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Microbial air quality assessment of some selected food industries in Oluyole Ibadan, Nigeria

Aderonke Oluwakemi Basil* and Blessing I. Nwadike

Department of Microbiology, University of Ibadan, Oyo, Nigeria.

*Corresponding author. Email: aderonkeadesemowo15@gmail.com, Co-author. Email: bi.nwadike@ui.edu.ng

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ABSTRACT: Air assessment is an essential component of environmental monitoring systems, helping to evaluate air quality, the health of personnel, and product safety in food industries. This study aimed to assess the microbial air quality of selected food industries in Ibadan and to investigate the presence of antibiotic-resistant bacteria. Microbial load enumeration was carried out using the settle plate method, followed by biochemical identification, pathogenicity, and antibiotic sensitivity tests. Selected isolates were also characterized molecularly. The results revealed that two out of the three sites exceeded the European Union (EU) and World Health Organization (WHO) Good Manufacturing Practices limit of 50–100 CFU for air microbial counts. The isolates identified in this study included Serratia, Bacillus, Staphylococcus, Proteus, Micrococcus, and Enterobacter. Three isolates exhibited positive reactions to hemolysis and DNase tests. While 100% of the isolates were susceptible to ciprofloxacin and 89.5% were susceptible to meropenem, resistance was observed against ceftriaxone, tetracycline, penicillin, vancomycin, gentamicin, and trimethoprim/sulfamethoxazole. Alarmingly, 57.8% of the isolates displayed multiple antibiotic resistance patterns, posing significant threats to public health. Therefore, the finding indicates the need for enhanced air quality control and hygiene practices in food industries, as well as periodic monitoring of the air environment.

Keywords: Air assessment, environmental monitoring, EU, food industries, microbial quality, WHO GMP.

INTRODUCTION

The food industry represents an occupational environment that contains raw materials, flour, flavourings, and other ingredients. Workers in such environments may face exposure to bioaerosols, which include bacteria, viruses, fungi, algae, and dust (Theisinger and de Smidt, 2017). The suspensions of microscopic solid or liquid particles in the air are defined as aerosols (Ferguson *et al*., 2019). The air is one of the microbial vectors that is thought to contribute to cross-contamination (Masotti *et al*., 2019). Therefore, microbial analysis of air is one of the most vital investigations for determining microbial air pollution (Moelling and Broecker, 2020). Bioaerosols contain microorganisms and their components such as fungi, bacteria, endotoxins, mycotoxins, and allergens. Such organisms are well-known as normal components of both indoor/outdoor air (Niazi *et al*., 2015).

Global expansion of drug resistance makes illnesses more difficult to cure and fatal, antibiotics are becoming less and less effective. Despite its emerging significance to public health concerns, the presence of antibiotic resistance genes (ARGs) in urban air has not received significant attention (Li *et al*., 2018). According to this research, airborne transmission may actively contribute to the environmental proliferation and exposure of antimicrobial resistance, in addition to other modes of transmission (Lis *et al*., 2009). Most of the time, complex mixes of allergens, toxins, and other diverse substances result in the development of bioaerosols (Humbal *et al*., 2018). Exposure to bioaerosols is frequently linked to several negative health impacts (e.g., Cancer, allergies, acute toxic effects, and infectious diseases). The most extensively researched topic has been respiratory symptoms and lung function impairment, which are among the most significant health issues brought on by bioaerosols (Chretien *et al*., 2015).

Bio-aerosol is a source of biological hazards in food

production environments and, antibiotic-resistant bacteria in the air is an emerging health concern. Therefore, microbial contamination of air in food production facilities is a major problem. There is a dearth of information about bioaerosols in the food industry and with the COVID-19 pandemic, it became essential to observe the aerosols in our environment, which have an adverse effect on the health of the public. This study aimed to assess the microbial air quality and product quality of different food industries in Oluyole Ibadan, as well as determine the presence of antibiotic-resistant bacteria.

MATERIALS AND METHODS

Sample site

The study sites are located at the Oluyole industrial axis, in Oluyole Local Government Area, Ibadan, Southwestern Nigeria. Ibadan is the capital of Oyo state and the third largest metropolitan area by population also one of the fastest growing industrial states in Nigeria, the largest metropolitan geographical area, Ibadan is located between latitude 7^{o} 02' 49'' and 7^{o} 43' 21''N longitude 3^{o} 31' 58'' and 4^{o} 08' 20''E. The mean annual temperature is 28^{o}C, ranging between 37^{o}C and the mean annual rainfall is 1,205mm, with a relative high humidity of about 74.5% all year round (UNDATA, 2013).

