
Bacterial Contamination of Drinking Water in Selected Dairy Farms in Sudan

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Abstract :

This study was conducted to investigate contamination of drinking water in selected dairy farms in Sudan based on bacterial isolation and total viable count. A total of 50 farms were examined. The farms were from five areas in Khartoum State namely Shambat, Alsamrab, Alhalfaia, Helat Koko and Helat Kogaly. Ten farms from each area were examined. A total of 50 drinking water samples (one from each farm) were collected. All water samples were examined for bacterial viable count and cultured to isolate common bacteria present. Sixty three bacterial isolates were recovered from all samples. The isolated bacterial genera were *Bacillus*, *Corynebacterium*, *Enterobacteria*, *Staphylococcus*, *Streptococcus*, *Actinobacillus*, *Campylobacter*, *Moraxella*, *Aeromonas*, *Cardiobacteria*, *Pseudomonas* and *Branhamella*. All water samples examined showed moderately high viable count. The mean viable count from the 10 farms in each area was 12×10^7 , 37×10^6 , 22×10^6 , 22×10^6 , 20×10^6 (cell/ ml) for Shambat, Helat Kogaly, Alsamrab, Alhalfaia and Helat Koko areas respectively. Most of the examined farms were with bad hygiene specially surround drinking water troughs. It could be concluded that drinking water quality in selected dairy farms was poor.

Introduction:

An adequate supply of clean, fresh drinking water is widely considered essential for optimal cow health and maximum milk production. Physico-chemical properties of water suitable for livestock have been documented but, despite the fact that waterborne transmission of pathogen among livestock has been long recognized. Little information is actually available concerning the microbiological quality of water offered to cattle (Reilly, 1981; Hanninen *et al.*, 1998). Logically, livestock drinking water heavily contaminated with enteric bacteria could serve as a common source of exposure to potential pathogens to cattle that could result in infection of large numbers of animals during a relatively brief period. The extent to which water troughs serves as reservoirs for enteric microorganisms and the frequency that waterborne transmission of these pathogens occurs from

water to cattle is not fully understood. Clean hygienic water is a major factor contributing to good dairy cattle.

Water is said to be bacteriologically contaminated or polluted either due to presence of certain pathogens or due to high increase of total viable count or due to presence of what is called indicators bacteria at certain levels (WHO, 1984, Alrofaei, 2000). Many bacteria are used as indicator to demonstrate presence of bacterial pollution of drinking water. The microbiological examination of drinking water is normally conducted to assess hygienic quality of water. Microbiological parameters such as viable count at 37°C are used not for disease risk estimation but rather as indicator for the treatment water process. In polluted water, a major type of bacteria found is coliform bacteria (Amy and Jeffrey, 2006). The most important species of the group include *Escherichia coli*, *Klebsiella spp* and *Enterobacter spp*. At the same time, non coliform bacteria were also found in polluted water such as *Sterptococcus*, *Proteus* and *Pseudomonas* species (Alcano, 1997; Jeffrey *et al*, 2001; Murinda *et al*, 2004).

Some areas of Khartoum State are known for their high population density of dairy cattle; these cattle are of local, cross and foreign breeds. There are different sources of drinking water in these dairy farms like ground water and city water sources. Although the significant of the problem, no previous study was carried out in these areas to investigate dairy farms drinking water contamination. The main objective of the present study was to investigate the quality of drinking water commonly present in selected dairy farms in Khartoum State.

Materials and methods:

Farms:

A total of 50 farms were examined for drinking water contamination. The farms were distributed in five areas in Khartoum State (Sudan). The areas were Elhalfaia, Elsamrab, Helat koko, Helat Khogaly and Shambat. Ten farms from each area were examined.

Samples:

A total of 50 water samples (one from each farm) were collected. Thirty water samples were from farms with city water supply while 20 water samples were from farms with underground water supply. All samples were taken by sterile 10 ml syringe and then put into sterile closed glass bottles. All water samples were examined for bacterial viable count and cultured to isolate common bacteria present.

Culturing:

Primary culturing for all water samples was done onto blood agar media. All water sample were taken by disposable pipettes and put into Eppendorf tubes then centrifuged at 8000 rpm for 5 minutes and the sediments were cultured onto blood agar media. Then cultures were incubated at 37C⁰ for 24 hours.

