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Airborne bacterial and fungal species in workstations of salmon processing plants

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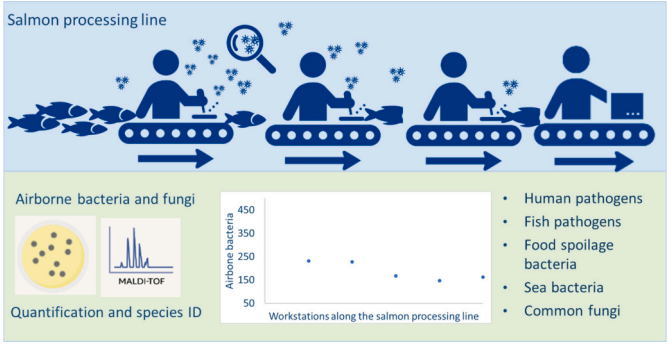
HIGHLIGHTS

- Airborne bacterial and fungal species identified in nine salmon processing plants
- Concentrations and species compositions differed between working stations
- General trends in species composition were found across plants
- Low exposure but high bacterial species diversity with many gram-negative species
- Airborne human and fish pathogens and food spoilage bacteria

GRAPHICAL ABSTRACT



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ABSTRACT

Significant quantities of salmon are processed daily in the industry's indoor facilities. Occupational exposure contributes to an individual's exposome. The aim of this study is to obtain knowledge about potential exposure to viable airborne species of bacteria and fungi as related to workstations in the salmon processing industry. The study was conducted in nine salmon plants along the Norwegian coast over one or two days with a one-year interval. The MAS100 was used for sampling and MALDI-TOF MS for species identification. The geometric mean concentrations of bacteria and fungi were 200 CFU/m^3 and 50 CFU/m^3, respectively, with the highest concentrations of bacteria found in slaughtering areas and fungi in trimming of fillets. In total 125 gram-negative and 90 gram-positive bacterial and 32 different fungal species were identified. Some genera were represented by several species e.g. *Chryseobacterium* (15 species), *Flavobacterium* (13 species), *Microbacterium* (12 species), *Pseudomonas* (37 species), and *Psychrobacter* (13 species). Risk class 2 (RC2, human pathogens) were found in all types of workstations and plants. Seventeen bacterial species belong to RC2, some were fish pathogens, food spoilage bacteria, or species causing foodborne disease. Among fungi, *Aspergillus nidulans* was frequently detected

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across different workstations and plants. In conclusion, bacterial and fungal concentrations were low. Fish and sea-related bacteria were found along the salmon processing line. Bacterial concentrations and species compositions differ between workstations. No particular bacterial or fungal species constituted a large fraction of all airborne species. Based on the presence of human pathogens, using protective gloves is important for the workers. The presence of human and fish pathogens and food spoilage bacteria reveals air as a transmission route for bacteria, potentially affecting workers, consumers, fish, and hygiene of processing equipment. To limit the spread of these bacteria an interdisciplinary cooperation with a One Health perspective may be relevant.

1. Introduction

The salmon industry represents a significant sector within the global food production chain, contributing substantially to economies worldwide (Anderson et al., 2017; Asche et al., 2018). Occupational health problems related to the fish industry include occupational respiratory problems and seafood allergy (Bang et al., 2005; Bertelsen et al., 2016; Jeebhay and Bang, 2017; Jeebhay and Cartier, 2010). In the salmon processing industry, large quantities of salmon are handled, which has been associated with exposure to endotoxin from bacteria and fish proteins (Shiryaeva et al., 2014). This suggests that aerosolization of components from the salmon, including viable bacteria, may occur.

With the development of better methods for identification of bacteria and fungi, studies have within the last years shown that occupational exposure of the airways to airborne bacteria and fungi differs between occupational settings not only in terms of exposure levels but also of species composition (Madsen et al., 2021; Mucci et al., 2022; White et al., 2019). The exposure to airborne microorganisms is of interest because they are inflammogenic, some are allergenic, and some may cause infections, which are at least partly related to the species. In environments where water has been recirculated or has been stagnant for a while, microbial exposure has been suspected to be a causing agent of hypersensitivity pneumonitis (HP) (Arnow et al., 1978; Huhulescu et al., 2011; Kane et al., 1993; Koschel et al., 2005; Kämpfer et al., 2005; Suda et al., 1995). Cases of HP have also been reported as associated with work in slaughterhouses (Vasileiou et al., 2022). In the salmon processing industry, we have found no reports on microbial associated HP, but a case associated with exposure to fish proteins has been reported (Tjalvin et al., 2018).

