anyone in the household reported a positive COVID-19 result. Statistical analysis: Multivariate regression model including household number, number sharing bedroom, number eating together at home daily, exposure to second-hand smoke, public transport use and high tortas consumption.	COVID-19 infection per unit increase in household size: • odds ratio = 1.58 (95% CI 1.12 to 2.23, p <0.01). COVID-19 infection per unit increase of persons sharing a bedroom: • odds ratio = 1.05 (95% CI: 0.66 to 1.68, p=0.82) COVID-19 infection per unit increase in number of persons eating together daily: • odds ratio = 1.06 (95% CI: 0.73 to 1.56, p= 0.75)	Risk of bias: • selection bias: participants were selected from cohort studies recruited primarily from hospitals • confounding: ecological bias and no adjustment for basic variables age or sex. • measurement of outcome: self-reported household COVID-19 infection. QCC rating: low Study design class: D
Mohan and others, 2017 (23) Rotavirus Infection and Disease in a Multisite Birth Cohort: Results From the MAL-ED Study	Study design: Prospective cohort Participants: N=1,737 children from: Bangladesh (n=213) Brazil (n=167) India (n=228) Nepal (n=228) Peru (n=198) Pakistan (n=252) South Africa (n=240) Tanzania (n=211)	Exposure: Overcrowding in the family (defined as more than 2 people per room). Outcome measurement: Rotavirus infection measured by symptoms and confirmed by blood test and stool samples. Statistical analysis: Poisson multilevel, site- and age-adjusted regression models with random effects to account for within-site and within-child correlations were used to estimate the incidence rate ratios (IRRs) for rota-virus infection and diarrhoea, adjusted for:	Rotavirus infection in overcrowded conditions: • incident rate ratio: 1.174 (95% CI 0.983 to 1.403, p=0.077) Rotavirus diarrhea in overcrowded conditions: • incident rate ratio: 1.401 (95% CI: 1.072 to 1.830, p=0.014)	Risk of bias: Baseline participant demographics not available to assess selection bias QCC rating: medium Study design class: B

Reference	Study design	Methods	Key findings	Risk of bias
	Countries: Bangladesh, Brazil, India, Nepal, Peru, Pakistan, South Africa, Tanzania Study period: April 2009 to February 2014. Participants followed up for 2 years from birth.	• sex • weight at first month • history of child death in the family • maternal age at childbirth • education and nutrition status • duration of exclusive breastfeeding • SES • overcrowding • child nutritional status during the first year • average number of pathogens detected per stool specimen		
Munywoki and others, 2021 (11) Seroprevalence and risk factors of SARS-CoV-2 infection in an urban informal Settlement in Nairobi, Kenya, December 2020	Study design: Cross-sectional Participants: • n=511 adults (18 years or older) • age: below 10 years n=120 (23.5%) and 60 years or older n= 7 (1.4%) • sex: n= 212 (41.5%) males and n= 299 (58.5%) females Country: Kenya Study period: 27 November 2020 to 5 December 2020	Exposure: Household size Outcome measurement: COVID-19 seroprevalence confirmed by laboratory testing Statistical analysis: Pearson chi square test used to measure association of categorical variables. The final multivariable logistic regression model included age, sex and household size, accounting for sampling weights and clustering by household	Household size (number of individuals living in the same house): • 1 to 2 versus 3 to 4 OR = 2.31 (95% CI 0.93 to 5.74), p=0.072 • More than or equal to 5 versus 3 to 4 OR = 1.98 (95% CI 1.17 to 3.34), p=0.011	Risk of bias: Selection bias: adult males were under-represented in the sample population as they were often working at the time of household visits and sampling. QCC rating: medium Study design class: D
My and others, 2013 (24) Endemic norovirus infections in children, Ho Chi Minh City, Vietnam, 2009-2010	Study design: Case-control Participants: • n=1419 cases, children under 5 years with acute diarrhoea	Exposure: Number of children in household. Self-report questionnaire. Outcome measurement: Norovirus infections measured through PCR test of stool sample.	• odds ratio for norovirus infection for those having 3 or more children in the household versus less than 3 = 1.70 (95% CI: 1.0 to 2.9, p=0.052) • odds ratio for norovirus infection for those having 5 or more adults in the household was	Risk of bias: None identified QCC rating: high Study design class: C

Reference	Study design	Methods	Key findings	Risk of bias
	• n=609 controls, children attending clinic for routine check-up or conditions unrelated to gastroenteritis Mean age (norovirus positive patients): • cases= 13.3 years (range 2 to 45) • controls= 15.8 years (range 2.3 to 52) Sex (norovirus positive patients): • cases= 147 (61%) males and 94 (39%) females • controls= 8 (53.3%) males and 7 (46.6%) females Country: Vietnam Study Period: May 2009 to December 2010	Statistical analysis Multivariable logistic regression model used to adjust for confounding variables such as, age, sex, and income level.	not associated with an increased risk of infection.	
Van Ingen and others, 2022 (12) Neighbourhood-level socio-demographic characteristics and risk of COVID-19 incidence and mortality in Ontario, Canada: A population-based study	Study design: Ecological Population: N = 28,808 Ontario residents (population level analysed: neighbourhoods between the 10th and 90th percentile of socio-demographic characteristics). Country: Canada	Exposure: Housing characteristics: Average household size, multigenerational families, unsuitably crowded housing, apartment in duplex or flat, low-rise apartment, high-rise apartment. Outcome measurement: COVID-19 incidence reported in national surveillance system.	COVID-19 incidence comparing 90th percentile to 10th percentile by increase in average housing size Relative risk = 1.9 (95% CI: 1.7 to 2.1) COVID-19 incidence comparing 90th percentile to 10th percentile by those living in unsuitably crowded housing Relative risk = 2.1 (95% CI, 2.0 to 2.3)	Risk of bias: Confounding: ecological bias QCC: medium Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
	Study period: 23 July 2020 to 28 July 2020	Statistical analysis: Multivariable regression models to produce incidence relative risk adjusted for age, sex, and urban/rural stratification.		

