# Assessing milk quality by evaluating total bacterial count in bulk milk in selected commercial dairy farms in Chattogram



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# Assessing milk quality by evaluating total bacterial count in bulk milk in selected commercial dairy farms in Chattogram



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# TABLE OF CONTENTS

# List of Tables

<b>Table 3.1</b> Descriptive statistics of five categorical and two continuous farm level variables
in ten commercial dairy farms in Chattogram district9
Table 3.2 Summary statistics of total bacterial count and $log_{10}TBC$ (CFU/mL) presented
in mean, minimum, maximum, median, quartile estimates, and standard deviation for BM
samples collected from ten commercial dairy farms of Chattogram every month12
Table 3.3 Association of five variables with total bacterial count using univariable
generalized linear regression model using random effect (farm ID) in ten commercial dairy
farms in Chattogram14
Table 3.4 Association of three variables with total bacterial count using multivariable
generalized linear regression model using random effect (farm id) in ten commercial dairy
farms in Chattogram14

# List of Figures

Figure 2.1 Geographical location of ten enrolled commercial dairy farms in Chattogram.
Figure 2.2 Diagram of a 10- fold series dilution process for the evaluation of total
bacterial count from bulk milk sample6
Figure 2.3 a. 10-fold series dilution of milk sample, b. Vertexing of sample before
dilution, c. Pouring of 1 mL of samples in a petri dish after dilution, d. Pouring of agar in
petri dish, e. Bacterial colony after incubation at 37°c for 72 hours, f. Counting of bacterial
colonies7
Figure 3.1 Comparison of total bacterial count (log <sub>10</sub> CFU per mL) in different milking
technique. Standard error (vertical black line on top of each bar) displayed in the figure.
Figure 3.2 Comparison of total bacterial count (log <sub>10</sub> CFU per mL) in crossbreed and
indigenous breed. Standard error (vertical black line on top of each bar) displayed in the
figure
Figure 3.3 Bacterial contamination in bulk milk in ten dairy farms in Chattogram13
Figure 3.4 Comparison of total bacterial count (log <sub>10</sub> CFU per mL) among different herd
size dairy farms in Chattogram. Standard error (vertical black line on top of each bar)
displayed in the figure15
Figure 3.5 Comparison of total bacterial count (log <sub>10</sub> CFU per mL) among three sampling
year from ten dairy farms in Chattogram. Standard error (vertical black line on top of each
bar) displayed in the figure
Figure 3.6 Seasonal comparison of total bacterial count (log <sub>10</sub> CFU per mL) samples
collected from ten dairy farms. Standard error (vertical black line on top of each bar)
displayed in the figure17

Abbreviation	Elaboration
TBC	Total bacterial count
SCC	Somatic cell count
BM	Bulk milk
CFU	Colony forming unit
mL	Milliliter
WHO	World health organization
FAO	Food and agricultural organization
DW	Distilled water
BSTI	Bangladesh standard testing institute

#### Abstract

Milk is an essential component in many healthy diets but it may lead to public health risks if contaminated by microorganisms. So, evaluation of the microbiological quality of raw milk is crucial before using it for human consumption. However, limited studies have been prioritized to assess the microbiological quality of bulk milk (BM) on the primary production site in the dairy farms in Bangladesh. For that, a study was conducted on ten selected commercial dairy farms in Chattogram during January 2021 to May 2023. The study aimed to evaluate the microbial quality of BM by assessing the total bacterial count (TBC) and determine the association of risk factors with the microbial quality of raw milk. The data was collected from the enrolled dairy farms through face-to-face interviews while receiving the samples in the laboratory, TBC was estimated following the pour plate technique. The mean value of TBC among 185 samples was 2.7 x 10<sup>7</sup> CFU per mL, ranging from 4.8 x  $10^4$  to 1.5 x  $10^9$  CFU per mL. The study finding indicated that most of the BM samples showed a higher bacterial count than a satisfactory level in terms of public health standards (1x 10<sup>5</sup> CFU per mL). Random-effect generalized linear regression model shows that season (P < 0.001), sampling year (P < 0.001), and herd size (P < 0.20) were associated with an increase in TBC of bulk milk. A significant increase in TBC was observed in summer than in the rainy and winter season. Higher TBC was found in medium-scale farms than in small and large-scale farms. This study revealed that TBC can be influenced by several factors such as, season and herd size therefore, additional hygienic considerations of the farms need to be monitored in future studies to ensure hygienic milk production and public health safety.

