Science Publications

Open Journal of Food and Nutrition, 2023, 1, 595
www.scipublications.org/journal/index.php/ojfn
DOI: 10.31586/ojfn.2023.595

Article

Microbial Quality of Home Prepared Complementary Foods in Slum Households with Children of Age 6-24 Months in Addis Ababa: A Community Based Cross-sectional Study

Abiyot Tenna [1,*], Esubalew Tesfahun [2], Dejene Derseh [3], Gebremedhin Yenehun [1], Teshome Nigussie [1]

[1] Public health Research and Emergency Management Directorate, Addis Ababa Health Bureau, Addis Ababa, Ethiopia

[2] Department of Public Health, College of Health Science, Debre Berhan University, Debre Berhan, Ethiopia

[3] Department of Public Health, Menelik II Health Science and Medical College, Kotobe Metropolitan University, Addis Ababa, Ethiopia

*Correspondence: Abiyot Tenna (Abiyottenna@gmail.com)

Abstract: Background: Foodborne disease is a worldwide challenge. It causes a huge burden of diarrhea in children mostly in developing countries and this is common during the complementary feeding periods. As home serve as the proliferation ground for microbial pathogens, home- prepared complementary foods, coupled with unhygienic feeding practice and contamination, it is the cause of child morbidity and poor nutritional status. This is worse in slum households. However, recent evidence is very scarce and further study is very necessary. **Objective:** To investigate the microbiological quality of home-prepared complementary foods in slum households with children of 6-24 months in Addis Ababa, 2021. **Methods:** A community-based cross-sectional study design was used and a total of 91 households were included. Three sub-cities in Addis Ababa and slum settlements within each sub-city were randomly selected by lottery method. Households with children of age from 6-24 months were selected by systematic random sampling. Laboratory investigation was used for microbial identification and excel sheet was used for data entry and cleaning. SPSS V. 23 was used for data analysis. **Result:** The median and interquartile range of aerobic plate count, *S.aureus*, yeast, molds and total coliforms are log5.75cfu/ml, Log1.84cfu/ml; Log4.7cfu/ml, Log5.46cfu/ml; Log5.29 cfu/ml, Log3.68cfu/ml; Log4.17cfu/ml, Log4.70cfu/ml; and Log0, Log3.5cfu/ml, respectively. Fecal coliform and *E.coli* were observed in 19% and 10% of complementary food samples. **Conclusion:** The load of aerobic plate count, *S.aureus*, yeast, molds, and total coliform are high in samples of complementary foods. Therefore, intervention studies for further identification of contamination sources should be made in order to minimize contamination of complementary foods and associated infections.

Keywords: Complementary foods, Microbial quality, Slum households

How to cite this paper:
Tenna, A., Tesfahhun, E., Derseh, D., Yenehun, G., & Negussie, T. (2023). Microbial Quality of Home Prepared Complementary Foods in Slum Households with Children of Age 6-24 Months in Addis Ababa: A Community Based Cross-sectional Study. *Open Journal of Food and Nutrition*, *1*(1), 40–50. Retrieved from https://www.scipublications.com/journal/index.php/ojfn/article/view/595

Received: December 26, 2022
Accepted: February 2, 2023
Published: February 4, 2023

1. Introduction

Microbiological threats in precarious food can make people sick, causing acute or chronic illness that in risky cases lead to death or enduring disability. Contaminants mainly of bacteria, viruses, and parasites constitute the major cause of food-borne diseases [1].

In developing countries, such contaminants are responsible for a wide array of diseases, including cholera, campylobacteriosis, *E.coli* gastroenteritis, salmonellosis,

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shigellosis, typhoid and paratyphoid fevers, brucellosis, amoebiasis, and poliomyelitis [2]. For instance, food contaminated with pathogenic *E. coli* causes up to 25 % of all diarrheal episodes in infants and children, while *Campylobacter jejuni* and *Shigella spp.* account for 10-15% and 5-15 %, respectively [3-5]. Food-borne bacterial diseases reported in Ethiopia were mainly caused by *Salmonella spp., Campylobacter, Listeria, E.coli* and *Mycobacterium* [6].