Table C.1b: Dormitories

Reference	Study design	Methods	Key findings	Risk of bias
Akaishi and others, 2021 (26) COVID-19 Transmission in Group Living Environments and Households	Study design: Cross-sectional Participants: • n= 4,550, individuals who attended a COVID-19 drive through test centre and had data regarding place of contact. Median age: • contact at dormitory= 24 years (IQR 22 to 27 years) • contact at home= 36 years (15 to 54 years) • close contact outside residence= 23 years (15 to 44 years) • lower risk contact outside residence= 15 years (6 to 28 years) Sex: • contact at dormitory: n=105 (87.5%) males and n=15 (12.5%) • contact at home: n=485 (42.4%) males and n=659 (57.6%) • close contact outside residence: n=573 (55.4%) males and n=461 (44.5%) • lower risk contact outside residence: n=1168 (51.9%) males and n=1084 (48.1%) females Country: Japan Study period: July 2020 to March 2021	Exposure: Place of contact, number of individuals per room in dormitory and implementation of infection control measures in dormitory. Comparison of dormitory and home-living. Outcome measurement: COVID-19 infection confirmed through positive PCR test at drive through testing centre Statistical analysis Binary logistic regression to assess potential predictors of COVID-19, with (1) 'contact at dormitory' used as an explanatory variable and (2) household contact used as an explanatory variable. For 'contact at dormitory', the variables included were age, sex (male), close contact history and contact at dormitory. For 'household contact', the variables included were age, sex (male), close contact history and household contact. Crude (unadjusted) risk ratios and 95% Cis were then calculated in each group with different group living environments including having a contact in the dormitory, a dormitory with no infection control measures, a dormitory with appropriate infection control measures, having a household contact, and having a lower-risk contact outside the residence.	Risk of COVID-19 infection for those who had contact at a dormitory versus close contact outside residence: Risk ratio = 2.43 (95% CI: 1.74 to 3.40, P <0.0001) Risk of COVID-19 infection in those living in a dormitory with no infection control measures versus those who had a close contact outside of the residence: Risk ratio = 5.12 (95% CI: 3.87 to 6.77, p<0.0001) Risk of COVID-19 infection in those living in a dormitory with appropriate infection control measures versus those who had a close contact outside the residence: Risk ratio = 0.10, 95% CI: 0.01 to 1.52, p=0.10). Risk of COVID-19 infection among dormitory-living students compared with home-living students: Risk ratio = 6.14 (95% CI: 3.83 to 9.84)	Risk of bias: Confounding: no adjustment for basic variables (age, sex or some measure of socioeconomic deprivation) in calculation of risk ratios. QCC rating: medium Study design class: D
Bigouette and others, 2021 (27) Association of Shared Living Spaces and COVID-19 in	Study design: Cross-sectional Participants: • n = 2,187 students living in university provided dormitory accommodation • mean age: 19.3 years (SD 1.1 years)	Exposure: Data obtained from university records. Sharing a bedroom = students sharing a bedroom with one or more than one student Outcome measurement: COVID-19 infection by positive PCR test.	Sharing bedroom: • sharing= 423 (80.1%) • not sharing= 105 (19.9%) • odds ratio for COVID-19 infection = 1.52 (95% CI: 1.15 to 2.03)	Risk of bias: None identified QCC rating: high Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
university students, Wisconsin, USA, 2020	• sex: n=1326 (60.6%) females, n=820 (37.5%) males and n=41 (1.9%) unknown sex • race = n=1737 (79.4%) white, n=13 (0.6%) Alaska Native or Native American, n=86 (3.9%) Asian, n=99 (4.5%) Black or African American, n=33 (1.5%) Native Hawaiian or other Pacific Islander, n=23 (1.1%) others, and n=196 (9%) unknown • ethnicity: n=127 (5.8%) Hispanic or Latino, n=1744 (79.7%) not Hispanic or Latino and n=316 (14.5%) unknown ethnicities Country: US Study period: 2 September 2020 to 19 December 2020	Shared living space = More than 2 students sharing a suite or defined as having a shared bedroom. Dormitory floor level occupancy = the number of occupied rooms divided by the number of rooms per floor. Statistical analysis: Multivariable logistic regression was used to adjust for age, sex, race, ethnicity, all dormitories, and dormitory floor level occupancy.	Sharing living space: • sharing= 472 (89.4%) • not sharing= 56 (10.6%) • odds ratio = 1.80 (95% CI: 1.28 to 2.55)	
Li and others, 2011 (28) Epidemiological investigation of an outbreak of pandemic influenza A (H1N1) 2009 in a boarding school: serological analysis of 1570 cases	Study design: Retrospective cohort Participants: • n=1,570 students • age range: 15 to 21 years • gender: n=1,078 (69%) males and n=492 (31%) females Country: China Study period: 21 August 2009 to 15 October 2009	Exposure: Boarding school dormitories with a capacity of 6 to 13 students per room, including students with fever residing in the same dormitory compared to those who were not exposed to fever in the same dormitory. Outcome measurement: Influenza infection confirmed by laboratory testing. Statistical analysis: Attack rates (as percentages) and generation periods (interval between boarding school enrolment and incident peak) calculated. Multivariable regression analysis adjusting for: • patients with fever in the same classroom • patients with fever in the same dormitory • opening window frequently	Odds ratio of influenza infection for students with a fever sharing the same dormitory = 2.048 (95% CI: 1.57 to 2.68, p<0.01)	Risk of bias: Confounding: no adjustment potential confounders in multivariate analysis, for example dormitory despite how dormitory room 9 had 30 out of 38 students infected. Additionally, variables such as age and sex were not adjusted for. QCC rating: medium Study design class: B

