

Isolation identification and distribution of bacteria in Dairy Effluent

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ABSTRACT

*This research work determined the bacteriological characteristics of the dairy effluent. Bacteriological studies were carried out from 2008 at four stations. Totally 18 bacteria were isolated. *Alcaligenes faecalis*, *Lueconostoc lactis*, was predominant in other species. Out of this species *Alcaligenes faecalis* had most abundant followed by *Lueconostoc*, *Lactobacillus* was higher number of species were obtained in summer season. Results of one year ecological study revealed that altogether species of bacteria from 18 genera were isolated from the records. Among the bacteria *Alcaligenes faecalis* was dominant in dairy effluent and in all the four seasons. The dominant genus followed by *Lactobacillus*, *Lueconostoc lactis*. The abundance of *Alcaligenes faecalis* in dairy effluent has due to favorable content of oxidizable organic matter, rich calcium, magnesium and abundance nutrients such as nitrates, phosphates, sulphates content of less dissolved oxygen and alkaline pH. The utilization of dominant species of *Alcaligenes faecalis* to monitor pollution in dairy effluent has also been recorded.*

Key words: Dairy effluent, biodiversity, *Alcaligenes faecalis* and pollution.

INTRODUCTION

Nowadays various types of fermented milk products exist, throughout the world (Stanley and cheese 1998; Tamime and Marshal 1997). Their nature depends on the type of milk used, the pre-treatment of the milk and the conditions of fermentation and subsequent processing. They mainly involve *Lactic acid bacteria* (LAB). At present LAB (Lactic acid bacteria) species of the genera *Lactobacillus*, *Lactococcus*, *Lueconostoc lactis*, *Pediococcus*, *Streptococcus*, and *Bifidobacterium* have been identified in fermented milk. Mainly strains of *Lactobacillus*, *Streptococcus* and *Bifidobacterium* are used in commercial starter cultures. (Cogan and Accolas 1996, Mogensen and Smith 1993).

In recent years *Alcaligenes faecalis* bacteria have been drawing tremendous attention due to the ability to degrade dairy effluent thereby improving effluent quality. Taking the above facts into consideration a survey was undertaken in dairy effluent to explore the nature of microbial diversity of bacteria used in treating dairy effluent.

MATERIALS AND METHODS

Dairy effluent was collected from Thanjavur Co-operative Milk Products and supply, situated at Thanjavur Tamil Nadu India. A sampling programme consisting of series of four seasons. Quality and microbial survey was conducted for a one year period from March to September. Populations of bacteria were isolated from the effluent samples by serial dilution technique. Bacteria were identified based on colony characteristics, gram staining methods and by various biochemical studies as given by Bergey's (1984) manual of determinative bacteriology.

Four places were selected in the effluent treatment plant Samples were collected from places along with the effluent in plastic boxes. The standard microbiological methods were followed for the isolation and identification of study bacteria. Effluent samples were collected in duplicate from each station in pre sterilized bottles.

RESULTS AND DISCUSSION

Bacterial diversity has not been studied in detail in dairy effluent. However a few reports are available on the bacterial flora of certain effluents. Jain et al (2001) isolated three different bacterial species such as *Bacillus megateriu*, *B. cereus* and *Xanthomonas fregariae* from distillery wastes effluent. Similarly, Abed et al., (2002) isolated bacteria belonging to different groups, mainly the *Cytophaga*, *Flavobacterium* – *Bacterioides* group r and b sub class of the class *proteobacteria*, and the green non sulphur bacteria from a heavily polluted site in a coastal stream. In the present study 19 bacterial genera isolated from the dairy effluent in all seasons (Table 1). Most of the isolated genera are potential pathogens. Some of these bacteria have previously reported to be present in waste water.

The less number of bacterial communities was apparently due to the environmental stress caused by the high level of pollutants, which allowed only a restricted number of species that tolerant such conditions but the *Alcaligenes faecalis* survive in all seasons.

Similar finding recorded that Sree kumar and soundarajan and Krishnan (2010) have successfully isolated a new strain of spore forming Bacilli that it capable fermenting lactose from dairy effluents.