Foodborne pathogens take advantage of immature immune systems and therefore; infants and young children are particularly at risk of contracting and dying from common foodborne or food-related diseases [3]. They bear an unequal share of the burden of food born diseases (FBD); accounting for 9% of the global population, but 38% of all cases of illness and 40% of disability-adjusted life years (DALYs) [3]. It cause up to 70% of the roughly 1.5 billion annual episodes of diarrhea, and 1.8 million deaths in children under the age of five [3, 4].

Complementary feeding period is the time when the child is introduced to additional food that complements breast milk. It is also the time when the child is most exposed to infection and malnutrition essentially in settings when pathogens are introduced to a child through contaminated foods and/or tools used in feeding [7]. As home provides favorable environment for proliferation of microbial pathogens and it is a main location where contamination and cross contamination occurred, home prepared complementary foods can be easily contaminated though it remains unacknowledged [8-10]. This is common in slum environments which are characterized by overcrowding, poverty, inadequate sanitary conditions and poor general hygiene [11].

Coliforms (31.2%), staphylococci (30.1%), *Bacillus* spp. (19.1%), and micrococci (14.2%) were identified from contaminated weaning foods prepared at home. Poorly cleaned and frequently re-used utensils, contamination during refilling and feeding bottles themselves were sources of contaminations [12].

In developing countries like Ethiopia, where commercial complementary food is out of reach of the poor, home prepared complementary foods are commonly practiced. Although Ethiopia has a regulatory service for commercial complementary foods, there is no means to control quality of home prepared complementary foods [13]. Moreover, recent information on microbial quality of complementary food is very limited and continuous research on hygiene of complementary food has been recommended [11, 14].

Therefore, the aim of this study is to investigate the microbial quality of home prepared complementary foods in slum households of Addis Ababa, Ethiopia.

2. Materials and Methods

2.1. Description of the study setting

The study was conducted in Addis Ababa. Addis Ababa lies 9°1′48″N latitude and 38°44′24″E longitude. The city occupies a total area of 540 Sq.Km² [15]. It is divided in to 11 sub-cities and 116 Woredas for administrative reasons. Namely, Addis Ketema, Akaki-Kality, Arada, Bole, Gulelle, Kirkos, Kolfie-Keraniyo, Lideta, Nefas Silk-Lafto, Lemi kura and Yeka Sub-city.

Kirkos, Arada and Yeka Sub-city were selected for this study. The total population of the three sub-cities are 291, 001; 278,194, and455, 998 with area of 14.62, 9.91,85.98/Km^{2,} respectively [16].

2.2. Study design and period

A community based cross-sectional study was conducted from March to May, **2021.**

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2.3. Sample and data source

Samples of home prepared complementary foods were collected and investigated in the laboratory.

2.4. Inclusion and exclusion Criteria

Slum households that possess children of age from 6-24 months and use home prepared complementary foods were included and mothers /caregivers who are seriously ill during the time of data collection, and have children who are placed on special case feeding due to diseases such as malnutrition/ and TB were excluded from the study.

2.5. Operational definition

Satisfactory result: test results indicating good microbiological quality.

Borderline result: test results indicating acceptable microbiological quality

Unsatisfactory result: test results indicating poor and unacceptable microbiological quality [17]

2.6. Sample size determination

Since microbial investigation of food is resource intensive, 91 complementary food samples were collected and analyzed for this research.

2.7. Data collection tools and procedures

Sample collection format which contains type of sample, location of sample site, date and time of collection, name of sample collectors and number of samples collected was prepared. For food sample collection, all materials used was washed, appropriately rinsed for any residues and sterilized. The food sample was collected by the principal investigator with two senior microbiologists. Then, 100gm sample was collected from each household with 6-24months children by using properly labeled sterile zipped plastic bag and is transported by using ice-bag (triple package) to Addis Ababa Health Bureau Public Health Microbiology Laboratory which is found in Zewditu Memorial Hospital, and analyzed within 2hrs of collection.