Reference	Study design	Methods	Key findings	Risk of bias
Maina and others, 2021 (31) Tuberculosis infection among youths in overcrowded university hostels in Kenya: a cross-sectional study	Study design: Cross-sectional Participants: 51 (out of 57 eligible) index students receiving treatment at Kilifi County Hospital from which 156 student contacts were recruited, screened, and provided a sputum sample. Country: Kenya Study period: January 2016 to December 2017	Exposure: Sharing accommodation or off-campus hostel (bunk beds accommodating 2 to 4 students per room) and close contact to a tuberculosis index case (household or social contacts) Outcome measurements: Prevalence of tuberculosis among all contacts (determined by GeneXpert test positive/clinical diagnosis) Statistical analysis: Multivariable regression model to calculate risk ratio of tuberculosis transmission. Crude risk ratios were calculated including the variables: contact type, age, gender, time spent with index case, sharing a bed with index case, sleeping in the same room as an index case, clinical signs, underling medical conditions and HIV status. Adjusted risk ratios were calculated using age, gender, sharing a bed with an index case, clinical signs.	Sharing a bed with an index case compared to not sharing: Risk ratio = 22.2 (95% CI: 2.45 to 202, p=0.008)	Risk of bias: • confounding: adjusted risk ratios did not include some measure of socioeconomic deprivation (such as underlying medical conditions included in crude risk ratio model) QCC rating: medium Study design class: D
Metintas and others, 2004 (32) Frequency and risk factors of dermatophytosis in student group living in rural areas in Eskisehir, Turkey	Study design: Cross-sectional Participants: • n = 2,384 students • age range: 11 to 19 years • gender: n=945 (39.6%) females and n=1439 (60.4%) males Country: Turkey Study period: Not stated	Exposure: Questionnaire on household characteristics Outcome measurement: Dermatophytosis, identified through symptoms and confirmed by laboratory testing of skin samples. Statistical analysis: Multivariate regression model controlling for age, gender, level of maternal education, hand hygiene and family member infection.	Infection for students living in a school dormitory versus those living at home: odds ratio = 2.943 (95% CI: 1.717 to 5.045, p<0.0001).	Risk of bias: Measurement of exposure self-reported QCC rating: medium Study design class: D
Raza and others, 2009 (33)	Study design: Case-control	Exposure: Questionnaire including bed-sharing and personal hygiene.	Itching in family or colleagues living in same dormitory: • cases = 42 (21%)	Risk of bias: Measurement of exposure: self-reported (personal hygiene