This study was conducted in three food industries where they produce vegetable cooking oil, bread and drinking water. These three food industries were coded as Sites A, B and C respectively. To ensure that all locations were covered, samples were collected at various sections of the food industry. Points where the samples were collected include the laboratory, stores, crushing section, refinery plant, solvent extraction plant, reception, and packaging unit.

Collection of samples

Air samples were collected using the settle plate method, as described by Olaitan and Bashir (2018). Standard Petri dishes containing media were exposed to the air for 15–30 minutes to collect biological particles that settled on the media. All samples were immediately transported to the Department of Microbiology laboratory, University of Ibadan, for incubation and further analysis. Sampling was conducted between March and July 2022. For each industry, samples were collected in two batches: one during the dry season and the other during the rainy season. This approach was based on previous studies, such as Pepper and Gerba (2015), which demonstrated differences in microbial load between the two seasons.

Enumeration of bacteria and fungi

The aerobic mesophilic bacteria and fungi counts from the air samples were determined using the settle plate method, involving standard Petri dishes containing appropriate media. The Petri dishes were exposed to the air for 15–30 minutes to collect biological particles that settled on the media. Nutrient agar and potato dextrose agar were prepared and used as the culture media. After the collection of air samples, they were transported to the University of Ibadan for incubation and further analysis, following the protocol described by Olaitan and Bashir (2018).

Identification of bacteria

The biochemical tests conducted include Catalase, Oxidase, Gram's staining, Indole, Triple Sugar Iron (TSI), Methyl Red (MR), Urease, Carbohydrate fermentation test, Starch hydrolysis test, Citrate utilization test. This test was done to identify the bacteria. Molecular Characterization of bacteria isolates was done using 16S rNA sequencing. Hemolysis, Gelatinase, Lecithinase and DNase test was conducted to determine the pathogenicity of the bacteria.

Antibiotics susceptibility profile

The antibiotic susceptibility patterns of the isolates were determined using the disc diffusion method on Mueller-Hinton agar. Inhibition zone sizes were interpreted using standard recommendations of the Clinical Laboratory Standard Institute (CLSI, 2021). Eight antibiotics discs were used, and these include Tetracycline (TE; 30ug), penicillin (PG; 10ug), ciprofloxacin (CIP; 30ug), ceftriaxone (CFM; 30ug), trimethoprim/sulphanethoxazole (SXT; 1.25ug/23.75ug), gentamicin (CN; 10ug), vancomycin (VA; 30ug), meropenem (MEM; 10ug) (Kabir *et al*., 2016). A fresh culture of the isolate was obtained to carry out the antibiotic susceptibility test, a sterile cotton swab was dipped into the sterile test tube containing the suspension, and the cotton swab was rotated at the edge of the test tube to remove the excess liquid. The swab was spread across the petri dish containing Mueller Hinton agar, then the antibiotic disc was impregnated on the agar. The plates were inverted and incubated at 37^{o} C after 18 -24 hours the plates were observed, and the inhibition zones were measured using a meter rule to the nearest whole millimetre (mm) and interpreted using (CLSI, 2021).

RESULTS

The results of the total aerobic mesophilic bacteria and fungi count present in the air of the three food industries are shown in Table 1. The highest microbial air count is 164 CFU for site A and the lowest is 32 CFU for site C. According to the result, the rainy season which is 2nd batch has more microbial load due to the activities in the air that season due to low temperature.

Table 1. Aerobic mesophilic bacteria and fungi count for the two batches of samples.

Parameters	Samples	Sites	Mean of 1st batch	Mean of 2nd batch	Standard Deviation	Limit for viable Particles
AMBC	Air (CFU)	A	144	164	56.5	50-100 CFU (EU&WHO GMP)
		B	95	138	97.3	
		C	32	44	36.6	
AMFC	Air (CFU)	A	8	11	3.8	50-100 CFU (EU&WHO GMP)
		B	7	10	4.4	
		C	6	6	4.3	

Key: AMBC=Aerobic Mesophilic Bacteria Count, AMFC= Aerobic Mesophilic Fungi Count.