2.8. Preparation of samples

Bacterial growth media such as Peptone water, MaCconkey Broth, MaCconkey agar, Brilliant Green Bile Broth (BGBB), EC broth, Nutrient broth, Plate count agar, selenite cysteine broth, XLD, Mannitol salt agar, buffered peptone water, Lysine Iron Agar, Triple sugar Iron agar, potato dextrose agar, Kovac's reagent, coagulase reagent, and oxidase reagent was used for laboratory investigation. Media preparation were carried out according to manufacturer's instruction and the instruction in the ISO 7218 method of microbiology of food and animal feeding stuffs [18]. Ten gram of each of the sample was weighed and mixed with 90ml of sterile maximum recovery diluents (MRD). This was used as the 10^{-1} dilution for each of the samples. Then, it was swirled gently for 20 minutes using Orbit shaker (lab-line instruments.inc, Model 3521, USA) to form a homogenate. Then, it was further diluted to 10^{-5}. Vortex was used at each dilution step before the next dilution was made to keep homogeneity of the samples. This process was repeated until the number of colonies per plate ranged between 30-300. Ten gram of each of the sample was weighed and mixed with 90ml of sterile peptone water (PW) and incubated over night for Salmonella detection. To avoid contamination, sterile gloves (surgical) were used (ANHUIZHONGJIAN PLASTIC AND RUBBERCO., LTD, CHINA).

For all microbial parameters involving colony count, two consecutive dilutions were used, as n_1 and n_2 to calculate the results. Total bacteria colony count was

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presented as Colony Forming Units per ml of complementary food samples (CFU/ml). The average plate count was calculated using the formula [19]:

$$N = C/V\ (n_1 + 0.1n_2)\ d$$

Where

C = is the sum of colonies on all plates counted
V = is the volume applied to each plate
n_1= is the number of plates counted at first dilution.
n_2= is the number of plates counted at second dilution,
d = is the dilution from which first count was obtained.

2.9. Microbial analysis

2.9.1. Analysis of food samples for Aerobic plate count

For analysis of aerobic plate count, method specified in ISO 4833-1 was used. From the sample homogenate, a serial dilutions from 10^{-4} to 10^{-5} was used. Accordingly, 0.1 ml portions from these dilutions were spread plated on pre-dried surface of plate count agar (PCA)(PARK Scientific APHA, USA) using a sterile glass rod and incubated at 37^0C for 48hrs (296, South Africa). All available and distinguishable colonies were counted as APC using colony counter (YLN-30, UK) [20].

2.9.2. Analysis of food samples for Total coliforms, Faecal coliforms and *Escherichia coli.*

The enumeration of total coliforms was carried out by the pour plate method using violet red bile agar (VRBA)(HIMEDIA laboratories, India). As indicator of presence pathogens in food, coliforms rarely occurred in complementary foods. Therefore, serial dilutions from 10^{-2} and 10^{-3} were utilized for this research. The VRBA media was mixed with 1 ml of the sample dilutions and allowed to set. Finally, an overlay was prepared using VRBA and incubated at 37^0C for 24hrs [21]. For confirmation of total coliform and fecal coliform, typical colonies were taken from VRBA and inoculated to Brilliant Green Bile Broth and EC Broth (HIMEDIA laboratories, India) and incubated for 37^0C and 44^0C for 24 hours, respectively. For detection of *E.coli*, a loopful from EC broth was taken and inoculated to nutrient broth (HIMEDIA laboratories, India) and incubated at 44^0C for 48hrs. Then, indole test was performed. Two-three drops were used for each test.

2.9.3. Analysis of samples for *Staphylococcus aureus*

Similarly, for enumeration *of Staphylococcus aureus,* serial dilutions of 10^{-2} and 10^{-3} were used. From each dilution, 0.1 ml portions were spread plated on pre dried surface of manitol salt agar (Difco Laboratories, USA) using a sterile glass rod and incubated at 37^0C for 48hrs [22]. Golden yellow colonies with yellow zones were considered as *staphylococcus aureus.* Further confirmation was done with coagulase test. Enumeration of all microbial analyses followed the counting rules by American Public Health Association [23].

