



**International Journal of Biology, Pharmacy
and Allied Sciences (IJBPAS)**

'A Bridge Between Laboratory and Reader'

www.ijbpas.com

MICROBIOLOGICAL STUDY OF MILK: A REVIEW

CHAUHAN K¹, ANDHARE P², MARCHAWALA F², BHATTACHARYA I² AND
UPADHYAY D^{2*}

1: Student, M. Sc. Microbiology, Parul Institute of Applied Sciences, Parul University, Post
Limda, Waghodia, Gujarat, 391760

2: Assistant Professor, Parul Institute of Applied Sciences, Parul University, Post Limda,
Waghodia, Gujarat, 391760

*Corresponding Author: Dr. Dhvani Upadhyay; E Mail: dhvani.updhvay82123@paruluniversity.ac.in;

Tel: +919558021474

Received 22nd Jan. 2021; Revised 24th Feb. 2021; Accepted 25th March 2021; Available online 1st April 2021

<https://doi.org/10.31032/IJBPAS/2021/10.4.1036>

ABSTRACT

Here, we tend to review what's familiar concerning the microorganisms gift in milk, together with milk from cows, sheep, goats and humans. Milk, because of its high nutritional content, will support a rich microbiota. These microorganisms enter milk from a spread of sources and, once in milk, will play variety of roles, like facilitating dairy farm fermentations (e.g. *Lactococcus*, *eubacterium*, *eubacterium*, *Propionibacterium* and flora populations), inflicting spoilage (e.g. bacteria genus, true bacteria, true bacteria and different spore-forming or thermophilic microorganisms), promoting health (e.g. lactobacilli and bifidobacteria) or inflicting illness (e.g. *Listeria*, *Salmonella*, *escherichia*, *Campylobacter* and mycotoxin-producing fungi). there's additionally concern that the presence of antibiotic residues in milk results in the event of resistance, significantly among unhealthful microorganism. Here, we tend to comprehensively review these topics, whereas comparing the approaches, each culture-dependent and culture-independent, which might be taken to analyze the microbial composition of milk.

Keywords: Dairy; spoilage; safety; health; probiotic; milkborne pathogens

INTRODUCTION

Milk is that the lacteal secretion obtained by the entire milking of class animals. thanks to its high biological process worth for people in general, it's a big food of nutrition of large population on earth. once temperature is appropriate for growth of microorganisms, the milk seems as a wonderful medium for his or her growth. The milk is contaminated terribly simply if it's handled carelessly and created unhygienically ends up in its early spoilage [1, 2].

Some of these nutrients square measure directly on the market to any or all microorganisms, whereas others square measure provided following the metabolism of major components by specific populations to unharness parts and metabolites that square measure utilized by others [3]. it's usually accepted that the carboxylic acid microorganism (LAB), a bunch of microorganism that ferment disaccharide to nurse, square measure a dominant population in bovine, goat, sheep and buffalo milk, before pasteurization. the foremost common workplace genera in milk embrace *Lactococcus*, *eubacteria*, *Leuconobacteria*, *eubacterium* and *Enterococcus*. Psychrotrophic populations, that significantly establish themselves during cold storage, are a significant part and oft

embrace *bacteria* genus and *Acinetobacter* spp. different strains of non-LAB genera are encountered in milk, furthermore as varied yeasts and moulds [4]. Human milk on the opposite hand is usually dominated by *eubacterium*, *staph*, *eubacteria* and *Bifidobacterium* spp. [5]. Probiotics live microorganisms that square measure useful to health once consumed. Milk and milk merchandise square measure typically related to probiotic microorganism, which give supplements for the useful maintenance of the viscus system [6].

There has been associate degree increasing attention within the use of various strains of workplace as probiotics, in the main *Lactobacilli* and *Bifidobacteria* that square measure residents of the commensal microorganism in the gut of human showing sensible therapeutic functions [7]. they will manufacture antimicrobial substances (e.g.: -organic acid, peroxide and bacteriocins) which may influence the expansion of the potential harmful microorganisms.