Some bacteria and fungi are classified into risk classes, of which risk class 2 (RC2) are microorganisms that can cause human disease and might be a hazard for directly exposed persons but are unlikely to spread to the community (European Parliament, 2006; Unfallversicherung, 2024). Several bacterial species associated with fish have been identified as causative agents of infections in humans (Gauthier, 2015). Cases of occupational infections are reported among aquarium cleaners and fishermen (Rim and Lim, 2014). Clusters of cases of *Streptococcus iniae* infections of people who had handled fresh, whole fish from farms have been reported (Weinstein et al., 1997). Similarly, cases of soft skin and tissue infections with *Mycobacterium marinum* have been reported among individuals who handle whole fish, particularly those sustaining hand injury during handling (Yacisin et al., 2017). Both *Mycobacterium marinum* and *Streptococcus iniae* are classified in RC2 posing a potential hazard to employees (Unfallversicherung, 2024). These two species are also pathogens of fish (Delghandi et al., 2020; Weinstein et al., 1997). Hand infections occurring during marine-related activities may involve uncommon bacteria that are not susceptible to conventional antibiotic treatment (Young-Afat et al., 2013). Consequently, it is important to obtain knowledge about occupational exposure to not only well-known pathogens but also other bacterial species. In spite of the several reports on infections related to handling of fresh fish, we have found no papers on cases of infections associated with work in salmon processing plants. This may be due to the absence of infectious species or infections, the use of effective protective equipment such as use of work gloves, or the underreporting of cases.

Fish spoilage pathogens are microorganisms that can contaminate fish and lead to its deterioration, making it unsafe or unpalatable for consumption. In the fish industry, airborne bacteria are not only relevant to study in relation to occupational and fish health but also in relation to product quality. While salmon processing plants are constructed with water-resistant materials and undergo daily cleaning, high humidity may still facilitate fungal growth, warranting further investigation.

With the MALDI-TOF MS method, it is possible to identify many bacteria and fungi down to species level by comparing the proteome profile with a library of profiles. The method is recognized for its efficacy in clinical settings (Seng et al., 2009), and has been successfully employed for identification of microorganisms in occupational settings (Daae et al., 2023), for fish pathogens (Jansson et al., 2020), seafood spoilage bacteria (Böhme et al., 2010), and aquatic bacterial isolates (Popović et al., 2017). In this study, we have identified airborne bacteria and fungi in the salmon processing industry using MALDI-TOF MS. The aim of this cross-sectional study is to obtain knowledge about airborne bacterial and fungal species in Norwegian salmon processing plants as associated with different workstations. The data are interpreted in relation to potential occupational health effects, but the presence of airborne fish pathogens and fish spoilage bacteria is also addressed.

2. Methods

The study is part of a multicenter study described elsewhere (Höper et al., 2023).

2.1. The plants and workstations

In total, 9 salmon processing plants were included in this study. The plants were present in rural areas along the Norwegian coastline. On the largest plants, more than 200 workers were employed. The measurements of airborne microorganisms were done from September 2021 until May 2023. Salmon processing plants can be divided into two main production departments: slaughtering and filleting. Slaughtering department included the work tasks cutting gill arches, gutting, sorting, and packing of the salmon while the filleting department included the work task, cutting of heads, filleting, trimming fillets, further processing such as pin-boning and removal of skin, and packing (here together called filleting). Therefore, air samples were taken close to workers in these areas, and we have grouped it into four workstations (Table s1).

The temperature and relative humidity (RH) were measured using Gemini Tinytag loggers. One logger was placed close to a workstation in the different departments, logging for a week. Data was collected for the two-hour period of the day where the airborne microorganisms were taken. Across plants, the average temperature in the cutting gill arches station was 8.5 °C (range 5.2–12.1) and the RH 82.2 % (range 62.0–100), in the gutting station 9.3 °C (range 5.4–17.6) and the RH 83.3 % (33.9–100), and in the filleting department 10.3 °C (5.7–15.0) and the RH 84.3 % (48.6–100 %).