Identification of isolates :

Purified isolates were identified to the genus level according to Barrow and Feltham (1993). The identification was based mainly on the colony characteristics, staining, motility and biochemical reactions.

Bacterial viable count:

The viable count was done according to (Quinn, *et al* 2000) using method of Miles-Misra. The water samples were serially diluted 5 times (10⁻¹- 10⁻⁵). A fresh sterile tips were used to mix the content of the each dilution by sucking up and down ten times, then 0.02 ml of each dilution were transferred to nutrient agar plates and then distributed (The surface of the plates were previously dried for 24 hours at 27°C with the plate lid closed, followed by 2 hours at 37°C with the lid and the base separated). the plates were labeled by the number of the dilution. An average colony count was obtained; the conversion factor was 50 to obtain a figure for the bacterial/ml in the original sample. The formula used for counting was (The total number of bacteria=The average of colonies count X dilution factor X 50).

Data about farms examined was collected. The data encompassed farm system, water sources, hygiene of water trough, water additives and common diseases in the farms.

Results :**Bacterial isolation**

Sixty three bacterial isolates were recovered from the 50 drinking water samples. The highest rate of the isolation was *Bacillus* (28.57%). The isolated genera were *Corynebacterium*, *Enterobacteria*, *Staphylococcus*, *Sterptococcus*, *Actinobacillus*, *Campylobacter*, *Moraxella*, *Areomonas*, *Cardiobacteria*, *Pseudomonas* and *Branhamella* (Table 1).

Table (1)
Percentage of isolated bacterial genera

Genus	No.	%
<i>Bacillus</i>	18	28.57
<i>Corynebacterium</i>	16	25.40
<i>Enterobacteria</i>	11	17.46
<i>Staphylococcus</i>	3	4.76
<i>Streptococcus</i>	3	4.76
<i>Actinobacillus</i>	3	4.76
<i>Campylobacter</i>	3	4.76
<i>Moraxella</i>	2	3.17
<i>Areomonas</i>	1	1.59
<i>Cardiobacteria</i>	1	1.59
<i>Pseudomonas</i>	1	1.59
<i>Branhamella</i>	1	1.59
Total	63	100%

From the 63 isolates, 48 (76.2%) were Gram positive while 15 (23.8%) were Gram negative. Fourty seven (74.6%) isolates were recovered from water troughs of general city water sources while 16 (25.4%) were isolated from water troughs of under ground source.

Viable count :

The mean viable counts from the 10 farms in each area were 12×10^7 , 37×10^6 , 22×10^6 , 22×10^6 , 20×10^6 (cells/ ml) for Shambat, Helat Kogaly, Alsamrab, Alhalfaia and Helat Koko areas respectively.

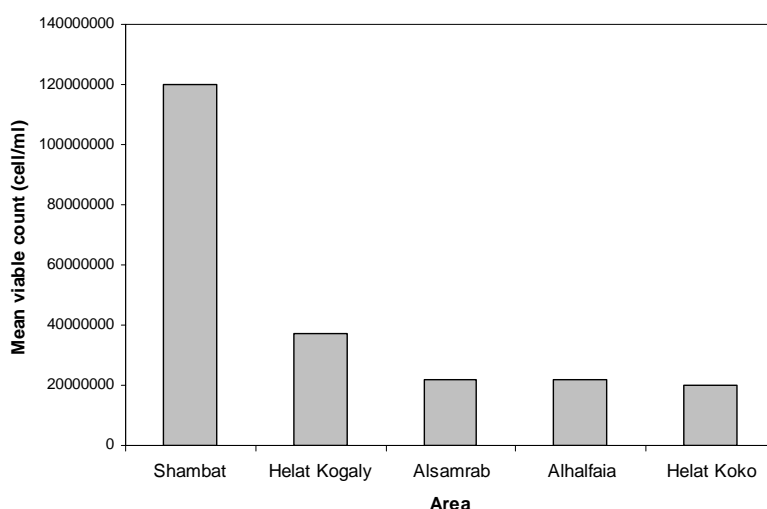


Figure 1 : Mean viable count of different areas

Discussion :

Little information is actually available concerning the microbiological quality of water offered to cattle (Hanninen *et al*, 1998; Reilly, 1981).The present study was designed to describe the microbiological quality of water commonly present in dairy cattle drinking water troughs in Sudan based on bacteriological isolation and total viable count. The mean viable counts were found 12×10^7 , 37×10^6 , 22×10^6 , 22×10^6 , 20×10^6 (cells/ ml) for Shambat, Helat Kogaly, Alsamrab, Alhalfaia and Helat Koko areas respectively.