Table 2. Pathogenicity tests of bacteria isolates obtained from air samples at different points in Sites A, B, and C.

Organisms	Haemolysis	DNase	Lecithinase	Gelatinase
Micrococcus luteus	-	-	-	-
Staphylococcus sp.	+	+	-	-
Proteus sp.	-	-	-	-
Enterobacter hormaechi	-	-	-	-
Serratia marcescens	+	+	-	-
Myroides marinus	-	-	-	-
Providencia sp.	-	-	-	-
Pluralibacter gergoviae	-	-	-	-
Bacillus sp.	+	+	-	-

Table 3. The frequency of occurrence of isolates obtained from the air sample of Sites A, B and C. (n=38).

Probable organisms	Site A	Site B	Site C	Con	Total	Percentage (%)
Proteus mirabilis	3	1	-	1	5	13.2
Proteus vulgaris	3	2	1	-	6	15.8
Micrococcus luteus	4	5	-	1	10	26.3
Bacillus aerius	2	1	-	1	4	10.5
Bacillus paramycoides	2	-	-	-	2	5.3
Staphylococcus spp.	2	2	-	-	4	10.5
Enterobacter hormaechi	2	-	-	-	2	5.3
Myroides Marinus	-	1	-	-	1	2.6
Serratia marscens	1	-	-	-	1	2.6
Providencia spp.	2	-	-	-	2	5.3
Pluralibacter gergoviae	-	-	2	-	2	5.3

Key: Con: - Controlled environment.

A total of 38 microorganisms were isolated from all plant air samples and they were characterized and identified through biochemical tests. Some isolates were identified as *Proteus, Micrococcus luteus, Staphylococcus, Providencia, Enterobacter, and Bacillus.* The pathogenic activity of the isolates was examined in Table 2, three isolates showed pathogenic activity and were identified as *Serratia marcescens* and *Bacillus paramycoides*.

The percentage frequency of occurrence of the isolates obtained from the air assessment of site A, site B, site C and Controlled Environment is shown in (Table 3) which shows that *Micrococcus luteus* had the highest frequency of occurrence (26.3%), followed by *Proteus vulgaris* (15.8%) with *Myroides Marinus* and *Serratia marscens* being the least (2.6%).

All isolates were susceptible to ciprofloxacin as the highest (100%) followed by meropenem (89.5%) and penicillin as the least (2.6%). The Antibiotics Susceptibility Profiling (%) of the bacteria isolates from Site A, Site B, Site C and Controlled Environment was shown in (Table 4). From the antibiotics susceptibility profiling test, eight antibiotics were used for the analysis the antibiotics

Table 4. Antibiotics susceptibility profiling (%) of bacteria isolates from air samples of sites A, B and C.

Antibiotics	N	Resistant	Intermediate	Susceptible
Ciprofloxacin	38	0	0	38(100%)
Tetracycline	38	24(63%)	2(5.3%)	12(31.6%)
Trimethoprim/Sulfamethoxazole	38	8(21.1%)	2(5.3%)	28(73.7%)
Meropenem	38	1(2.6%)	3(7.9%)	34(89.5%)
Ceftriaxone	38	24(63.2%)	0	14(36.8%)
Penicillin	38	12(31.6%)	25(65.8%)	1(2.6%)
Vancomycin	24	20(83.3%)	3(12.5%)	1(4.7%)
Gentamicin	14	4(28.6%)	7(50.0%)	3(21.4%)

Key**: -** N: - Number of isolates.

Table 5. Multiple Antibiotic resistance profile of isolates from different sites.

Isolates	Resistance pattern	Multiple R-type	Frequency
Proteus spp.	TE, CRO, VA	3	5
	TE, SXT, CRO, VA	4	2
Micrococcus luteus	TE, CRO, VA	3	2
	SXT, PG, VA	3	1
	TE, SXT, VA	3	1
	TE, CRO, VA, CN	4	1
Staphylococcus spp.	TE, CRO, VA	3	2
	SXT, CRO, VA	3	1
Bacillus spp.	SXT, CRO, PG	3	1
	TE, CRO,PG, VA	4	1
Pluralibacter spp.	TE, CRO, VA	3	1
	TE, PG, VA	3	1
Enterobacter spp.	TE, CRO, PG, VA	4	1
	TE, CRO, VA	3	1
Myroides marinus	TE, CRO, PG, VA, CN	5	1
Providencia spp.	TE,CRO, VA	3	1
Serratia marcescens	TE, PG, VA	3	1