2.2. Airborne microorganisms

Concentrations of airborne bacteria and fungi were measured in workstations in the nine salmon processing plants, in six of these plants airborne microorganisms were measured twice, and in three plants once.

The six plants with repeated measurements were visited with one year in between each measurement. All samples were taken in the noon.

The microorganisms were sampled using the active sampler, MAS100 (sampling 100 lpm; Merck), which samples directly on agar media. Sampling was done on Nutrient agar (in the following called NA; from Oxoid, Basingstoke, England) containing 50 mg/l actidione (cycloheximide, Serva, Germany). NA supports the growth of a wide variety of bacteria, making it suitable for general-purpose use in microbiology laboratories. Sampling was also done on Dichloran Glycerol agar (Dichloran-Glycerol Agar Base (DG18-agar); Thermo Fisher Scientific Oxoid, Basingstoke, UK). DG18 is a medium for numeration of fungi from various samples, particularly in food and environmental microbiology. Sampling times between 1 and 2.5 min were used, and between 100 and 250 l air were sampled. The samples were sent to NRCWE-dk, and upon arrival at the laboratory, the agar plates were incubated at 25 °C and inspected every second day for 14 days. Sixteen agar samples for bacteria and seventeen for fungi were taken out of the study because the agar had been exposed to temperatures below 0 °C or the plates were in another way in a bad condition during arrival at the laboratory. In total, 90 samples were analysed for bacteria and 87 for fungi (Table s1).

Colonies on the agar plates were counted. Bacterial isolates were identified using the extended direct transfer method according to the manufacturer's recommendations in a matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) Biotyper System (Bruker Daltonics, Bremen, Germany) as described previously (Madsen et al., 2023) with Bruker library v.11. Fungal isolates were identified using a modified version of a previously described ethanol extraction protocol. The modifications consisted of pellet drying times at 30–60 min after the removal of ethanol from the mycelia. Furthermore, following the addition of formic acid and then acetonitrile, the tubes were vortexed for 30 s at 2000 rpm (Multi Reax, Heidolph, Schwabach, Germany).

MALDI-TOF MS analyses were performed on a Microflex LT mass spectrometer (Bruker Daltonics) using the Bruker Biotyper 3.1 software with the BDAL standard library and filamentous library 4.0. A bacterial test standard (Bruker Daltonics) was used to calibrate the instrument. Each isolate was analyzed in duplicates using MALDI-TOF MS. The following cut-offs were used to report the results of the analyses: Based on own experiences as well as others (Fedorko et al., 2012; Stein et al., 2018), isolates with scores lower than 1.75 were unidentified. Isolates with scores between 1.75 and 1.85 were identified at the genus level. Isolates with scores of 1.85 or higher were identified at the species level.

2.3. Treatment of data

Concentrations of bacteria and fungi are presented as CFU/m^3 air. Concentrations at different workstations were compared in SAS 9.4 using general linear models (GLM) with the log-transformed data. Differences in bacterial community composition were explored using redundancy analysis (RDA) with a Hellinger pre-transformation on the concentrations using R v. 4.2.1 (R Core Team, 2022) with the package vegan (Oksanen et al., 2019) and the function anova.cca (with 'by = margin') (Legendre and Legendre, 2012). The species compositions constrained by workstation was studied.

3. Results

The concentrations of airborne bacteria and fungi differed between different workstations of the plants, with highest exposure to bacteria found during cutting gill arches and gutting, and with highest concentrations of fungi during sorting fish and fillet trimming (Table 1).

In total, 214 different airborne bacterial species were found in the working environment of the 9 salmon processing plants, and these species were distributed into 66 genera. Some genera were represented by several species e.g. *Chryseobacterium* (15 species), *Flavobacterium* (13 species), *Microbacterium* (12 species), *Pseudomonas* (37 species), and *Psychrobacter* (13 species). Several bacterial species belong to RC2 with the highest concentrations found during cutting gills. Several species are described as pathogens of fish (Table 2). Some species were found in all plants, *Dermacoccus nishinomiyaensis*, *Microbacterium maritypicum*, *Micrococcus luteus*, *Psychrobacter immobilis*, and *Rhodococcus erythropolis*, and species belonging to RC2 were also found on all plants (Table s3).