The presence of high viable bacteria from drinking troughs was indication of the contamination at these sites. The extent of bacterial contamination observed in the drinking water troughs might demonstrate animals' daily exposure to bacterial infections from water sources (LeJeune *et al*, 2001).

The association between water quality and water contamination factors that influence the survival and proliferation of the bacteria in the system of drinking water troughs was very close (Hancock *et al* 1994). All of dairy farms examined in this study were open system so chances of water troughs contaminations with feeding, faeces, urine, dust and any out factors contamination were high. Also water trough material was poor and the troughs were put directly on cattle house floor closely to the mud and faeces. In Addition outer troughs environment was very humid with cattle

urine which increased contamination chances. It has been reported that water sample from direct source of underground water supply was completely free from coliform bacteria (El Tom, 1997). So water troughs will be contaminated after poured in troughs for the following reasons:- bad hygienic measures in the farms, persistence of water for long time in troughs, water troughs were not cleaning regularly, disinfectants or detergents were not used for washing or cleaning the troughs. Accordingly, all of the above reasons were noticed in the examined farms which explain the high viable count.

The viable count technique used in this study was Miles-Misra. This method has advantages of being economical and sensitive also it requires less laboratory equipments and glass wares comparing with other techniques (Quinn, 2000).

Based on bacterial isolation in this study, the highest isolated bacteria in all water troughs samples were *Bacillus* (28.57%), *Corynebacterium* (25.39%) and *Enterobacteria* (17.46%). These genera are pathogenic and their isolation might be of importance due to their contribution to water borne infections. *E coli* was one of the bacteria usually found to be the main contaminant in dairy farms ((Fairbrother, and Nadeau, 2006; LeJeune, and Wetzel 2007). And *Enterobacteria* was isolated at rate of 17.46% and identified as general group not to species level. It could be concluded that drinking water quality was not good in the examined farms.

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التلوث البكتيري لمياه الشرب في مزارع أبقار في السودان

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الملخص :

أجريت هذه الدراسة لتقصي تلوث مياه الشرب في بعض مزارع أبقار إنتاج الألبان في السودان. تم اعتماد التلوث على أساس العزل و العد الكلي للبيكتريا. تم فحص ٥٠ مزرعة موزعة في خمس مناطق في ولاية الخرطوم. المناطق هي: شمبات، السامرأب، الحلفايا، حلة كوكو و حلة خوجلى. فحصت عشرة مزارع من كل منطقة. جمعت ٥٠ عينة ماء شرب بمعدل عينة من كل مزرعة. كل العينات فحصت لعد البيكتريا الحي وتمت زراعتها لعزل البيكتريا الموجودة. تم الحصول على ٦٣ عزلة بيكتريا من كل العينات. أجناس البيكتريا المعزولة كانت كالاتي: الباسلس، كوراني باكتريم، انتيروباكتريم، استافلوكوكوس، استربتوكوكوس، اكتينوباسلس، كامبيلوباكتر، موريكسلا، ارينومونس، كارديوباكتر سودومونس وبراهميلا. كل عينات مياه الشرب المفحوصة أظهرت عد كلى مرتفع نسبياً. متوسط العد الكلى للعشر مزارع في كل منطقة كان كالاتي: (cell/ ml) 12×10^7 , 37×10^6 , 22×10^6 , 22×10^6 , 20×10^6 . الشمبات، حلة خوجلى، السامرأب، الحلفايا، حلة كوكو بالتتابع. الصحة العامة و النظافة كانت سيئة في اغلب المزارع المفحوصة خاصة حول أحواض مياه الشرب. يمكن الخلاصة إلى أن جودة مياه الشرب ضعيفة في المزارع المفحوصة.