Keywords: Microbial quality, milk hygiene, bacterial count, season, farm size.

#### **Chapter 1 : Introduction**

Milk is the most easily affordable complete source of nutrition for developing countries like Bangladesh, due to its easiest availability and lowest cost compared to meat (Beal, 2021). About 90 % of the total amount of produced milk in Bangladesh and 81 % of the total milk yield globally comes from dairy cows (DLS, 2021-22; FAO, 2023). Cow milk is a complex mixture of nutrients such as water (85.5-89.5) %, total solid (10.5-14.5) %, fat (2.5-6) %, protein (2.9-5) %, lactose (3.6-5.5) %, and mineral (0.6-0.9) %. The composition of cow milk can vary in response to different factors e.g., breed, age, stage of lactation, milking interval, season, and health status of the cow (Cortes, 2023). According to World Health Organization (WHO), the recommended requirement of milk is 250 mL for per person per day. However, in Bangladesh, the milk availability is only 45.2 mL for each person which is extremely lower than the requirement. It indicates the current production can meet only 18.1% of the total requirement, which means there is still a huge gap between the requirement and availability of milk (Ritchie et al., 2017). Despite the huge demand and growth capacity of the dairy industry in Bangladesh, milk production is not up to the mark yet here due to a lack of dairy development interventions e.g., the absence of high-yielding cow breeds, higher cost of milk production than the selling price due to higher feed cost (Hussain, 2022).

According to OECD/FAO (2022), about 53 % of the world's total milk is produced from developing countries, which will continue to increase 59 % over the next ten years as consumption of milk and milk products are readily growing. A study conducted in Bangladesh found that average net return from dairy farming is US \$58 per cow per month; from that around 97 % monthly revenue comes from selling of milk (Datta et al., 2019). Despite having large potential, there are several challenges in dairy farming likely in many developing countries, including Bangladesh, are ignorant about the maintenance of standard quality of milk hygiene practices e.g., poor handling of milk during storage and transportation, poor worker hygiene that leads to different zoonotic and foodborne infections (Hasan et al., 2015; Mpatswenumugabo et al., 2019; Singha et al., 2023).

Milk is usually considered sterile when it is produced from the alveoli of the udder of a healthy cow. After leaving from the healthy udder, milk usually contains low microbial count which mainly comprises lactic acid bacteria (LAB) under the genera *Lactobacillus, Lactococcus, Leuconostoc* and *Bifidobacterium* spp that act as a probiotic for human (Reuben et al., 2019; Taye et al., 2021). The microbial count of raw milk may increase mainly as a result of three preeminent sources, i) infected lactating cow, ii) unhygienic milking, and iii) inappropriate transportation and storage or processing of milk (Mpatswenumugabo *et al.*, 2019). Many other factors may also influence the microbiological count of milk e.g., herd hygiene, degree of cleanliness, health status of workers, milk storage temperature, season, farm size, geographical location, and type of milking. (Costello et al., 2003; Parekh and R, 2008). When undesirable microorganisms like *Escherichia coli , Pseudomonas fluorescens , Pseudomonas fragi, Bacillus* spp., *Clostridium* spp. , *Streptococcus* spp. get access in milk, they multiply and produce different proteolytic and lipolytic enzymes that degrade milk's protein, carbohydrate and fat ultimately leading to the deterioration of milk quality (Ferrer, 1996).

Milk quality is the state of milk considering it's physical, chemical, and microbiological characteristics at in admissible level. Milk quality directly affects the profitability of dairy producers by reducing milk shelf life and deteriorating the processability of milk (Ndambi et al., 2018; Deshapriya, 2019). The quality of raw milk can be determined by measuring different on-farm or laboratory tests such as, assessment of the nutritional composition of milk (e.g., fat, protein, and lactose), inspection of udder health by either bacteriological culture or somatic cell count (SCC) and routine surveillance microbiological evaluation of milk by total bacterial count (TBC) (Ruegg and Reinemann, 2002). Total bacterial count (TBC) is the quantitative eneumeration of bacterial colonies present in BM (Jayarao and Wolfgang, 2003) and it is one of the most recognized methods to evaluate the milk quality in routine milk testing laboratories, categorizing raw milk for human consumption and processability of milk into different dairy products. In Bangladesh, the standard limit for microbial count is in the range of 5 x 10<sup>4</sup> CFU per mL to 1 x10<sup>5</sup> CFU per mL set by the Bangladesh Standard and Testing Institution (BSTI) (BFSA, 2022). Ahmed et al.