In the cutting gills arches, gutting, and filleting workstations, many different *Pseudomonas* species were found, but some of these species were found only a few times. The number of gram-negative species out of the total number of species was highest during cutting gills arches and gutting followed by filleting. The species compositions differed between workstations ($p = 0.001$) (Fig. 1).

Different fungal species were found with *Aspergillus nidulans*, *Penicillium brevicompactum* and *Penicillium commune* found often (Table 3), and these species were found in seven of eight plants (Table s4). A single species, *Aspergillus fumigatus*, belongs to RC2.

4. Discussion

This study was performed to obtain knowledge about potential exposure to bacteria and fungi during work in salmon processing plants. In general, low concentrations of airborne bacteria and fungi were found. However, human and fish pathogens and food spoilage bacteria were found, and these results will be discussed with a focus on potential occupational exposure.

The sampling was done in three different workstations as measures of potential work task exposure; a fourth station, sorting/packing, was included to a less degree. Different concentrations of bacteria were found in the different workstations, with the highest concentrations occurring in the early steps of the process chain. However, the concentrations of bacteria were in general low, and lower than found in different areas of poultry slaughtering facilities (Liang et al., 2013; Paba et al., 2014). We have found no other studies investigating airborne bacterial species in fish processing plants, but some studies have counted bacterial sedimentation on agar media in occupational settings with fish (Bagge-Ravn et al., 2003; Quintanilla-Martínez et al., 2022). Several species found in the air have previously been found in the sea and on/in fish, and many species were gram-negative. The presence of gram-negative bacteria in moderate concentrations is in accordance with previous findings of airborne endotoxin in salmon plants (Bang et al., 2005; Shiryaeva et al., 2014). In total, 125 gram-negative and 89 g-

Table 1
Concentrations (CFU/m^3) of bacteria and fungi in 9 salmon processing plants and numbers of different species.

Workstation	Bacteria			Gram-negative bacteria			No. of species		Fungi			No. of
	GM	AV	n	GM	AV	n	Gram$^+$	Gram$^-$	GM	AV	n	species
Cutting gill arches	232$^{a1)}$	285	26	41^{ab}	88	26	46	86	15^{c}	38	23	14
Gutting	228^{a}	295	33	49^{a}	87	33	51	76	51^{b}	129	34	23
Sorting/packing	153^{ab}	155	6	16^{b}	18	6	19	14	1008^{a}	1035	2	5
Filleting	162^{b}	211	28	28^{b}	39	28	54	63	120^{a}	258	31	17
All stations	201	257		38	70		–	–	51	167		–

[1)] Numbers in the same column followed by the same letter are not significantly different. GM = Geometric mean value, AV = average, n = numbers of samples.

Table 2
Heat map of geometric mean concentrations of samples positive for the bacterial species and numbers of positive stations (n) out of the total number of each type of workstation[1)]. The species are selected because they have previously been described as associated with fish or as human pathogens. Samples are taken in workstations at 9 salmon processing plants. Darker red means higher concentrations, and darker green means more positive samples.