THE MICROBIAL COMPOSITION OF VARIOUS MILK SORT

Although the big production of commercially made milk worldwide comes from cows, there area unit variety of alternative animal sources of milk that's used for human

consumption. These embody quite common sources like goats, sheep, buffalo and alternative utilised in additional specific regions like even-toed ungulate milk in african and arab countries and yak milk.

Cow's milk

Cow's milk is made in large scale. variety of alternative Microorganism will be gift in important proportions. These embody Psychrotrophs, like bacteria genus, Acinecobacter and Aeromonas spp. that flourish throughout cold storage [8]. Recently applied high-throughput within the microorganism population of raw cow's milk that was to be used for cheese production (9) our analyses indicate that the northermoduric bacterium that area unit gift among these population area unit doubtless to be in a very broken, nonculturable kind.

Goat's milk

Goat's milk production represents regarding a pair of.1% of worldwide milk production [10]. It's a very important artefact that has gained multiplied interest as an alternate to cow's milk, thanks to proof that it's doubtless to induce allergies. Goats milk additionally disagree from cow's and sheep's milk by virtue of getting bigger levels of iron diversity [11] still as containing smaller fat globules, having the next content of fatty acids and forming a softer curd throughout

ulterior fermentation, successively resulting in bigger edibleness [12].

Goats milk is most often used for cheese creating typically at fain level or in tiny dairies. it absolutely was relied on the utilization of selective microbiological media, spp analysis still as fragment length polymorphism(RFLP) typewriting of isolates to look at the microbic diversity of 118 goats milk samples taken from goats milk samples taken from one herds throughout one lactation year to reveal the presence of a various microorganism population within the milk [13]. additionally to microorganisms unremarkably encountered in milk, like those listed on top of some species were known that aren't generally related to goats milk or that had antecedently solely been related to goats milk or that had antecedently solely been related to cheeses, together with variety of a corynobacteria and brachybacteria. Whereas these variation will be attributed to distinction in feed, the authors prompt that alternative factors like climate {and the|and therefore the|and additionally the} health of the animal were also vital [13].

Sheep milk

Sheep milk is never consumed however still constitutes c.1.3% of worldwide milk production because it is usually used throughout Europe within the development f

cheese. Studies assessing the impact of storing sheep milk at refrigeration temperature highlighted will increase in Psychrophiles, however additionally in Mesophiles. Unsurprisingly, the Thermotolerant population didn't increase.

These general trends are full of temperature and also the length of storage. Alternative bacterium that is detected occasionally will embody organism of concern from milk safety perspective together with E.coli, Salmonella, coccus aureus, Bacilli and eubacteria [14]. In populations of Streptococci and S.aureus there was a rise and a decrease in counts, severally in regions wherever the milk was additional acidic and nutrient levels were lower [15].

Some insight into the biology of sheep milk was additionally provided by a recent study of the milk cheese, Oscypek that is factory-made while not a starter culture [16]. As this naturally hard milk cheese it's doubtless that these cheese-associated bacterium were additionally gift within the corresponding milk. This approach additionally revealed variety of minor population together with *Ferroglyphus halophilus*, eubacteria, *Salivarius*, *S.thermophilus* and eubacteria *vertibularis*. A high output sequencing-based approach revealed the presence of forty totally different genera together with six kind

the order Lactobacillales that grooved ninety seven of appointed sequences.

The benefits of using this technology were once more highlighted once antecedently unmarked populations of *Kocuria*, *Saguibacter*, *Flavobacteria*, *Thryseobacterium*, *Exigouobacterium*, *Staphulococcus* and *Chromonalobacter* were defected. Notably a substantial proportion 2 hundredth of sequence reads couldn't be appointed, and then the identity of those bacterium and also the importance of the opposite sub populations can needed futher attention [16].

Bluffalo milk

Buffalo milk is consumed in varied countries round the world with India and Islamic Republic of Pakistan being the very best shoppers. it's not as common in Europe, however it will have a very important market in some Mediterranean countries wherever it's utilize in creating ancient cheese cheese. The microbic content of raw bluffalo milk has been assessed, through culturing, and located to contain an oversized population of laboratory, together with Lactococci and Lctohailious, as can as Coliforms. E.coli, S.aureus and microorganism endospores, light that technologically relevant bacterium area unit gift, microorganisms of concern with relevancy quality and safety also can be found [17]. More recently, high output

sequencing has been applied to identify the microorganism populations gift in buffalo milk and throughout the manufacture of cheese cheese[18].