Key: CIP:- ciprofloxacin; TE:- tetracycline; SXT:- trimethoprim/sulphanethoxazole; MEM:- meropenem; CRO:- ceftriaxone; PG:- penicillin; VA:- vancomycin; CN:- gentamicin.

include: Ciprofloxacin, Tetracycline, Trimethoprim/ Sulphanethoxazole, Meropenem, Ceftriaxone, Penicillin, Vancomycin. Gentamicin. Vancomycin was used for gram-positive isolates and gentamicin was used for gram-negative isolates. The results show that most of the isolate was not resistant in nature with the highest resistant antibiotic as ceftriaxone (63.2%) followed by Tetracycline (63%), with the least as Ciprofloxacin which showed no resistance at all.

Sixteen (42.1%) of the isolates obtained were resistant to two or more of the eight antibiotics, and 22(57.8%) showed multiple antibiotic resistance (MAR) patterns of varying degrees. Seventeen (44.7%) were resistant to three of the antibiotics, 4(10.5%) were resistant to four antibiotics and 1(2.6%) of the isolate obtained was resistant to 5 antibiotics which is shown in (Table 5)

The MAR index of the isolates is shown in Table 6. The result showed that 34.2% were found to have an index less than 0.2 while none had an index of 0.7-1.0 (not being resistant to all the antibiotics tested against the isolates). Sixty-five-point seven percent (65.7%) were greater than 0.2.

The crude material and product from each site were examined to ascertain the quality of the product. The results shown in Table 7 show that the product from Site A and Site C is safe for consumption and are within the European Union and World Health Organization, good manufacturing practice limits, the highest microbial load was Site B product (15.5CFU) with the least as the product from site A with (3 CFU) this product passes through high temperature before it is packaged.

Molecular characterization was done for some of the isolates that showed unique features. Figure 1 shows the phylogenetic tree of the isolates. The isolates were

Table 6. Multiple Antibiotics Resistant (MAR) index of isolates obtained from air samples of Sites A, B and C.

MAR Index	No. of isolates (%)
0.0	1 (2.6%)
0.1	7(18.4%)
0.2	5(13.2%)
0.3	3(7.89%)
0.4	17(44.7%)
0.5	4(10.5%)
0.6	1(2.61%)
0.7	0(0)
0.8	0(0)
0.9	0(0)
1.0	0(0)

Table 7. Microbial load of raw materials and product of sites A, B and C.

Parameters	Sample	Site	1st Batch	2nd Batch	Average	Limit for viable particles
Crude (CFU/Plate)	Palm oil	A	46	79	62.5	25-50 (CFU/25cm^2)
	Untreated tap water	B	23	60	41.5	
	Flour	C	20	21	20.5	
Product (CFU/plate)	Vegetable oil	A	5	1	3	25-50 (CFU/25cm^2)
	Treated drinking water	B	10	21	15.5	
	Bread	C	2	5	3.5	

identified as *Proteus mirabilis* (Con4), *Myroides marinus* (B7), *Enterobacter hormaechi* (A9), *Proteus mirabilis* (B8), *Bacillus aerius* (A21), *Pluralibacter gergoviae* (C1), *Proteus mirabilis* (A16) and *Bacillus paramycoides* (A6).

DISCUSSION

In this study, air samples that were collected from selected food industries in Ibadan showed that the rainy season had more microbial load than the dry season. Table 1 result is consistent with the work of Oyet *et al.* (2020) who obtained a higher microbial load during the rainy season in their assessment of different foods such as yam, fish and plantain from food vendors in Port Harcourt, Nigeria. Oyet *et al.* (2020) stated that the dry season had lower bacteria counts compared to the rainy season and attributed it to the distribution of microorganisms by environmental factors such as temperature, humidity of the season, pH, and intensity of sunlight.