Bacterial species	Cutting gills CFU/m³	n/12	Gutting CFU/m³	n/14	Sorting/Packing CFU/m³	n/2	Fillet CFU/m³	n/14	RC[2)]	FB/FSP[3)]	Fish[4)] pathogen
Acinetobacter guillouiae	9	3					11	3	2		
Acinetobacter johnsonii	19	3	10	1					2	FSP	Other
Acinetobacter lwoffii	4	1	4	1					2		Other
Aerococcus viridans	10	1							2		Other
Aeromonas bestiarum			4	1							Salmon
Aeromonas eucrenophila			4	1							Other
Aeromonas salmonicida			4	1							Salmon
Brevundimonas vesicularis	4	1							2		
Bacillus cereus			4	1			10	1	2	FB/FSP	
Brevundimonas diminuta	24	1	128	1			48	1			
Brochothrix thermosphacta			60	1	6	1				FSP	
Carnobacterium maltaromaticum	7	2			4	1	4	2	2	FSP	Other
Chryseobacterium chaponense	6	2	4	1							
Chryseobacterium oncorhynchi	28	1	12	4			22	2			
Chryseobacterium piscium	42	4	10	6						FSP	
Chryseobacterium scophthalmum	13	5	25	3			8	2	2		
Chryseobacterium shigense	10	1	13	3	2	1	8	3			
Chryseobacterium tructae	10	1	10	1							
Corynebacterium suicordis							10	1	2		
Delftia acidovorans	10	1	8	1			4	1			Other
Empedobacter brevis	4	1							2		
Flavobacterium araucananum			10	1			10	2			
Flavobacterium hydatis	12	1	10	2			4	1			Salmon
Flavobacterium lindanitolerans	4	1									Salmon
Gordonia bronchialis	4	1	4	1					2		
Hafnia alvei			7	2					2	FB/FSP	
Janthinobacterium lividum	9	2	14	6			10	1			Other
Kocuria rhizophila	4	1	12	6	16	1	4	4			Salmon
Moraxella osloensis	14	6	12	7	18	1	13	4	2		
Myroides odoratus	10	1							2		
Proteus vulgaris			132	1					2		Salmon
Pseudomonas chlororaphis	7	2	8	3	4	1	18	2			Other
Pseudomonas fluorescens	10	3	15	2			7	2			Salmon
Pseudomonas fragi	14	2	10	1			18	2		FSP	
Pseudomonas gessardii	4	2	20	10			9	6		FSP	
Pseudomonas koreensis	4	1	41	4			4	1			
Pseudomonas oleovorans							4	1			Other
Pseudomonas orientalis							4	1			Other
Pseudomonas proteolytica	6	3	11	4			7	4			
Psychrobacter immobilis	16	7	113	8	2	1	12	4		FSP	
Psychrobacter pulmonis	10	2	8	1					2		
Rhodococcus erythropolis	48	8	37	8	30	1	20	9			Salmon
Shewanella baltica	4	2	4	1			10	2		FSP	
Serratia liquefaciens			28	1					2	FB/FSP	Salmon
Serratia proteamaculans	16	2	4	1					2	FB/FSP	
Stenotrophomonas maltophilia	4	3							2		Other
Vagococcus salmoninarum	4	1									Salmon

A full list of all bacteria can be found in Table s2. [1)] Each sampling day are considered separately, [2)] 2, if in risk class (RC) 2 according to Gestis; [3)] Food spoilage pathogens (FSP), or cause foodborne disease from salmon to human (FB); [4)] Described to cause infections in 'salmon' or 'other' fish.

positive bacterial species were found. As examples, *Carnobacterium maltaromaticum* and *Chryseobacterium scophthalmum* were in this study found in three types of workstations and have previously been found in the intestines of healthy fish (Alvarez-Pellitero et al., 2004; Løvmo Martinsen et al., 2011). Many different *Pseudomonas* species, some *Aeromonas, Chryseobacterium*, and *Flavobacterium* species were found in the salmon processing plants, and these species have previously been found in seawater and/or in the air in drilling waste plants also present along the Norwegian seacoast (Daae et al., 2023). *Pseudomonas* and *Chryseobacterium* species were found in all types of workstations. Bacteria found on surfaces of processing equipment in the food processing industry are often referred to as the residential bacteria. A review paper shows that residential bacteria in the fish industry include the genera *Hafnia, Micrococcus, Psychrobacter, Rhodococcus,* and *Serratia* (Møretrø and Langsrud, 2017), and species within these genera were all found in the air in this study, identifying air as a transmission route of these bacteria. Human skin and airway-related bacteria were found in all types of workstations and on all plants even though the workers used coveralls and gloves.