2.9.4. Analysis of food samples for Salmonella and shigella *spp*

For detection of salmonella, method specified in 1SO 6579 was used**.** Ten gram of each sample was weighed into 90ml of Buffered Peptone Water (BPW) (Sisco research laboratories Pvt.Ltd, India) and incubated at 37^0C for 24 hrs. For *salmonella and shigella,*the first dilution (10^{-1}) was used after overnight incubation. For each sample, 1ml from BPW was transferred into selenite cysteine broth which is used as secondary enrichment and incubated at 37^0C for 24hrs.Then, a loopful (5µl) from selenite cysteine enrichment broth (HIMedia laboratories, India) was streaked to

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Xylose lysine deoxycholate agar (XLD)(BIOMARK Laboratories, India). Typical colonies with red/pink in color and black at center were identified for salmonella and red colonies were identified as shigella [24]. Further confirmation was carried out via batteries of biochemical tests. Lysine iron agar, triple sugar iron agar, urea agar, oxidase test, Motility-Indol-ornithine agar and citrate agar (HI-Media laboratories, India) were used [25].

2.9.5. Analysis of food samples for Yeasts and molds

For enumeration of yeast and mold, methods identified in ISO 21527-1: 2008 was employed. Dilutions were made from the homogenate and 0.1 ml portions from 10^{-3} to 10^{-4}dilutions were spread plated on pre-dried surface of potato dextrose agar (BIOMARK Laboratories, India).and incubated 20^{0}C for 5days. Creamy to white colonies were considered as yeasts whereas the others were considered as molds [26].

2.10. Data management and quality control

All materials used for laboratory investigations (bottles, petri dishes, test tubes, pipettes and other materials) was washed properly, rinsed for any residues that may have bacteriological effect and was sterilized. This process continued in each day of sample collection and analysis. Samples was transported by using triple package and improperly labeled and broken containers, last arriving samples and samples with insufficient volumes was excluded. Media sterility was checked by overnight incubation prior to use and quality control was used in all batch of the samples.

2.11. Data analysis

Excel sheet was used for data entry and completeness and consistency was checked. Then, it was transported to SPSS version 23. Both descriptive and inferential statistics were used. Descriptive statistics such as frequency distribution, median, Interquartile range and percentage were used. Tables, graphs and charts were used for result presentation.

2.12. Ethical consideration

Letter of approval was obtained from Kotobe Metropolitan University, Menelik II Health Sciences and Medical College. Ethical letter was obtained from Addis Ababa Health Bureau Public Health Research and Emergency Management directorate and verbal consent was found from each household where the samples and associated information were collected. During data collection, all COVID-19 protection protocol was obeyed. All data collectors and supervisors were oriented about face masking, hand washing, use of sanitizers and distancing (>1m). A follow up was made and appropriate action was taken.

3. Result

3.1. Microbial contamination of complementary foods

In this study, 91 home prepared complementary food samples were collected and analyzed to assess the microbial contamination. As indicated in figure 1, the samples comprises 40.7% cereal based foods, 18.7% mixed foods, 15.4% milk, 8.8% vegetables and root-tubers and 12% enjera with shiro and firfir and the rest proportion is egg and meat.

The median and interquartile range of Aerobic plate count, *S.aureus*, yeast, molds and total coliforms are log5.75cfu/ml, Log1.84cfu/ml; Log 4.7 cfu/ml, Log5.46 cfu/ml; Log5.29 cfu/ml, Log 3.68 cfu/ml; Log4.17 cfu/ml, Log4.70 cfu/ml; and Log0 cfu/ml, Log3.5 cfu/ml, respectively (Table 1).

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Table 1. Median and Interquartile range of aerobic plate count, *S.aureus*, yeast, molds and total coliform enumerated from samples of home prepared complementary foods (n= 91).

Variables	Result in Logcfu/ml	
	Median	Interquartile range
Log APC	5.75	1.84
Log *S.aureus*	4.17	5.46
Log Yeast	5.29	3.68
Log Molds	4.17	4.70
Log Total coliform	0	3.5

Growth prevalence is another tool used to estimate microbial load in samples of complementary foods. Growth frequency of aerobic plate count and yeast is observed in greater than 80% of the samples followed by *S.aureus* and molds which shows growth in half of the samples (Table 2).