(2019) conducted a study in Chattogram and found unacceptably high TBC, where higher and lower value was  $1 \times 10^6$  and  $3 \times 10^4$  CFU per mL, respectively. If the TBC exceeds than the standard level, it may also degrade fat, protein and lactose in BM that directs towards the poor quality of the milk products (Spreer, 1998; Ndahetuye et al., 2020).

According to author's knowledge, there are only limited number of studies (Hasan et al., 2015; Ahmed et al., 2019; Singha et al., 2023) carried out in Bangladesh to evaluate the microbial quality of raw milk and the associated risk factors. However, these studies did not follow-up the bacterial contamination in bulk milk over a period time therefore could not completely reflect the temporal variation particularly in commercial dairy farms. To meet this scientific gap, this study aimed to estimate the periodical variation of bacterial contamination in BM in ten commercial dairy farms of Chattogram.

Specifically, the objectives of this study were to,

- 1. Estimate the variation of bacterial contamination in BM from selective commercial dairy farms by measuring total bacterial count (TBC).
- 2. Identify the association of different variables with increase in TBC in commercial dairy farms of Chattogram area.

## **Chapter 2 : Materials and Methods**

#### 2.1 Description of study area and population

The study was carried out in Chattogram district, its geographical location is  $22.3375^{\circ}$  N 91.8389<sup>o</sup> E at south-eastern region of Bangladesh. Chattogram district is one of the important dairy zones in Bangladesh. Ten commercial dairy farms were selectively enrolled for this study for a duration of 28 months (January 2021 to May 2023).



Figure 2.1 Geographical location of ten enrolled commercial dairy farms in Chattogram.

The yellow area indicates the selected district of the study (Chattogram) The red area indicates the selected farms in Chattogram district (Anowara, Baraiyarhat, Bhatiary, Chandanaish, Fauzderhat, Karnafuli, Manikchari, Station Road, Kattoli)

#### 2.2 Ethical approval and epidemiological data collection

Interested commercial dairy farmers were invited in Department of Medicine and Surgery, Chattogram Veterinary and Animal Sciences University and farmers who finally agreed were enrolled in this study. Written consents were given by the farmers and the participation in the study was voluntary and could be withdrawn at any time. A short questionnaire was prepared to collect data from the enrolled dairy farms. Data was collected once in every month during sample submission through face-to-face interviewing of farmers during receiving the sample in laboratory. The gathered information was farmer's demography, farm name, location, farmer's name, no. of milking animal at farm, and available breed in farm (cross\ indigenous). It also included information on milking hygiene; milking technique (hand\machine), transportation media (ice\ other) and required time between milk collection to transport it to the laboratory.

#### 2.3 Sample collection

Bulk milk (BM) (25-50 mL) was collected separately from each of the ten enrolled dairy farms on monthly basis from January 2021 to May 2023. Before collection, farmers thoroughly mixed the bulk milk from all the lactating cows for about 5 minutes to ensure homogeneity and then 30mL of milk was taken in 50 mL sterile falcon tube and transported to Udder Health Laboratory, Department of Medicine and Surgery, CVASU using ice box maintaining 4<sup>o</sup>C.The milk sample was stored at -20<sup>o</sup>c prior to microbiological analysis.

#### 2.4 Laboratory analysis

## 2.4.1 Media preparation

At first, 17.5 gm of plate count agar was dissolved in 1L of distil water (DW) by heating. After dissolving, media was sterilized for 15 min in the autoclave set at  $121^{\circ}$ c.After sterilization, media was kept in hot water bath at  $45^{\circ}$ c prior to pouring it in petri dish for inoculation.