One of the most important investigations to ascertain the level of microbial air pollution in the environment is the microbiological quality assessment of industrial air. The settle plate method was used to assess the bacterial and fungal aerosol concentrations in the atmosphere of the food industries in Ibadan, and the results obtained ranged from 30.5–163.6 CFU. This is within the range obtained by Olaitan and Bashir (2018). The overall bioaerosol of the food industries (Site A and B) with a mean microbial load of 154 CFU and 116.5 CFU respectively exceeded the acceptable limits of World Health Organization Good Manufacturing Practices (WHO, 2000; European Union, 2008) with 50-100 CFU as the standard microbial load of food industries. Table 1 result also indicates that the hygiene of food industries is not taken seriously.

Staphylococcus sp., *Serratia marcescens* and *Bacillus* sp. were positive for the pathogenicity test, the Table 2 result correlates to the findings of Kabir *et al*. (2016) who showed the presence of pathogenic bacteria (*Staphylococcus* sp.) from the air samples of a university environment, in Bangladesh. Bioaerosols usually harbour microorganisms as Gram-positive cocci and Gram-negative rods are present alongside their components such as β glucans, mycotoxins, endotoxins, and allergens (Kim *et al*., 2018). These bioaerosols are capable of causing serious diseases in humans such as respiratory diseases, cancer and infection when they are been inhaled or ingested (Kim *et al*., 2018).

It was observed that *Micrococcus luteus* was the predominant isolate followed by *Proteus vulgaris*, *Bacillus*

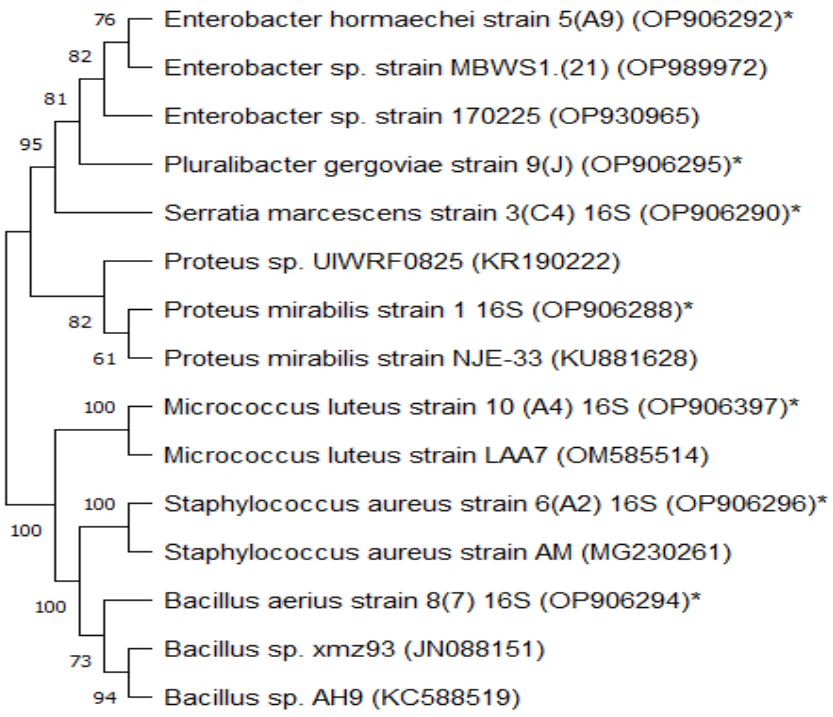

Figure 1. Phylogenic tree of isolates obtained from air samples of Sites A, B and C in relation to isolates in the gene bank.

sp. and *Staphylococcus* sp. This finding in Table 3 agrees with the works of Olaitan and Bashir (2018) and Oyet *et al*. (2020), who discovered that *Micrococcus luteus* was predominant in the air of pharmaceutical industries in Kano, Nigeria. *Micrococci luteus* can grow well in an environment with little water or high salt concentration. They occur in a wide range of environments, including dust (air), water and soil. *Micrococcus* is generally thought of as a harmless bacterium, though there have been rare cases of *Micrococcus* infection in people with compromised immune systems, as occur in HIV patients. Similar work was reported by Sabharwal and Sharma (2015) who observed *Micrococcus luteus* and *Staphylococcus* sp. as the predominant isolates obtained from the air of a school environment. Other isolates obtained include *Providencia* sp., *Enterobacter* sp., *Serratia marcescens, Citobacter freudii* and *Pluralibacter* sp.