Table 2. Growth prevalence of aerobic plate count, *S.aureus*, yeast, molds, and total coliform, fecal coliforms and *E.coli* in samples of complementary foods (n=91).

Microorganisms	No growth (%)	Growth (%)
Log APC	12.1	87.9
Log *S.aureus*	42.2	57.8
Log Yeast	19.8	80.2
Log Molds	44	56
Log Total coliforms	65.9	34
Fecal coliform	81	19
E.coli	90	10
Salmonella/shigella	100	0

Table 3 shows the mean count of microbial quality parameters exceeding the standard limit stated by standard guidelines. Accordingly, 71, 50, 53.8, 12.9 and 23.7% proportions of samples are unsatisfactory for aerobic plate count, *S.aureus count*, yeast count, molds count and total coliform count, respectively. Fecal coliform and *E.coli* were found in 19% and 10% of the samples, respectively and *salmonella/ shigella* was not detected in all the samples.

Table 3. Comparison of microbial quality with standards (n=91)

Variables	Satisfactory (%)	Borderline (%)	Unsatisfactory (%)	Standard Mean Logcfu/ml
Log APC	12.9	16	71	>5
Log *S.aureus*	42.4	7.6	50	>4
Log Yeast	25.8	20.4	53.8	>5
Log Molds	46.2	40.9	12.9	>5
Log Total coliforms	66.7	9.7	23.7	>4

3.2. Microbial load based on types of complementary foods

Growth of microorganisms in food also depends on the types of foods. As indicated in Table 4, the median of APC ranges from Log4.88cfu/ml in vegetables and tubers to Log 6.11 cfu/ml in cereal based foods. The IQR of APC is Log 1.91 cfu/ml in cereal based foods and Log 6.45 cfu/ml in Injera with shiro/ firfir. The median of *S.aureus* ranges from Log0cfu/ml in enjera with shiro/firfir and vegetebles/ tubers to

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Log4.77cfu/ml in mixed foods. The IQR of *S.aureus* is Log 4.78 cfu/ml in enjera with shiro/firfir and Log 5.69 cfu/ml in mixed foods. The median of total coliform is Log0cfu/ml in all food types and the IQR is Log0cfu/ml in egg/meat and vegetables, and Log5cfu/ml. The median yeast count ranges from Log0cfu/ml to Log5.61cfu/ml in milk. The IQR of yeast count is Log1.82cfu/ml in mixed foods and Log 6.05 in enjera with shiro or firfir. The median of molds ranges from Log0cfu/ml in milk to Log4.51 in vegetables or tubers and the IQR is Log3.88 in vegetables and Log5.45cfu/ml in egg/meat (Table4).

Table 4. Median and interquartile range of measured microbial parameters from samples of different food types (n=91).

Measured microbial parameters	Statistics	Types of food samples (n)					
		Milk(14)	Cereal based foods (37)	Enjera with shiro/ firfir (11)	Vegetables/ tubers(8)	Mixed foods(17)	Egg and meat (4)
Log APC	Median	5.95	6.11	5.52	4.88	5.47	5.91
	IQR	2.82	1.91	6.45	5.37	1.48	2.15
Log *S.aureus*	Median	4.00	4.60	0	0.00	4.77	2.23
	IQR	5.45	5.63	4.78	5.36	5.69	4.92
Log total coliform	Median	0	0	0.00	0	0	0
	IQR	4.19	4.88	5.00	0	0.96	0
Log Yeast	Median	5.61	5.43	5.20	0.00	5.50	4.75
	IQR	2.13	3.13	6.05	3.99	1.82	6.02
Log Molds	Median	0	3.50	4.00	4.51	4.30	2.45
	IQR	4.35	4.73	4.60	3.88	4.65	5.45

Table 5 shows proportions of different food types unsatisfactory for LogAPC, Log *S.aureus*, Log Yeast, Log mold and Log total coliforms. Accordingly, high proportions (>50%) of samples of all types of foods are unsatisfactory for LogAPC. Similarly, except enjera with shiro/ firfir and vegetables/ roots, >50% of other food types are unsatisfactory for *S.aureus*. More than 50% of samples of milk, mixed foods and meat/egg are unsatisfactory for Log yeast and cereal based foods and enjera with shiro/firfir are unsatisfactory for Logmolds. Less than 20% of all food types are unsatisfactory for Log total coliforms (Table 5).