#### 2.4.2 Enumeration of total bacterial count (TBC)

The pour plate technique was used for estimating total number of aerobic bacteria in the raw milk samples. The Plate Count Agar was used to perform TBC for microbial quality analysis of raw milk. Media was prepared according to the instructions provided by the manufactures (Oxoid, Basingstoke, UK). Samples were mixed properly by inverting the milk vial 20 to 25 times, then samples were serially 10-fold diluted up to  $10^{-7}$  by transferring 1 mL of BM sample from the original sample tube (after vertexing at 1500 rpm for 15 seconds) to a 2<sup>nd</sup> tube containing 9 mL of 0.9 % sterile saline. From the 2<sup>nd</sup> tube again 1 mL was transferred to the 3<sup>rd</sup> tube with 9 mL of 0.9 % sterile saline and thus continued where finally 1mL was discarded from the last tube. Then from each 10-fold dilution prepared 1 mL of sample was mixed with 15-20 mL of plate count agar in a sterile petri dish and incubated aerobically at 37°C for 72 hours. Then bacterial counts were made considering the countable dilution of 25-250 colonies and the counts from the last countable dilution was considered for the estimation using following formula (Figure 2.2) (Singha et al., 2023)

The number of bacteria in a milliliter of milk was determined by using the formula (CFU/mL),



Colony count in the last countable dilution

**Figure 2.2** Diagram of a 10- fold series dilution process for the evaluation of total bacterial count from bulk milk sample.

Volume of the inoculum in mL  $\times$  dilution factor of per mL of milk  $\times$  1.1



**Figure 2.3 a.** 10-fold series dilution of milk sample, **b.** Vertexing of sample before dilution, **c.** Pouring of 1 mL of samples in a petri dish after dilution, **d.** Pouring of agar in petri dish, **e.** Bacterial colony after incubation at 37<sup>o</sup>c for 72 hours, **f.** Counting of bacterial colonies.

#### 2.5 Statistical analysis

Findings from the laboratory analysis were entered into an MS Office 2021 Excel spreadsheet (Microsoft Corp., Redmond, WA, USA). The study period was categorized into three seasons, summer (March to May), rainy (June to October) and winter (November to February) and number of milking animal recoded into farm size; small (1 to 50), medium (51 to 200) and large scale (more than 200). Total bacterial count (TBC) data was manually transformed into log<sub>10</sub> in MS Excel to achieve a normal distribution for the downstream statistical analysis. Descriptive analysis was performed for TBC, where frequency numbers with percentages were calculated for the categorical variables i.e., farm size, time

elapsed after collection (hours) were presented in mean, range, and median. A summary (mean, minimum, maximum, quartile estimates) of TBC and  $log_{10}$  transformed TBC was conducted for each studied farm. Random effect generalized linear regression model were built up using farm Id as the random effect to identify the farm level variables associated with the TBC. Univariable analysis was performed to identify the associated variables (P < 0.20) that included in the multivariable regression models. The model was constructed following a stepwise forward selection procedure of variables. Confounding and collinearity were assessed through detecting a significant change (> 30 %) in coefficients and standard error upon adding a new variable each time.

## **Chapter 3 : Results and Discussion**

#### **3.1** Descriptive analysis

One hundred and eighty-five BM samples were received from ten farms on month basis. In the year of 2021, 2022, 2023; total received BM samples were 81, 68 and 36, respectively. Samples were received on three seasons; summer (n = 57), rainy (n = 55) and winter (n = 73). In the selected farms, number of cows ranged between 1 to 480 (median 35). Received samples were comprised of indigenous breed (n = 5) and mostly cross breeds (n = 180). All the farms used the milking twice daily. Regarding milking type, among 185 samples, 136 samples were received from farms with hand milking and remaining 49 samples from farms with machine milking. Time elapsed between sample collection to receiving in the laboratory ranging from 1 to 10 hours (median 6) (Table 3.1).

Variable name	Categories	N (%)	Mean (Min-Max)	Median
Season	Summer	57 (30.8)	-	-
	Rainy	55 (29.7)	-	-
	Winter	73 (39.4)	-	-
Milking Technique	Hand	136 (73.5)	-	-
	Machine	49 (26.4)	-	-
Breed	Cross	180 (97.3)	-	-
	Indigenous	5 (2.7)	-	-
Year	2021	81 (43.7)	-	-
	2022	68 (36.7)	-	-
	2023	36 (19.4)	-	-
Time elapsed after collection	-	178	5.4 (1-10)	6
(hours)				
Farm size	-	185	101.43 (1-40)	35

**Table 3.1**. Descriptive statistics of five categorical and two continuous farm level variables in ten commercial dairy farms in Chattogram district.