Reference	Study design	Methods	Key findings	Risk of bias
Risk factors for scabies among male soldiers in Pakistan: Case-control study	Participants: N= 200 cases and 200 controls matched by age, sex and socioeconomic status (all male participants) Mean age: • cases = 29.17 years (SD: 7.13 years) • controls = 29.19 years (SD: 7.27 years) Country: Pakistan Study period: February 2006 to April 2006	Outcome measurement: History of scabies infection (self-reported) Statistical analysis: Multivariable logistic regression model including itching in same family/ colleagues, changing clothes less than 2 times a week, sharing beds, bathing less than one time a day, low education and leave/ temporary duty	• controls = 1 (0.5%) • odds ratio = 95.41 (95% CI 9.97 to 912.91, p<0.05) Sharing beds: • cases = 83 (41.5%) • controls = 54 (27%) • odds ratio = 4.44 (95% CI 2.19 to 9.10, p<0.05) Residence in unit barracks: • cases = 180 (90%) • controls = 149 (74.5%) • odds ratio = 3.08 (95% CI 1.75 to 5.39) Sharing towels: • cases= 32 (16%) • controls= 39 (19.5%) • odds ratio =0.78 (95% CI 0.47 to 1.31) • Family size more than 10: • cases = 80 (40%) • controls = 85 (42.5%) • odds ratio = 0.90 (95% CI 0.60 to 1.34)	subject to potential social desirability bias) QCC rating: medium Study design class: C
Sun and others, 2011 (29) In China, students in crowded dormitories with a low ventilation rate have more common colds: evidence for airborne transmission	Study design: Cross-sectional Participants: n=3,712 students residing in dormitories Country: China Study period: 2006 to 2007	Exposure: Room occupancy, how many times the window is open by self-report. Measures of temperature, relative humidity and CO2 by PS31 monitor. Outcome measurement: Incidence and duration of the common cold. Self-reported questionnaire covering previous 12-month. Statistical analysis: Multivariable model adjusting for gender, age, hours spent indoors, family member allergy history and exposure to environmental tobacco smoke.	(All data extracted from graphs, figure 1 and 2) Incidence of common cold in last 12 months: 6 to 10 times: • 3 people per room= 4.5% • 4 people per room= 5.2% • 6 people per room= 8.3% More than 10 times: • 3 people per room= 1.2% • 4 people per room= 2.2% • 6 people per room= 3.1%	Risk of bias: Measurement of exposure: self-reported (potentially subject to recall bias) QCC rating: medium Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
			Association between crowdedness and incidence more than or equal to 6 times (adjusted odds ratio): • 3 people per room= 1.01(95% CI not given) • 4 people per room= 1.55 (95% CI 0.74 to 3.32) • 6 people per room= 2.58 (95% CI 1.07 to 6.26) Incidence of common colds increased with the number of people per room (p=0.002)	
Yang and others, 2021 (30) Spread of respiratory infections in student dormitories in China	Study design: Cross-sectional Participants: • n= 2952 students living in dorm rooms • gender: 42.7% females and 57.3% males Country: China Study period: Phase 1: 27 May 2015 to 20 June 2015 Phase 2: • Summers: 23 July 2015 to 20 July 2015 • Winters: 24 December 2015 to 23 January 2016	Exposure: self-administered questionnaires on dorm room environment (such as, dampness problems), lifestyles (such as, cleaning frequency, opening window frequency) Outcome measurement: Retrospective self-reported common cold and influenza frequency Statistical analysis: • Chi square tests used to analyse the association of demographics and respiratory infections (Such as age, gender, smoking status, occupancy level and living habits) • Generalized estimation equation models adjusted for living habits and demographics was used to evaluate association of infections with ventilation and dampness	Annual common cold incidence: Less than 6 times: • 3 or less students in a room (n=291) = 67% • 4 students in a room (639): 64.9% • 5 or more students in a room (n=1310) = 62.1% Between 6 and 10 times: • 3 or less students in a room (n=291) = 29.6% • 4 students in a room (639): 33.5% • 5 or more students in a room (n=1310) = 30.8% More than 10 times: • 3 or less students in a room (n=291) = 3.4% • 4 students in a room (639): 1.6% • 5 or more students in a room (n=1310) = 7.1% Annual influenza incidence: Less than one time: • 3 or less students in a room (n=299) = 68.2% • 4 students in a room (627): 65.7% • 5 or more students in a room (n=1287) = 63.3% 1 to 6 times: • 3 or less students in a room (n=299) = 28.4%	Risk of bias: • confounding: no adjustment for basic variables (age, sex or some measure of socioeconomic deprivation) • exposure and outcome measurement self-reported (potential for recall bias) QCC rating: medium Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
			• 4 students in a room (627): 32.2% • 5 or more students in a room (n=1287) = 31.5% More than 6 times: • 3 or less students in a room (n=299) = 3.3% • 4 students in a room (627): 2.1% • 5 or more students in a room (n=1287) = 5.1%	

Table C.1c: Vessels

Reference	Study design	Methods	Key findings	Risk of bias
Fernandes and others, 2002 (34) Influenza B outbreak on a cruise ship off the Sao Paulo Coast, Brazil	Study design: Case-control Participants: • n=104 acute respiratory illness cases, 54 (51.9%) crew members and 50 (49.1%) passengers. • n=33 cases (crew members with influenza like illness) • n=192 controls (asymptomatic crew members) Age: • younger than 18 years= 16 (32%) passengers • 18 to younger than 60 years= 33 (66%) passengers and 54 (100%) crew • 60 or older than 60 years= 1 (2%) passenger Sex: • male= 19 (38%) passengers and 29 (53.7%) crew Country: Brazil Study period: 1 February 2012 to 27 February 2012	Exposure: Conditions of deck including number of occupants per room and number of windows. Outcome measurement: Influenza like illness. Statistical analysis: Only symptomatic crew members were included in case-control analysis. Multivariable regression model adjusting for age, sex, and duties on ship.	Housing deck: Higher decks 4 to 7: • cases= 11 (33.3%) • controls= 103 (52.6%) Lower decks 2 and 3 (poor ventilation, no windows and 2 to 4 people per cabin): • cases= 22 (66.6%) • controls= 91 (46.4%) Odds ratio of influenza like illness in lower deck versus higher deck = 2.39 (95% CI 1.09 to 5.25)	Risk of bias: None identified QCC rating: high Study design class: C
Harwood and others, 2013 (35) The attack rate of H1N1 in various berthing configurations on	Study design: Cross-sectional Participants: N=4596 vaccinated sailors (male: n=3910, female: n=686)	Exposure: Size of berthing areas defined as: • total number of people living in the berthing area • square feet of living area (total square feet in berthing space divided by the number of people living in the space)	Average attack rate of H1N1: 3% Correlation between attack rate and square feet of living area: Correlation coefficient R = 0.131, one tailed p=0.290	Risk of bias: • selection bias: females underrepresented in the sample population • confounding: no adjustment for age and some measure