Table 5. Percentage of food samples from different food types that contains unsatisfactory result for LogAPC, Log *S.aureus*, Log Yeast, Log Molds and Log Total coliforms counts (n=91).

Types of samples(n)	% food samples unsatisfactory for measured microbial parameters				
	Log APC	Log *S.aureus*	LogYeast	LogMolds	LogTotal coliform
Milk(14)	64.3	50	64.3	14.3	21.4
Cereals based foods(37)	70.3	52.8	29.7	54.1	10.8
Enjera with Shiro or firfir (11)	72.7	36.4	27.3	54.5	9.1
Vegetables/tubers(8)	50	37.5	12.5	12.5	12.5
Mixed foods(17)	82.4	58.8	64.7	11.8	17.6
Meat or egg(n=4)	75	50	50	25	0

Key: Enjera is an Ethiopian known traditional food made mainly from cereal flour such as teff, maize, sorgum etc. Firfir: is prepared by splitting enjera in to smaller pieces. Mixed foods: prepared from two and more of food types indicated above

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4. Discussion

In this study, 91 samples of complementary foods were collected and investigated for microbial contaminations. Accordingly, Log median count ranges from Log1.7±2.5cfu/ml for total coliform to Log5±2.1 in aerobic plate count. This result was comparable to study conducted in urban and rural parts of Zanzibar, Tanzania [27] in which aerobic plate count ranges from Log2.24cfu/g to Log4.58cfu/g, total coliform ranges from Log1.71cfu/g to log3.63cfu/g, and other *entrobactericea* ranges from Log1.73cfu/g to Log3.93cfu/g. The studies are similar in study setting and design but different in sample size which is relatively high in the latter. The present study is also in line with study made in Woldia Town [28] in which total viable count ranges from Log 4.14cfu/ml to 4.25Logcfu/ml, yeast ranges from Log4cfu/ml to Log4.2cfu/ml and molds ranges from Log4.1cfu/g to Log4.2cfu/g. But the latter one was done on fermented food from sorghum, walnut and ginger. Study conducted in Ghana, Accra reported total viable count in the range of Log2.35 to 3.5Logcfu/g and *S.aureus* in the range of Log2.35cfu/g to Log3.37cfu/g [29]. It is similar in sample size but the latter one is facility based. Other study in Saudi Arabia reported similar result. Total viable count in the range of Log3.65cfu/ml to Log3.86cfu/ml, and yeast and mold count in the range of Log3cfu/ml to Log4.3cfu/ml. *S.aureus* and lactobacillus were also identified. But the food is formulated from co-fermentation of Sorghum, pumpkin and carrot [30].

The total microbial count in the present study is higher than study made in south Ethiopia where total viable count and yeast and molds were identified from foods combined of kocho, sweet potato and haricot bean in the range of 0 to log0.63cfu/g and Log1.04 to Log1.13cfu/g [31]. It is also higher than other similar community based study in Asase, North Bank, Makurdi reported *S.aureus* in the range of Log1.4 to Log1.6cfu/g and total coliforms in the range of 0 to Log1.2cfu/g [32]. The nature of food samples, study setting and sample size are different.

In the present study, proportions of samples that showed growth is least for total coliforms (34%) and high for aerobic plate count (87.9%). Fecal coliform and *E.coli* were found in 19% and 10% of the samples, respectively and salmonella/ shigella was not detected in all the samples. Similar findings were obtained in the study in North Bank, Makurdi where 42% samples were positive for *S.aureus* and 59.2% were positive for total coliforms [32]. But sample size is twice higher in the latter study. In other study in rural village of Egypt, *E.coli* and *B.cerus* was found in 43.7% and 21.4% of the samples and similar to the present study, *salmonella and shigella* was not detected [33]. The difference in *E.coli* load may be due to differences in sample size, study settings and study period. In other study conducted in Ghana Accra, 2.2% and 14.4% of the samples contain *E.coli* and *Salmonella*, respectively [29]. In other study in Bangladesh, which has comparable sample size with the present study, large proportions of food samples is positive for aerobic plate count, total coliform, fecal coliforms, *E.coli*, and *S.aureus* which is 41.5, 28.3, 17.7, 25.4, 2.8%, respectively but there was no salmonella and shigella [34].