N = Observation, Min = Minimum, Max = Maximum

This study found that a higher TBC in the milk of the farms that practiced hand milking than in machine milking (Figure 3.1).Unclean milking, absence of pre-milking udder hygiene practices and poor cleaning of milking equipment could be the primary source of bacterial contamination of milk (Mpatswenumugabo et al., 2019). This study findings agreed to Naing et al. (2019) who found higher bacterial count in hand milking. Figure 3.2 showed that, higher TBC was found in the milk of the indigenous breed than in the crossbreed of the farms. According to author knowledge, no previous studies were found to evaluate the effect of breed on TBC of raw milk. Differences in farm management practices of indigenous and cross breed could be reason of variation of bacterial count in different breeds. Improper hygienic management during milking and milk handling could contribute to the variation of TBC in dairy farms (Iqbal, 2019; Singha et al., 2023).



**Figure 3.1** Comparison of total bacterial count ( $\log_{10}$  CFU per mL) in different milking technique. Standard error (vertical black line on top of each bar) displayed in the figure.



**Figure 3.2** Comparison of total bacterial count ( $\log_{10}$  CFU per mL) in crossbreed and indigenous breed. Standard error (vertical black line on top of each bar) displayed in the figure.

#### 3.2 Enumeration of bacteria in milk

Among all 185 BM samples, TBC varied between  $4.8 \times 10^4$  to  $1.5 \times 10^9$  CFU per mL of milk (4.68 log<sub>10</sub> CFU per mL to 9.18 log<sub>10</sub> CFU per mL) with an average of  $2.7 \times 10^7$  CFU per mL (5.92 log<sub>10</sub> CFU per mL) (Table 3.2). According to Bangladesh Standard and Testing Institution (BSTI) standard range of TBC is  $5 \times 10^4$  to  $1 \times 10^5$  CFU per mL (BFSA, 2022). Therefore, present study findings suggest that TBC levels in all BM samples exceeded the standard range. Uddin et al. (2011) conducted a study in Dhaka city and Hasan et al. (2015) carried out a study in Dinajpur, and found that bacterial count in the range from  $2 \times 10^8$  to  $2.36 \times 10^9$  CFU per mL (8.3 log CFU per mL to 9.4 log CFU per mL) and from 7.4 x  $10^5$  to  $1.3 \times 10^6$  CFU per mL (5.8 log CFU per mL to 6.1 log CFU per mL), respectively which are higher than this study findings. Differences in individual farm level management could be main reason for the variation of microbial count (Böhnlein et al., 2021). In present study, from ten dairy farms, highest mean TBC (8.09 log CFU per mL) was found in farm no. 10 and lowest mean TBC (5.55 log CFU/mL)

found in BM collected from farm no. 01 (Figure 3.3). Naing et al. (2019) reported that mean value of TBC in Myanmar, 2.55 x  $10^7$  CFU per mL, this average TBC count was nearly matched with our study findings. The standard level of TBC, according to Sri Lanka Standard Institute 1983, is less than 30,000 CFU per mL. A study conducted in Sri Lanka, found mean value of TBC of BM samples were in the range of 2.4 x  $10^6$  to 2.3 x  $10^7$  CFU per mL (6.38 log<sub>10</sub> CFU per mL to 7.11 log<sub>10</sub> CFU per mL) which was nearly similar with this study findings. Poor hygienic management in farms e.g., improper udder hygiene practices, and use of the conventional method of milking could contribute to the higher bacterial count in Sri Lanka (Gunasena and Siriwardhana, 2021), which is mostly similar to the farm management condition of Bangladesh that could be a reason of nearly similar bacterial count in both countries. A study in Northern Germany reported that TBC in raw milk was ranging from 3.9 x  $10^2$  to  $3.2 \times 10^7$  CFU per mL (2.6 log CFU per mL to 7.5 log CFU per mL) (Böhnlein et al., 2021). Different environmental condition, good sanitation and better farm management practices in Germany could contribute reduce the bacterial contamination in milk rather than other developing countries.

**Table 3.2**. Summary statistics of total bacterial count and  $log_{10}TBC$  (CFU/mL) presented in mean, minimum, maximum, median, quartile estimates, and standard deviation for BM samples collected from ten commercial dairy farms of Chattogram every month.