In this study, we used a general medium, NA, to grow bacteria. The salmon industry is in this study characterised by a high species richness, with the presence of many gram-negative species, and low concentration. The composition of airborne bacterial species in this industry is very different from e.g. what has been found in e.g. pig farms (White et al., 2019) and pigeon houses (Madsen et al., 2022), all dominated by *Staphylococcus* species, biowaste plants with many different species including *Leuconostoc mesenteroides* (Madsen et al., 2024), and home (Madsen et al., 2023) – even though NA was also used in these studies. Use of other growth conditions and selective media would have revealed other species. As suggested recently, new insights are required to

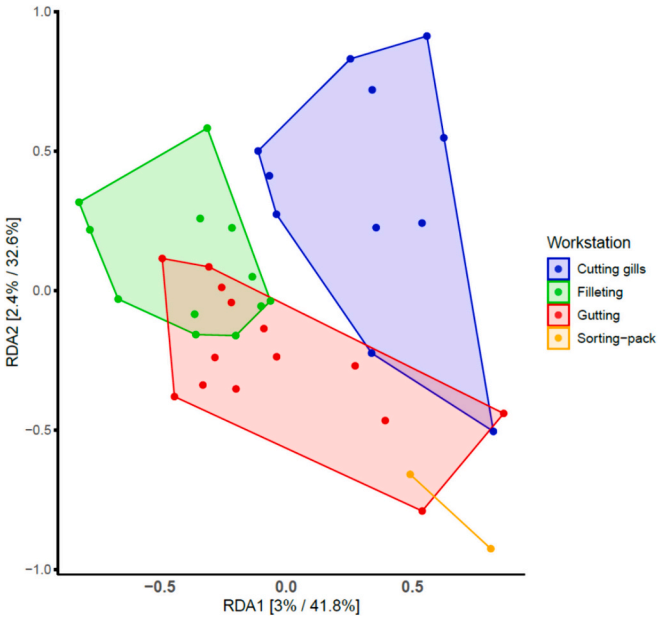

Fig. 1. RDA (redundancy analysis) plot of airborne bacteria constrained by the workstation; circles represent an individual sample. Percentages on the axes refer to the relative contribution (eigenvalue) of each axis to the total inertia in the data and the relative contribution of the particular axis to the total constrained space. Samples are colored by workstation.

Table 3
Heat map of geometric mean concentrations of fungal species in samples positive for the species and numbers of positive workstations (n) out of the total number of each type of workstation each day. Samples are taken in workstations at 8 salmon processing plants. Darker red means higher concentrations, and darker green means more positive samples.

Fungal species	Cutting gills		Gutting		Sorting		Filleting	
	CFU/m³	n/11	CFU/m³	n/15	CFU/m³	n/1	CFU/m³	n/14
Aspergillus fumigatus	4	1						
Aspergillus nidulans	9	4	18	5			33	7
Aspergillus sp.			10	1			10	1
Aspergillus terreus			4	1				
Aspergillus versicolor	30	1	19	3				
Botrytis cinerea							10	1
Cladosporium herbarum			4	1				
Cladosporium langeronii	10	1	4	1				
Cladosporium spp.	17	4	18	4			28	4
Didymella glomerata			11	2				
Mucor sp.			2	1				
Penicillium brevicompactum	11	5	17	7			16	7
Penicillium camemberti	13	3	8	5	2	1	21	5
Penicillium chrysogenum	8	1	32	1				
Penicillium citrinum							10	1
Penicillium commune	2	1	6	7	54	1	18	6
Penicillium corylophilum			17	2				
Penicillium digitatum	20	2	18	2	10	1	10	1
Penicillium discolor							10	1
Penicillium fellutanum							4	1
Penicillium glabrum			3	2			12	1
Penicillium italicum	6	3	18	1				
Penicillium nalgiovense			4	1				
Penicillium olsonii			4	3	10	1	13	3
Penicillium onobense	9	2						
Penicillium roqueforti			10	1				
Penicillium spp.			46	2	32	1	19	3
Penicillium terreus							10	1
Penicillium verrucosum	10	1						
Phoma herbarum	12	2						
Wallemia sp.			10	1			12	1
Yarrowia lipolytica							10	1
Yeast	116	2	78	2			40	1

understand how environmentally transmitted bacterial communities influence their counterparts in the respiratory and gastrointestinal tracts upon inhalation and ingestion (Jin et al., 2022).