Reference	Study design	Methods	Key findings	Risk of bias
board an aircraft carrier	Study period: 5 July 2009 to 30 July 2009	• occupancy rate (percentage of available beds occupied in a given berthing space) Outcome measurements: H1N1 influenza transmission between determined by presumptive diagnosis (patient demonstrating a core body temperature of 37.8ºC or higher and 2 or more H1N1 associated symptoms). Statistical analysis: Attack rate of H1N1 defined as the number of people affected as a percentage of the total number of people in a given command. Correlation coefficients were calculated to determine the relationship between attack rates and square feet of living area, occupancy rate, no of berthing racks occupied (maximum, mean and median), total berthing space and command size.	Correlation between attack rate and occupancy rate: Correlation coefficient R = -0.562, one tailed p=0.005 Correlation between attack rate and number of berthing racks occupied: • maximum number of racks occupied: correlation coefficient R = -0.418, one tailed p=0.34 • mean number of racks occupied: correlation coefficient R = -0.449, one tailed p=0.024 • median number of racks occupied: correlation coefficient R = -0.382, one tailed p=0.048 Correlation between attack rate and total space: Correlation coefficient R = -0.362, one tailed p=0.131	of socioeconomic deprivation in analysis. • statistical analysis: Information provided on statistical analysis was minimal and therefore not possible to determine if appropriate analysis was performed • measurement of outcome: self-reported symptoms of H1N1 QCC rating: low Study design class: D

Table C.1d: Emergency shelters and hostels for those experiencing homelessness

Reference	Study design	Methods	Key findings	Risk of bias
Ghinai and others, 2023 (37) Risk Factors for Severe Acute Respiratory Syndrome Coronavirus 2 infection in Homeless Shelters in Chicago, Illinois-March-May, 2020	Study design: Cross-sectional Participants: • n=1435 residents in homeless shelters • age: • less than 40= 387 (27.1%) • 40 to 55 = 462 (32.3%) • more than 55 = 580 (40.6%) • gender: n=389 (27.6%) female and n=1023 (72.5%) male • ethnicity: n=879 (65%) Non-Hispanic Black, n=228 (16.9%), Non-Hispanic White, n=184 (13.6%) Hispanic, and n=62 (4.6%) Non-Hispanic other Country: US Study period 1 March 2020 to 1 May 2020	Exposure: Self-completed questionnaire including sleeping arrangements (number per room), number of communal bathrooms, number of residents per 1000 square feet. Outcome measurement: COVID-19 infection confirmed by PCR test. Statistical analysis Multivariable log binominal regression model with prevalence ratios, adjusting for: smoking status, number of individuals per 1,000 square feet, number of people per room, communal bathrooms per 100 residents, private bathrooms per 100 residents, proportion of residents leaving and returning each day.	Shared room versus single room: • 2 to 4 people: prevalence ratio = 1.35 (95% CI: 0.87 to 2.11), p=0.19 • 5 to 8 people: prevalence ratio = 1.59 (95% CI: 1.00 to 2.53), p=0.05 • 9 to 20 people: prevalence ratio = 1.64 (95% CI: 1.00 to 2.70), p=0.05 • more than 20 people: prevalence ratio = 1.76 (95% CI: 1.11 to 2.80), p=0.02 Facility level: • residents per 1000 square feet: prevalence ratio = 0.86 (95% CI: 0.68 to 1.08), p=0.10 • communal bathrooms per 100 residents: prevalence ratio = 0.89 (95% CI: 0.74 to 1.07), p=0.22 • private bathrooms per 100 residents: prevalence ratio = 0.92 (95% CI: 0.87 to 0.98), p=0.02 • proportion of residents leaving and returning each day: prevalence ratio = 1.08 (95% CI: 1.01 to 1.16), p=0.03	Risk of bias: Measurement of exposure self-reported QCC rating: medium Study design class: D
Leibler and others, 2019 (41) Homelessness, Personal Hygiene, and MRSA Nasal Colonization among Persons Who Inject Drugs	Study design: Cohort study nested within RCT Participants: • n=78 injecting drug users • mean age: 38.7 years (SD: 11 years) • sex: n=50 (64%) male, n=28 (36%) female • race: n=41 (53%) white • ethnicity: n=14 (18%) Latino or Latina Country: United States	Exposure: Housing and hygiene conditions (homeless shelters, sleeping in more than one place in one week, sleeping on the street, use of public shower facilities). Outcome measurement: Nasal swabs for MRSA confirmed by laboratory testing. Statistical analysis: Univariate logistic regression with clustering of standard errors to evaluate risk factors for MRSA nasal colonisation across repeated sampling including the variables:	MRSA nasal colonisation risk factors: • sleeping in a homeless shelter in the past 3 months: odds ratio = 3.0 (95% CI: 1.2 to 7.6, p=0.02) • sharing bedding with other people: odds ratio = 2.2 (95% CI: 1.0 to 4.7, p =0.05)	Risk of bias: Confounding: no adjustment for basic variables (such as age, sex, and some measure of socioeconomic deprivation) QCC rating: medium Study design class: B