Variable	Mean (Min-Max)	Median	p25	p75	SD
TBC	$2.7 \times 10^7$	2.6 x 10 <sup>5</sup>	189,091	2,090,909	131,000,000
	(4.8 x 10 <sup>4</sup> -1.5 x 10 <sup>9</sup> )				
log <sub>10</sub> TBC	5.92	4.68	5.28	6.32	0.97

TBC = Total bacterial count, SD = Standard deviation, Min = Minimum, Max = Maximum



**Figure 3.3** Bacterial contamination in bulk milk in ten dairy farms in Chattogram. Mean value of each farm, overall mean (red dashed line), standard log<sub>10</sub>TBC (green dashed line), standard error (vertical black line on top of each bar) were displayed , respectively.

#### 3.3 Factors associated with bulk milk total bacterial count

Univariable random-effect linear regression shows that TBC of BM was significantly associated with season (P < 0.001), sample collection year (P < 0.001), and farm size or number of milking animals in the farm (P < 0.20). There was no significant effect of breed and milking technique on TBC (Table 3.3). Three independent categorical variables had a P < 0.2 in the univariable analysis, that were included in the multivariable analysis. In this model, summer (P < 0.001) compared to rainy and winter, milk collection year 2021 (P < 0.001) compared with other years (2022, 2023), and medium-sized farms (P = 0.15) were compared with small and large herd sizes (Table 3.4). In the model-building process, no confounding or interaction was detected. Variance inflation factors remained below 30, which indicated that the factors were not collinear and the regression model fitted well with the given data. There, summer season, sampling year 2021 and medium sized farm were associated with higher level of TBC. (Table 3.4)

**Table 3.3**. Association of five variables with total bacterial count using univariable generalized linear regression model using random effect (farm ID) in ten commercial dairy farms in Chattogram.

Variable name	Categories	Ν	Mean	β	95% CI	<b>Overall P</b>
Season	Winter	73	5.57	Reference		< 0.001
	Rainy	55	6.03	0.49	0.18 to 0.82	
	Summer	57	6.32	0.79	0.47 to 1.10	
Year	2023	36	5.49	Reference		< 0.001
	2022	68	5.61	0.12	-0.24 to 0.47	
	2021	81	6.38	0.88	0.53 to 1.22	
Farm size	Large	33	5.67	Reference		0.15
	Small	103	5.93	0.26	-0.12 to 0.63	
	Medium	49	6.09	0.42	-0.003 to 0.84	
Milking system	Machine	49	5.83	Reference		0.44
	Hand	136	5.95	0.12	-0.20 to 0.45	
Breed	Cross	180	5.92	Reference		0.81
	Indigenous	5	6.02	0.10	-0.79 to 0.96	

N: Observations,  $\beta$ : Co-relation coefficient, 95% CI: 95% confidence interval, P: Probability

**Table 3.4**. Association of three variables with total bacterial count using multivariable generalized linear regression model using random effect (farm id) in ten commercial dairy farms in Chattogram

Variable name	Categories	Ν	β	95% CI	Р
Season	Winter	73	Reference		
	Rainy	55	0.35	0.06 to 0.63	0.02
	Summer	57	0.92	0.64 to 1.20	< 0.001
Year	2023	36	Reference		
	2022	68	0.33	-0.01to 0.67	0.05
	2021	81	1.08	0.75 to 1.43	< 0.001
Herd size	Large	33	Reference		
	Small	103	0.08	-0.23 to 0.39	0.60
	Medium	49	0.26	-0.09 to 0.61	0.15

N: Observations, β: Co-relation coefficient, 95% CI: 95% confidence interval, P: Probability

#### 3.3.1 Herd size

Farm level microbial count of BM could be varied due to the hygienic management during collection, transportation and storage of milk (Costello et al., 2003). In this study, lower TBC was observed in large scale farms than small- and medium-scale dairy farms (Figure 3.4). In small and medium scale dairy farms, improper farm management and absence of cooling facilities during storage and transportation of raw milk could contribute to higher bacterial count. On the other hand, large scale commercial dairy farms were facilitated with clean milking equipment that could help reducing the bacterial count. The present study findings agreed with the Naing et al. (2019) that reported that lower bacterial count in case of large herd size of farm. A study conducted in intensive dairy farms in North Italy reported that lowest value of bacterial count in milk produced from high producing farms as there maintained proper udder hygiene before and after milking (Bava et al., 2021).