The concentrations of fungi varied considerably with most concentrations being low, but a high concentration was found during sorting of fish in a single plant; the source of the fungi is not known, and high concentrations of fungi were not found in other workstations of the same plant (data not shown). The species found in high concentration was *Penicillium commune,* and this species was found in most plants. The concentration of fungi across workstations was at the level of what has previously been found in salmon processing plants (Bang et al., 2005) and at the lower end of what has been found in poultry slaughterhouses (Paba et al., 2014). Several fungal species were found in the air, and most belong to the genera *Aspergillus* and *Penicilllium*. These genera have previously been found in samples taken from the surface of fish (Mirza Alizadeh et al., 2022). As no species were found consistently in the plants, and *Aspergillus* and *Penicillium* are not normally associated with fish we expect they have other sources. The salmon plants were all present on the Norwegian coasts. Therefore, comparing the fungal species list with what has previously been found in companies in the same areas is relevant. Of the 32 fungal species identified from the air samples from the salmon plants, 17 species have previously been found in the working environment in drilling waste plants also along the Norwegian coast (Daae et al., 2023). Several of the found species including *A. nidulans* are halotolerant and some of the *Penicillium* species are xerotolerant which may be related to seawater in the environment, however, these species are commonly found in many working environments and homes. Furthermore, the used agar medium, DG18, supports growth of fungi able to grow at a low water activity, and use of other growth conditions may have supported growth of other species. *Penicillium camemberti* was found repeatedly but not consistently and only in low concentrations; this species has been found in occupational environments with high exposure, which caused HP (Marchisio et al., 1999). However, this species is also common in the air in homes.

In total, 17 different bacterial species found in the air of the plants classified in RC2 and as such have previously caused human infections. The RC2 pathogen, *Acinetobacter johnsonii*, was found in the cutting gills and gutting workstations. This species has in a few reported cases caused skin infection in healthy people (Henao-Martínez et al., 2012), and has been described as a food spoilage pathogen of tuna (Wang and Xie, 2020). *Myroides odoratus* was found in the air during cutting gills; it has been found in seawater, and the species belongs to RC2, and infections by *Myroides* species have mainly occurred in wet environments (Benedetti et al., 2011; Endicott-Yazdani et al., 2015). *Proteus vulgaris* found during gutting, is described as a human and salmon pathogen. The species inhabits the intestinal tracts of humans and animals and has previously caused infection in a person after skin penetration by a catfish barb (Huang et al., 2013). Therefore, it is important for the workers not only to use gloves for food hygiene but also to protect themselves. *Stenotrophomonas maltophilia* belongs to RC2 but is also described as a fish pathogen (Hajam et al., 2022); we have found no reports of work-related infections with this species. *Bacillus cereus* was found in the gutting and fillet workstations. It is classified in RC2, as it can cause gastrointestinal problems, particularly foodborne illnesses. The species can grow on slices of salmon, and cases of foodborne illness due to *B. cereus* with salmon as the vehicle has been reported (Labbé and Rahmati, 2012). It has been found in shrimp shell and codfish powder from a plant in which a worker experienced occupational airway problems (Bertelsen et al., 2016). In this study, it was only found in a few samples, and it is commonly found in the air in many working environments and also homes (Madsen et al., 2023), and not especially related to salmon plants. *Aeromonas eucrenophila* was found in one gutting workstation; it can cause diarrhea in humans (Albert et al., 2000) though it is not classified in RC2, and the species is also a pathogen of salmon (Bhowmick and Bhattacharjee, 2018). *Gordonia bronchialis* found in workstations cutting gills and gutting, belongs to RC2,

but it is also described as beneficial for fish (Shabanzadeh et al., 2016).

In addition to infections, bacteria may also cause development of HP. In occupational settings, HP typically develops gradually over time with repeated exposures to the causative agent. The frequency and intensity of exposure, as well as individual susceptibility factors, seem to play a role in determining whether or not an exposure leads to the development of HP. In the salmon processing plants, some bacterial species were found repeatedly, but in low concentrations, but we have found no papers reporting these species as causing agents of HP in other occupational settings. Exposure to *Pseudomonas* has previously been associated with development of HP (Yi, 2002); in the salmon plant, 37 different *Pseudomonas* species were found, but in low concentrations.