Reference	Study design	Methods	Key findings	Risk of bias
	Study period: October 2016 to April 2018	• sleeping in a homeless shelter in the last 3 months • sleeping at more than one place during the last week • use of public shower facilities in the last week • sharing bedding with other people		
Mosnier and others, 2023 (39) Cumulative incidence of SARS-CoV-2 infection within the homeless population: insights from a city-wide longitudinal study	Study design: Prospective cohort Participants: • n=1,241 homeless adults • median age: 38 years (IQR: 22 years) • gender: n=874 (70.4%) men and n=367 (29.6%) women Country: France Study period: Two sessions: (1) 5 June 2020 to 5 August 2020 (2) 11 September 2020 to 18 December 2020	Exposure: Communal accommodation (rough sleeping in squats, slums, stabilisation shelters and emergency shelters or hostels). Outcome measurement: COVID-19 infection identified through rapid serological test (Biosynex COVID-19 BSS). Statistical analysis: Multivariable Cox regression to calculated adjusted hazard ratios, including the variables: • household status • having financial resources • percentage of time spent in emergency shelters • number of daily contacts • difficult access to hygiene products • smoking status • psychiatric or addictive comorbidity	Risk of infection compared to individuals who spent less than 33% of their time in an emergency shelter: • between 33 to 66% of their time in emergency shelters: • adjusted hazards ratio = 1.70 (95% CI: 1.11 to 2.62) • more than 66% of their time: adjusted hazards ratio = 1.93 (95% CI: 1.18 to 3.15)	Risk of bias: • confounding: no adjustment for age and sex in multivariate regression model. • attrition: study reports that a large number of people were lost to follow up (n=1241 at baseline and n=721 at follow up, follow up rate: 58%) and that participant characteristics at baseline and follow up were different (specifics not provided) QCC rating: medium Study design class: B
Roederer and others, 2023 (40) Seroprevalence and risk factors of exposure to COVID-19 in homeless people in Paris, France:	Study design: Cross-sectional Participants: • n=818 homeless residents of emergency shelter • mean age: 39 years (50% participants younger than 35)	Exposure: Crowding in place of residence based on a simple cumulative crowding indicator taking into account the number of people sharing a room, sanitary facility, kitchen and number of close contacts per day.	Crowding in place of residence: • medium crowding versus low crowding odds ratio = 2.7 (95% CI 1.5 to 5.1), p=0.0020 • high crowding versus low crowding odds ratio = 3.4 (1.7 to 6.9), p<0.0001	Risk of bias • selection bias in the methods of recruitment of sites (convenience sampling) and participants • outcome measurement: unreliable with low sensitivity or specificity

Reference	Study design	Methods	Key findings	Risk of bias
a cross-sectional study	• sex: n=651 (80%) men and n=167 (20%) women Country: France Study period 23 June 2020 to 2 July 2020	Type of residence comparing those living in emergency shelters, in worker's residence and in the food distribution site. Outcome measurement: Seropositivity for COVID-19 confirmed by laboratory testing. Statistical analysis: Multivariable logistic regression model adjusted for sex, frequency of leaving the place of residence, crowding in place of residence, tobacco consumption, transit through gymnasium before or during lockdown, and type of recruitment site.	Type of site: • emergency shelter versus food distribution site odds ratio =1.7 (95% CI 1.1 to 2.7), p=0.025	• exposure measurement: self-reported (potential social desirability bias) QCC rating: low Study design class: D
Alvarez-Fischer and others, 2021 (36) Spreading of SARS-CoV-2 Among Adult Asylum Seekers in Refugee Shelters in Germany	Study design: Cross-sectional Participants: • n=97 refugees • mean age: 37·7 years (range 19 to 67, SD 11·7 years) • gender: 57.9% males and 42.1% females Country: Germany Study period: • time point 1: 23 November 2020 to 3 December 2020 • time point 2: 17 February 2021 to 24 February 2021	Exposure: Residence in refugee shelter Outcome measurement: COVID-19 infection confirmed by RT PCR Statistical analysis: Chi squared test was performed to compare the frequency of positive infections, reporting absolute numbers and percentages (also reporting p values and Cis). The authors adjusted for age, sex, or facility equipment.	PCR positivity at time point 1: • refugees: 2 out of 97 (2.1%, 95% CI: 0.4 to 6.3%) • control group: 3 out of 2547 (0.1%, 95% CI 0 to 0.3%), p value for difference between groups p<0.001 Seropositivity at time point 1: • refugees: 4 out of 97 (4.1%, 95% CI 1.4 to 9.2%) • control group: 12 out of 2547 (0.5%, 95% CI 0.3 to 0.8%), p value for difference between groups p<0.001 PCR positivity at time point 2: • refugees: 2 out of 67 (3%, 95% CI 0.5 to 9.1%) • control group: 2 out of 2371 (0.1%, 95% CI 0 to 0.3%),p value for difference between groups p<0.001 Seropositivity at time point 2: • refugees: 25 out of 67 (37.3%, 95% CI 27.4 to 48.1%) • control group: 38 out of 2371 (1.6%, 95% CI 1.2 to 2.1%), p value for difference between groups p<0.001	Risk of bias: • selection bias: only 97 of 675 (14%) eligible refugees aged over 18 years willing to participate. • outcome measurement: between the 2 time points, a mass outbreak in one of the shelters in which 51/129 residents confirmed PCR positive QCC rating: medium Study design class: D