Antibiotic-resistant genes have been examined and discovered in the air (Li *et al*., 2018). Hence, after the collection and isolation of bacteria from the air samples, the isolates were subjected to an antibiotic susceptibility test with eight antibiotics namely, Ciprofloxacin, Meropenem, Gentamicin, Ceftriaxone, Vancomycin, Tetracycline, Penicillin and Trimethoprim/Sulfamethoxazole. All the isolates were majorly susceptible to Ciprofloxacin (100%) while 89.5% were susceptible to Meropenem. Sixty-three per cent of the isolates were resistant to Tetracycline and 63.2% showed resistance to Ceftriaxone this finding is consistent with the study of Kabir *et al.* (2016) that reported 100% susceptibility by Meropenem and Ciprofloxacin with resistance to Ceftriaxone (50%) and Tetracycline (31.3%). A similar finding has also been reported by Hayleeyesus and Manaye (2014).

Sixteen (42.1%) of the isolates obtained were resistant to one or two of the eight antibiotics; 22(57.8%) showed multiple antibiotic resistance (MAR) patterns on varying degrees. Of the 22, 17(44.7%) were resistant to three of the antibiotics, 5(13.2%) were resistant to four antibiotics and 1(2.6%) of the isolate obtained was resistant to 5 antibiotics. Eleven (28.9%) of the isolate showed the same phenotypic antibiotic-resistant pattern as Tetracycline, Cetriaxone, and Vancomycin, as shown in Table 5 agrees with the work of Kabir *et al*. (2016). Isolates with multiple antibiotic-resistant patterns can serve as reservoirs for antibiotic-resistant genes through horizontal gene transfer which poses a great threat to humans.

The findings in this study revealed the highest multiple antibiotic resistance rates, in that 34.2% were found to have a MAR index less than 0.2 while none had an index of 1.0 (not being resistant to all the antibiotics tested against the isolates). This finding shown in Table 6 correlates with Ayandele *et al*. (2020), who showed that isolates from a tertiary institution in Oyo had no MAR index of 1.0.

The products from Site A and Site C are safe for consumption as their microbial load was within the European Union and World Health Organization, good manufacturing practice (WHO, 2000; European Union, 2008) limits. The highest microbial load was observed in Site B product (15.5CFU) and Table 7 shows the need for

proper hygiene in the food industries.

It is alarming to detect *Serratia marcescens* produced from the air of the laboratory air conditioner system in Site A. Which was both resistant to multiple antibiotics and pathogenic. This finding agrees with Kim *et al*. (2018) who obtained antibiotic-resistant bacteria from the dust air particles of indoor air conditioner filters indicating that the air conditioner system aids the spread of microorganisms in the environment. The personnel in the food industries are to ensure personal protective equipment is worn during operations.

Conclusion

This study highlights the critical need for improved hygiene in food industries, as two out of the three sites assessed did not comply with World Health Organization (WHO) Good Manufacturing Practices. The detection of pathogenic microorganisms and multiple antibiotic-resistant bacteria in the air poses a significant threat to human health. Additionally, the microorganisms present in the air could act as reservoirs for antibiotic-resistance genes. Therefore, further studies are necessary to identify the specific resistance genes in the bacteria isolated from the air. It is recommended that periodic air quality assessments be conducted in food industries to monitor bioaerosol compositions. The use of personal protective equipment (PPE) should be prioritized, particularly for workers in food industries, as exposure to airborne microorganisms can adversely affect human health. Furthermore, adherence to Good Manufacturing Practices (GMP), including stringent hygiene protocols and effective air filtration systems, should be enforced to ensure a safer industrial environment.

CONFLICTS OF INTEREST

The authors declare that they have no conflict of interest.

REFERENCE

Ayandele, A. A., Oladipo, E. K., Oyebisi, O., & Kaka, M. O. 2020. Prevalence of multi-antibiotic resistant *Escherichia coli* and *Klebsiella* species obtained from a tertiary medical institution in Oyo, state, Nigeria. *Qatar Medical Journal*, *2020*, Article number 9.

Chretien, J. P., Anyamba, A., Small, J., Britch, S., Sanchez, J. L., Halbach, A. C., Tucker, C., & Linthicum, K. J. (2015). Global climate anomalies and potential infectious disease risks: 2014-2015. *PLoS Currents Outbreaks*, *7*.