**Figure 3.4** Comparison of total bacterial count ( $\log_{10}$  CFU per mL) among different herd size dairy farms in Chattogram. Standard error (vertical black line on top of each bar) displayed in the figure.

#### 3.3.2 Sampling year

From three years trends of bacterial count of BM of dairy farms, the highest mean log<sub>10</sub> TBC was 6.38 observed in 2021, and the lowest mean was 5.50 found in 2023 (Figure 3.5). The reason for this decrement in TBC could be due to variations in sample size, milking system, and hygiene practices. Evaluation of long-term trends microbiological quality of BM could be influenced by geographical location of the farm, individual farm-level management, and sanitation practices of milk during storage and transportation (Costello et al., 2003).



**Figure 3.5** Comparison of total bacterial count ( $\log_{10}$  CFU\ mL) among three sampling year from ten dairy farms in Chattogram. Standard error (vertical black line on top of each bar) displayed in the figure.

#### 3.3.3 Season

This study represents the diversity in TBC due to seasonal effect, higher TBC found in summer than in rainy and winter seasons (Figure 3.6). In summer, due to warm and humid environment microbial multiplication increases, that could be the reason of higher bacterial count in summer than other seasons (Li et al., 2018). A higher TBC in raw milk

collected from different regions of Iran during summer has been reported by Hajmohammadi et al. (2021); found that higher TBC level in summer (6.25 log CFU \mL) than winter (6.10 log CFU\mL). Li et al. (2018) also reported that there was a higher risk of bacterial contamination in summer and lower in winter obtained from a 12 months series of monthly analysis of bacterial composition in China. It revealed that there was highest diversity in bacterial composition during summer due to changes of temperature and humidity. Nahusenay et al. (2023) found in a study in Ethiopia, bacterial count in raw milk was higher in wet season (January to March) than dry season (May to June) probably the high variation may also occur because of differences in milking and hygiene practices.



Figure 3.6 Seasonal comparison of total bacterial count ( $log_{10}$  CFU per mL) samples collected from ten dairy farms. Standard error (vertical black line on top of each bar) displayed in the figure.

## **Chapter 4 : Limitations**

The study gives an indication of variation in the total bacterial count in of the selected farms over a period of 28 months which was very high although this study ended with a relatively small number of variables. Therefore, in the future studies, a large-scale prospective study is further required encompassing the nutritional, chemical, other microbiological parameters with a wide number of variables related to the udder health and milk handling practices to identify the effective control measures to reduce microbial contamination in bulk milk on farm. Another arena for further research could be to evaluate milk quality by identifying foodborne zoonotic pathogen contamination in BM which could be directly related to the safety of milk consumers in Chattogram, Bangladesh.

#### Conclusion

The present study aims to determine the microbial quality of BM in the selected commercial dairy farms in Chattogram by using the most common microbial quality indicator TBC on the collected samples. The findings of the study clearly summarize that TBC was found high in all BM samples than the standard level set by BSTI ( $1 \times 10^5$  CFU per mL). There were seasonal variations of TBC in BM in the selected farms, all farms were shown to have a higher TBC during summer. In large scale farms lower level of TBC was revealed that could be due to implementation of pre-milking and post-milking hygienic measurements like cleaning and drying off of the udder before and after milking, use of machine milking system instead of conventional system for milking, and availabilities of cooling facilities during storage and transportation of raw milk.

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## **Biography**

I am Tishita Sen Ape, daughter of Tilak Kanti Sen and Shipra Rani Chowdhury. I passed my Secondary School Certificate examination in 2014 (G.P.A 5.00) from Jamal khan Kusum Kumari Girl's High School, Chattogram followed by Higher Secondary Certificate examination in 2016 (G.P.A 5.00) from Govt. Hazi Muhammad Mohsin College, Chattogram. Then I enrolled for Doctor of Veterinary Medicine degree at Chattogram Veterinary and Animal Sciences University, Chattogram, Bangladesh in the 2017-18 session. Now, I am an intern student at the Faculty of Veterinary Medicine, CVASU. In future, I would like to work in surgery and wild life-based research-related fields.