Reference	Study design	Methods	Key findings	Risk of bias
Kawano and others, 2016 (38) Shelter crowding and increased incidence of acute respiratory infection in evacuees following the Great Eastern Japan Earthquake and tsunami	Study design: Retrospective cohort Participants: • n=7,439 participants in 37 shelters, including n=418 patients with acute respiratory infection • median age: 32 years (IQR: 12 to 62 years) • gender: n=212 (51%) female Country: Japan Study period: 15 March 2011 to 4 April 2011	Exposure: Crowdedness of shelters and space per person, calculated by dividing living space area by number of evacuees. Shelters were classed as non-crowded if they had less than 5.5m^2 mean floor space per person and overcrowded if they had more than 5.5m^2 mean floor space per person. Outcome measurement: Cumulative and daily incidence rate of acute respiratory infections per 10,000 evacuees at each shelter, estimated by reviewing medical records of evacuees. Statistical analysis: Multivariable linear regression analysis of daily incidence rate of acute respiratory infections with the Huber White heteroscedasticity robust sandwich variance estimator, adjusting for: • crowded shelter or non-crowded shelter • number of rooms at the shelter • availability of heaters • flooded shelters	Incidence of ARIs in crowded compared to non-crowded shelters: • crowded shelters: n=21 (56.8%) • non-crowded shelters: n=16 (43.2%) Median cumulative incidence rate of acute respiratory infection: • crowded shelters: 5.4 per 10,000 person days (IQR: 0 to 24.6 days) • non-crowded shelters: 3.5 per 10,000 person days (IQR: 0 to 8.7 days) • p value for difference: p=0.04 Difference in daily incidence rate of acute respiratory infection: • crowded shelters compared to non-crowded shelters: 19.1 per 10,000 person days (95% CI 5.9 to 32.4) • p value for difference: p=0.01	Risk of bias: Confounding: no adjustment for basic variables (age, sex, and some measure of socioeconomic deprivation) QCC rating: medium Study design class: B

Annexe D: Quality criteria checklist

Table D1: Quality criteria checklist

Reference	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Score	Class	Notes
Ahmed and others 2020	Y	Y	N	NA	NA	Y	Y	Y	Y	Y	Medium	D	Q3: confounding (ecological bias)
Akaishi and others 2021	Y	Y	N	Y	Y	Y	Y	Y	Y	Y	Medium	D	Q3: confounding, no adjustment for basic variables (age, sex, or some measure of socioeconomic deprivation) in calculation of risk ratios.
Alvarez-Fischer and others 2021	Y	N	Y	Y	Y	Y	N	Y	Y	Y	Medium	D	Q2: selection bias, only 97 of 675 (14%) eligible refugees over 18 years willing to participate Q7: outcome measurement: between the 2 time points, a mass outbreak in one of the shelters in which 51/129 residents confirmed PCR positive
Baker and others 2000	Y	N	Y	Y	Y	N	Y	Y	Y	Y	Medium	C	Q2: selection bias (cases recruited differently to controls) Q3: exposure measures were self-reported (potential recall bias)
Baker and others 2008	Y	Y	N	NA	NA	Y	Y	Y	Y	Y	Medium	D	Q3: confounding (ecological bias)
Bennett and others 2022	Y	Y	Y	Y	Y	N	Y	Y	Y	Y	Medium	C	Q6: exposure measurement self-reported
Bigouette and others 2021	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	High	D	
Bigwan and others 2014	Y	N	N	Y	Y	N	Y	Y	Y	Y	Low	D	Q2: selection bias, lack of information on recruitment and baseline demographics Q3: confounding, no assessment of basic confounders (age, sex, and some measure of socioeconomic deprivation Q4: measurement of exposure is self-reported
Blakiston and others 2020	Y	Y	N	NA	NA	Y	Y	Y	Y	Y	Medium	D	Q3: confounding, ecological bias and no adjustment for basic variables (age, sex, and some measure of socioeconomic deprivation)
Boukari and others 2022	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	High	B	
Cerami and others 2022	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Medium	B	Q3: confounding, no adjustment for basic variables age and sex
Dasgupta and others 2020	Y	N	N	NA	NA	Y	Y	Y	Y	Y	Medium	D	Q2: selection bias, county level age, sex or other baseline demographic distributions not assessed Q3: confounding, ecological bias and no adjustment for basic variables (age, sex, and some measure of socioeconomic deprivation)
Fernandes and others 2002	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	High	C	
Ghinai and others 2023	Y	Y	Y	Y	Y	N	Y	Y	Y	Y	Medium	D	Q6: measurement of exposure self-reported

Reference	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Score	Class	Notes
Harling and Castro 2014	Y	Y	N	NA	NA	Y	Y	Y	Y	Y	Medium	D	Q3: confounding (ecological bias)
Harwood and others 2013	Y	N	N	Y	Y	Y	N	N	Y	Y	Low	D	Q2: selection bias, females underrepresented in the sample population Q3: confounding, no adjustment for age and some measure of socioeconomic deprivation in analysis Q7: measurement of outcome: self-reported symptoms of influenza Q8: statistical analysis, information provided on statistical analysis was minimal and therefore not possible to determine if appropriate analysis was performed
Irfan and others 2017	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	High	C	none identified
Kapoor and others 2016	Y	N	N	Y	Y	N	Y	Y	Y	Y	Low	D	Q2: selection bias, unclear how the controls were recruited Q3: confounding, no adjustment for basic variables (age, sex, and some measure of socioeconomic deprivation) Q6: unclear how exposure was measured
Kapwata and others 2020	Y	N	N	NA	NA	Y	N	Y	Y	Y	Low	D	Q2: selection bias, no information on population and demographic distributions Q3: confounding, no adjustment for age or some measure of socioeconomic deprivation Q7: reporting bias, self-reported tuberculosis diagnosis susceptible to reporting bias, possibly resulting in an inaccurate measure of tuberculosis infection levels
Kawano and others, 2016	Y	Y	N	Y	Y	Y	Y	Y	Y	Y	Medium	B	Q3: confounding, no adjustment for basic variables (age, sex, and some measure of socioeconomic deprivation
Lamichhane and others 2022	Y	N	N	NA	NA	Y	N	Y	Y	Y	Low	D	Q2: selection bias, no information on patient demographics at individual level Q3: confounding, no adjustment for basic variables (age, sex, and some measure of deprivation Q6 and 7: measurement of exposure and outcome: exposure data and outcome data collected 3 years apart (possible districts would have changed during this time)
Lee and others 2021	Y	Y	N	NA	NA	Y	Y	Y	Y	Y	Medium	D	Q3: confounding, ecological bias and no adjustment for minimal relevant variables (age, sex, or any measure of deprivation)
Leibler and others 2019	Y	Y	N	NA	Y	Y	Y	Y	Y	Y	Medium	B	Q3: confounding, no adjustment for basic variables (such as age, sex, and some measure of socioeconomic deprivation)
Leite and others 2021	Y	N	Y	Y	Y	Y	N	Y	Y	Y	Medium	C	Q2: selection bias: cases recruited differently to controls (cases recruited via national system of epidemiological surveillance, controls recruited by random digital dialling) Q7: measurement of outcome: controls self-reported if they had COVID-19 whereas cases had a PCR test
Li and others 2021	Y	Y	N	NA	Y	Y	Y	Y	Y	Y	Medium	B	Q3 confounding: no adjustment for dormitory in multivariate analysis, despite seeing a difference in dormitory room 9 which had 30 out of 38 students infected. Furthermore, no adjustment was made for the number of students per room, which despite the reported capacity in the main text of 6 – 13 students per room, ranges from 38 to 532.