CLSI (2021). Performance standards for antimicrobial susceptibility testing. 31st edition. ClSI supplement M100S. Wayne, PA: Clinical and Laboratory Institute.

European Union Good Manufacturing Practices (2008). Medicinal products for human and veterinary use. Annex 1: Recommended Limits for Microbiological Monitoring of Clean Areas During Operation.

Ferguson, R. M., Garcia-Alcega, S., Coulon, F., Dumbrell, A. J., Whitby, C., & Colbeck, I. (2019). Bioaerosol biomonitoring: Sampling optimization for molecular microbial ecology. *Molecular Ecology Resources*, *19*(3), 672-690.

Hayleeyesus, S. F., & Manaye, A. M. (2014). Microbiological quality of indoor air in university libraries. *Asian Pacific journal of Tropical Biomedicine*, *4*, S312-S317.

Humbal, C., Gautam, S., & Trivedi, U. (2018). A review on recent progress in observations, and health effects of bioaerosols. *Environment International*, *118*, 189-193.

Kabir, M. S., Mridha, F., Islam, S., & Shorifujjaman, M. (2016). Microbiological pollutants in air and antibiotic resistance profile of some bacterial isolates. *Jahangirnagar University Journal of Biological Sciences*, *5*(1), 47-56.

Kim, K-H., Kabir, E., & Jahan, S. A. (2018). Airborne bioaerosols and their impact on human health. *Journal of Environmental sciences*, *67*, 23-35.

Li, J., Cao, J., Zhu, Y. G., Chen, Q. L., Shen, F., Wu, Y., Xu, S., Fan, H., Da, G., Huang, R. J., & Yao, M. (2018). Global survey of antibiotic resistance genes in air. *Environmental Science and Technology*, *52*(19), 10975-10984.

Lis, D. O., Pacha, J. Z., & Idzik, D. (2009). Methicillin resistance of airborne coagulase-negative staphylococci in homes of persons having contact with a hospital environment. *American journal of infection control*, *37*(3), 177-182.

Masotti, F., Cattaneo, S., Stuknytė, M., & De Noni, I. (2019). Airborne contamination in the food industry: An update on monitoring and disinfection techniques of air. *Trends in Food Science & Technology*, *90*, 147-156.

Moelling, K., & Broecker, F. (2020). Air microbiome and pollution: composition and potential effects on human health, including SARS coronavirus infection. *Journal of environmental and public health*, *2020*(1), 1646943.

Niazi, S., Hassanvand, M. S., Mahvi, A. H., Nabizadeh, R., Alimohammadi, M., Nabavi, S., Faridi, S., Dehghani, A., Hoseini, M., Moradi-Joo, M., & Yunesian, M. (2015). Assessment of bioaerosol contamination (bacteria and fungi) in the largest urban wastewater treatment plant in the Middle East. *Environmental Science and Pollution Research*, *22*, 16014-16021.

Olaitan, M. O., & Muhammad, B. (2018). Microbial quality evaluation of two pharmaceutical companies in Kano State, Nigeria. *Journal of Pharmacy & Bioresources*, *15*(1), 84-91.

Oyet, G. I., Achinewhu, S. C., Kiin-Kabari, D. B., & Akusu, M. O. (2020). Microbiological quality of selected street vended foods during wet and dry season in parts of Port Harcourt metropolis, Rivers State, Nigeria. *Research Journal of Food Science and Nutrition*, *5*(2), 35-45.

Pepper, I. L., & Gerba, C. P. (2015). Aeromicrobiology. In *Environmental Microbiology* (pp. 89-110). Academic Press.

Sabharwal, E. R., & Sharma, R. (2015). Estimation of microbial air contamination by settle plate method: are we within acceptable limit. *Scholars Academic Journal of Biosciences*, *3*(8), 703-707.

Theisinger, S. M., & de Smidt, O. (2017). Bioaerosols in the food and beverage industry. In: *Ideas and applications toward sample preparation for food and beverage analysis*, INTECH Chapter 3, pp. 29-35.

UNDATA (2013). Statistics: Gender Inequality Index. Retrieved from http://data.un.org//documentData.aspx?d=361.

World Health Organization (WHO) (2000). Food safety: Resolution of the Executive Board of the WHO 105th Session. Retrieved 12th November 2022 from www.who.int/publications/item.