In the present study, unsatisfactory results that exceed the safe international guideline values are 12.9% of samples for molds and 71% of the samples for aerobic plate count. In a similar community based study in Zanzibar, Tanzania. proportions of samples exceeding international guideline values is 86% for aerobic plate count, 55% for total coliform and 2-60.5% for *enterobactericea* based on types of food samples [27].

Growth frequency of bacteria depends on the types of food. The available nutrients that support growth of microbes differ based on varieties of foods. In the present study, growth of aerobic plate count is higher in cereal based foods and egg/meat; *S.aureus* is the same for milk based food, cereal based foods and mixed foods; growth of yeast is higher in milk based and mixed foods as most mixed foods

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contains milk. Growth of molds is higher in vegetables and root tuber based foods and total coliform is higher for cereal based foods. But the number of samples may affect this estimate. Study made in eastern Nigeria showed that growth of bacteria differ across different food types. According to this study, four food types(Akamu, Jollotrice, Moi-Moi and Agidi) were compared and fecal coliform were higher in Agidi, E.coli were realtively high in Akamu and moi-moi and *Entrobacteriacea* is higher in Akamu [35]. Study made in Jimma Town showed that growth of aerobic plate count is higher in milk and cereal based foods; *entrobacteriacea* and coliform is higher in milk based foods and *S.aureus* and yeast is relatively higher in cereal based foods[36]. Similar study in integrated health centers in Mayahi, Niger revealed that aerobic plate count grow in mixed foods to the level of Log9.71cfu/g and Log8.4 cfu/g in single foods. But *E.coli* and salmonella grow more in single item foods than mixed foods [37]. Similar study in rural areas of Peru revealed that total coliform grows to the level of Log9cfu/ml in dairy foods and to the level of Log2cfu/ml in cereal based foods and similarly, *E.coli* was grown higher in dairy based foods and least in cereal based foods [38]. Further studies are needed to clearly indicate the cross evaluation of food types and types of microbes it can supports more.

5. Conclusion

Analysis result indicated high count of indicator organisms. This in turn indicated the likely presence of pathogenic organisms. Moreover, except salmonella and shigella, relatively high count of *S.aureus* was also obtained. The microbial load also differs among different types of food samples and the proportions of food samples that demonstrate unsatisfactory result for the measured microbial parameters were also high. This shows possibility of occurrence of infections in children and requirement of immediate actions.

Therefore, broadly, the findings can be utilized by all stakeholders involved in maternal and child nutrition programs, policy developers and decision makers. It can help nutrition professionals and other stakeholders as transition pathways from basic information to interventional studies in an effort made to improve the hygiene of complementary foods. It can also be used by Addis Ababa City Administration Health Bureau and sub city health offices for informing nutrition service providers about the issue and taking action accordingly. Lastly, it can also be used as a reference for those who need to repeat it or conduct similar study.

Ethical consideration

After proposal approval by Kotobe Metropolitan University, Menelik II Health Science and medical College, ethical letter was obtained from IRB of Addis Ababa Health Bureau Public Health Research and Emergency Management directorate and informed consent was obtained from each participant.

Data Availability

The types of data used to support the findings of this study are included within the article.

Conflict of Interest

The authors declare that they have no competing interests.

Funding

The author disclosed receipt of the following financial support for the research, authorship, and/or publication of this article: We are grateful to the Kotobe Metropolitan University, Menelik II Health Science and medical College for financial and logistic support.

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Authors' contribution: Abiyot Tenna-designed the project, organized data collection, analyzed data and wrote a report. GY and TN involved in laboratory investigation of samples and reporting whereas ET and DD involved in supervising overall activities and final review of the document.

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