S. No	Micro organisms	STATION 1				STATION 2				STATION 3				STATION 4							
		Post monsoon	Premonsoon	Summer	monsoon	Post monsoon	Pre monsoon	Summer	winter	Post monsoon	Pre monsoon	Summer	winter	postmonsoon	Pre monsoon	Summer	monsoon	Pre monsoon	summer	winter	
1	<i>Alcaligenes faecalis</i>	+	+	+	+	+	+	+	+	+	+	+	++	+	+	+	+	+	+	+	+
2	<i>Lueconostoc lactis</i>	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
3	<i>Meniscus</i>	-	-	+	-	-	+	-	-	-	-	+	-	+	-	-	-	-	-	-	-
4	<i>Silfido bacillus</i>	-	+	+	+	+	-	+	-	+	-	+	-	-	+	+	-	+	+	-	-
5	<i>Sparolacto bacillus</i>	+	-	+	-	+	+	+	-	-	+	+	-	-	-	+	-	-	+	-	-
6	<i>Trichococcus</i>	-	+	+	+	-	-	-	+	-	-	-	-	+	-	+	-	-	+	+	-
7	<i>Syntrophospara</i>	+	+	-	-	+	+	-	-	+	-	+	-	-	+	-	+	+	+	-	+
8	<i>Lactobacillus</i>	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
9	<i>Janthino bacterium</i>	-	-	-	-	-	+	-	-	-	+	-	-	-	+	-	-	+	-	-	-
10	<i>Podiococcus</i>	+	-	+	-	-	+	-	-	-	+	+	-	+	+	-	+	+	-	+	-
11	<i>Spirillum</i>	-	-	+	+	+	-	+	-	-	-	-	-	+	+	+	-	+	+	-	-
12	<i>Aquasprillum</i>	-	+	+	-	+	-	+	-	-	+	-	-	+	+	+	-	+	+	-	-
13	<i>Methylococcus</i>	-	-	+	+	-	+	+	-	-	+	+	-	+	-	+	+	-	+	+	+
14	<i>Psychrobacter</i>	+	+	-	-	-	+	+	+	+	-	+	+	+	+	+	-	+	+	-	-
15	<i>Campylobacter</i>	-	+	+	-	-	+	+	-	-	-	-	+	-	+	-	-	+	-	-	-
16	<i>Monococcusum</i>	+	-	+	-	+	+	+	+	-	+	+	+	+	-	-	+	-	-	-	+
17	<i>Phalylobacteri</i>	+	+	-	-	+	-	+	-	+	-	-	-	+	-	-	+	-	-	+	+
18	<i>Oceanosprillum</i>	+	-	-	+	-	-	-	-	+	-	-	-	-	+	-	-	+	-	-	-

Bod of effluent was higher in during summer than winter premonsoon and the present investigations, during summer the maximum numbers of species were recorded which might be due to the higher level of organic matter. Pell (1997) nominated the pathogens of most concern to the dairy industry as *Salmonellaspp*, *Escherichiacoli*, *Listeria monocytogenes*, *Mycobacterium*, *Paratuberculosis*, *Cryptosporidium parvum* and *Giardia spp.*, as a result confirmed are suspected links to outbreaks of disease in humans.

Among the species of bacteria *Alcaligenes faecalis* was the dominant one, which occurred in all the month in all seasons. In diary effluent the temperature may raise during summer as a result the species diversity could be increased. Contrary to this in present investigations the observed result showed that during summer the bacterial count was more. It was observed that *Alcaligenes faecalis* dominated the effluent during all the seasons.

Many of them emphasize the importance of light, temperature, pH, phosphates, chloride nitrate, sulphate as factors important in determining the distribution of bacteria. In the present investigation it observed that *Alcaligenes faecalis*, *Lactobacillus* bacteria dominated the effluent stream during all seasons. *Meniscus*, *Spirillum*, *Methylococcus* were observed in summer and winter season which not recorded in post monsoon and pre monsoon.

Bacterial diversity in diary effluent were *Alcaligenes faecalis*, *Lueconostoc lactis*, *meniscus*, *Silfidobacillus*, *Sparolacto bacillus*, *Trichococcus*, *Syntrophospara*, *Lacto coccus*, *Pediococcus*, *Sprillum*, *Aquasprillum*, *Methylococcus*, *Psychrobacter*, *Campylobacter*, *Monococcus*, *Phalylobacterium*, and *Ocnosprillum* have been observed presenting summer premonsoon and post monsoon in all the station (1,2,3).

In the present study *Alcaligenes faecalis* has been found to be tolerating to pollution which frequently inhibits the polluted water. The bacterium degrades urea, creating ammonia which increases the pH of the environment. Although *Alcaligenes faecalis* is considered to be alkaline tolerant, it maintains a neutral pH in its cytosol to prevent the damaging or *Alcaligenes faecalis* is normally found in soil, water, and environments in association with humans.

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