Reference	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Score	Class	Notes
Libby and others 2020	Y	Y	N	NA	NA	Y	Y	Y	Y	Y	Medium	D	Q3: confounding (ecological bias)
Lienhardt and others 2005	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	High	C	none identified
Lopez and others 2021	Y	Y	Y	N	Y	Y	N	Y	Y	Y	Medium	B	Q3: confounding, no adjustment for sex or some measure of deprivation Q7: outcome measurement, potential information bias, index cases reporting on household contacts
Maina and others 2021	Y	Y	Y	Y	Y	N	Y	Y	Y	Y	Medium	D	Q3: confounding, adjusted risk ratios did not include some measure of deprivation (such as underlying medical conditions included in crude risk ratio model)
Martin and others 2022	Y	N	Y	Y	Y	Y	Y	Y	Y	Y	Medium	D	Q2: selection bias, participants were self-recruited
Mendez and others 2021	Y	N	N	NA	NA	Y	N	Y	Y	Y	Low	D	Q2: selection bias, participants were selected from cohort studies recruited primarily from hospitals Q3: confounding, ecological bias and no adjustment for basic variables age or sex Q7: measurement of outcome, self-reported household COVID-19 infection
Metintas and other 2004	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Medium	D	Q6: measurement of exposure self-reported
Mohan and others 2017	Y	N	Y	Y	Y	Y	Y	Y	Y	Y	Medium	B	Q2: baseline participant demographics not available to assess selection bias
Mosnier and others 2023	Y	Y	N	N	Y	Y	Y	Y	Y	Y	Medium	B	Q3: confounding, no adjustment for age and sex in multivariate regression model Q4: attrition, study reports that a large number of people were lost to follow up (n=1241 at baseline and n=721 at follow up, follow up rate: 58%) and that participant characteristics at baseline and follow up were different (specifics not provided)
Munywoki and others 2021	Y	N	Y	Y	Y	Y	Y	Y	Y	Y	Medium	D	Q2: selection bias, adult males were under-represented in the sample population as they were often working at the time of household visits and sampling.
My and others 2013	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	High	D	
Raza and others 2009	Y	Y	Y	Y	Y	N	Y	Y	Y	Y	Medium	C	Q6: measurement of exposure, self-reported (personal hygiene subject to potential social desirability bias)
Roederer and others 2023	Y	N	Y	Y	Y	Y	Y	Y	Y	Y	Low	D	Q2: selection bias in the methods of recruitment of sites (convenience sampling) and participants Q6: exposure measurement, self-reported (potential social desirability bias) Q7: outcome measurement, unreliable with low sensitivity or specificity
Sun and others, 2011	Y	Y	Y	Y	Y	N	Y	Y	Y	Y	Medium	D	Q6: measurement of exposure self-reported (potentially subject to recall bias)
Van Ingen	Y	Y	N	NA	NA	Y	Y	Y	Y	Y	Medium	D	Q3: confounding (ecological bias)
Yang and others 2021	Y	Y	Y	Y	Y	N	N	Y	Y	Y	Medium	D	Q6 and 7: exposure and outcome measurement self-reported (potential for recall bias)

QCC questions

1. Was the research question clearly stated?
2. Was the selection of study subjects/patients free from bias?
3. Were study groups comparable?
4. Was method of handling withdrawals described?
5. Was blinding used to prevent introduction of bias?
6. Were intervention or therapeutic regimens or exposure factor or procedure and any comparison(s) described in detail? Were intervening factors described?
7. Were outcomes clearly defined and the measurements valid and reliable?
8. Was the statistical analysis appropriate for the study design and type of outcome indicators?
9. Are conclusions supported by results with biases and limitations taken into consideration?
10. Is bias due to study's funding or sponsorship unlikely?

QCC study design hierarchical classes (A-D)

- class A: randomised and quasi-randomised controlled trials
- class B: cohort studies
- class C: non-randomised controlled or crossover trial, case-control, time series, diagnostic, validity, or reliability studies
- class D: non-controlled trial, case study or case series, other descriptive study, cross-sectional study, trend study, before and after study

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Published: April 2024

Publication reference: GOV-16434