Several species that are described as pathogens of salmon or other fish were found in the air. An example is the species *Rhodococcus erythropolis*, described as a salmon pathogen (Olsen et al., 2006). It was found in all four types of workstations, on all plants, and it has previously been found in the air in drilling waste plants also along the Norwegian coast – but not in seawater (Daae et al., 2023). Other salmon pathogens, *Aeromonas bestiarum* and *Aeromonas salmonicida,* were found in the air during gutting. Of these species, DNA of *Aeromonas salmonicida* has previously been found in a Norwegian recycling aquaculture system from salmon (Drønen et al., 2022). *Flavobacterium hydatis* found in different workstations and *Flavobacterium lindanitolerans* found during cutting gills are described as pathogens of salmon (Faisal et al., 2011; Loch and Faisal, 2015). *Vagococcus salmoninarum* is considered one of the most significant cold-water pathogens (Saticioglu et al., 2021), and it was found during cutting gills.

Carnobacterium maltaromaticum was found in different workstations of the process line, including filleting, and the species is described as a salmon spoilage bacterium (Macé et al., 2013) and a pathogen in trout (Smith et al., 2023). *Hafnia alvei* found in the gutting workstation is also identified as a spoilage bacterium of fresh stored salmon (Macé et al., 2013). *Chryseobacterium piscium* and *Serratia liquefaciens* found in cutting gills and/or gutting workstations are described as spoiling bacteria in cold-smoke salmon (Joffraud et al., 2006). *Psychrobacter immobilis* found in all types of workstations, in highest concentrations in the gutting station, and on all plants; it is a fish spoilage bacterium of iced trout (González et al., 2000) and can grow even below 0 °C. It has previously been found on the skin, abdominal cavity, and muscle of different freshwater fish as well as in freshwater (González et al., 2000). *Pseudomonas gessardii* found in different workstations and in 8 of 9 plants can cause food spoilage in fresh fish (Parlapani et al., 2023). *Shewanella baltica* is also described as a food spoilage bacterium and was also found in different workstations.

The detection of fish, sea, and human-related bacteria in the air emphasizes the diverse sources contributing to airborne bacterial composition. The presence of human and fish pathogens, as well as bacteria associated with food spoilage, albeit in low concentrations, suggests a likely result of a high air change rate and that the plants were cleaned thoroughly every night – and underscores the importance of maintaining such conditions. Adopting a One Health approach, fostering collaboration across various sectors, appears crucial to curbing bacterial spread from salmon and safeguarding the health of workers, consumers, and fish alike.

5. Conclusion

With the measurements on nine salmon plants, this study shows that the overall concentrations of bacteria and fungi were low but with a high bacterial species richness. Fish and sea-related bacteria were found in the air along the salmon processing line, and across plants, and thus, workers were potentially exposed to bacteria from the salmon and seawater. The potential exposure differs between workstations in terms of species and concentrations. To obtain knowledge about potential exposure during sorting/packing more studies are needed. Both human and fish pathogens and food spoilage bacteria were present in the air, and some species were problematic for both workers and fish. Based on the presence of human pathogens, the use of protective gloves is important not only for food hygiene but also for workers' health. No particular bacterial or fungal species constituted a large fraction of all bacteria or fungi, indicating that bacterial growth in the salmon processing plants was limited.

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CRediT authorship contribution statement

Anne Mette Madsen: Writing – original draft, Visualization, Methodology, Formal analysis, Conceptualization. **Marte Renate Thomassen:** Writing – review & editing, Methodology, Investigation, Data curation. **Margit W. Frederiksen:** Writing – review & editing, Methodology, Investigation, Data curation. **Bjørg Eli Hollund:** Writing – review & editing, Investigation, Data curation. **Anna B.O. Nordhammer:** Writing – review & editing, Investigation, Funding acquisition, Data curation. **Hans T. Smedbold:** Data curation. **Berit Bang:** Writing – review & editing, Project administration, Methodology, Funding acquisition, Conceptualization.

Declaration of competing interest

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Data availability

Data will be made available on request.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.scitotenv.2024.175471.

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