Technologically relevant microorganism of milk

Raw milk will contain a various microorganism population. Several such microorganism will contribute subsequently to natural fermentations. In some things, specific strains are therefore eminent during this regard that they need been isolated from milk and consciously adscititious as starters or adjuncts designed to confer fascinating traits on soured product. this will be significantly important in things wherever rules need the utilization of change integrity milk, and thus, the re-introduction of farm microorganisms will complete the removal of comparable populations and therefore the associated adverse impact on the flavour of resultant product.

Lactococcus

Lactococcus lactis ssp. *lactis* biovar diacetylactis is additionally recognised for its production of flavour-developing compounds [19]. These microorganisms are distinguished from each other on the idea of essential amino acid and change state usage, growth temperature and salt tolerance. A comparison of twenty *Lactococcus lactis* strains, ten of

the ssp. *lactis* composition and ten of the ssp. *cremoris* composition, confirmed 2 major taxonomic group lineages that were distinguished on the idea of the presence or absence of 4571 cistron orthologs. Thus, it's calculable that these phenotypically similar taxonomic group diverged c. seventeen million years past [20]. microorganism of *Lactococcus lactis* ssp. *lactis* IL1403 unconcealed that every one glorious genes needed for energy metabolism were gift, together with variety of cistrons concerned in fermentation yet as a completely unique gene, *poxL*, encryption pyruvate enzyme, which can play a task in change between fermentation modes. xliii insertion parts were identified, the distribution of that suggests that recent recombination between 2 closely connected genomes might have occurred [21]. Sequencing of *Lactococcus lactis* ssp. *cremoris* MG1363 unconcealed some similarities to strain IL1403, together with chemical change systems and genes related to the usage of milk sugar.

Lactobacillus

The genus *Lactobacillus* is extremely various and, per the foremost recent estimations, consists of 174 completely different species and twenty seven taxonomic group (www.bacterio.cict.fr). *Lactobacilli* will be found in wealthy, carbohydrate-containing

niches, together with those related to plants, animals, provender and milk [22]. Associate degree ever bigger understanding of true bacteria biology has crystal rectifier to the utilization of strains of true bacteria for associate degree increasing vary of commercial farm applications. Specifically, their proteolytic activity and talent to supply aroma compounds and exopolysaccharides will contribute to the standard and nutritional worth of farm product. Lactobacilli that are of specific importance among the farm business are *L. helveticus*, *L. delbrueckii* ssp. *bulgaricus* and *L. delbrueckii* ssp. *lactis* (the latter 2 species are going to be cited as *L. bulgaricus* and true bacteria *lactis* hereafter). True bacteria *helveticus* was first delineated by Orla- writer in 1919 as associate degree isolate from associate degree Emmentaler cheese however it's since been evident that representatives of this species are usually isolated from milk and milk based mostly product [23]. True bacteria *helveticus* includes a range of traits that are fascinating with regard to cheese production. These embrace fast lysis of the strains, which ends within the unharness of animate thing enzymes and a discount in bitterness and inflated notes in cheese [24]. True bacteria *helveticus* is additionally characterized by its ability to

grow at comparatively high temperatures [25, 26] and is that the most chemical change of the workplace oft employed in the manufacture of farm product. The discharge of free fatty acids following lipolysis introduces vital vital compounds [27]. Ordination sequencing of *L. helveticus* DPC4571, a cheese isolate, unconcealed that the presence of a high share of pseudogenes that are related to loss-of-function events and presumptively adaptation to the farm niche [28]. The expansion of *L. helveticus* in milk depends on a fancy system of chemical change enzymes, that put together modify strains to access essential amino acids [29]. There are many true bacteria increase in range throughout the manufacture of farm product and might become significantly dominant throughout the ripening of cheese.

Streptococcus

The bacteria genus consists of ninety-seven species and seventeen sub-species (www.bacterio.cict.fr). Though several genera of streptococci are unhealthful, *S. thermophilus* carries a 'GRAS' standing [30] and is usually isolated from farm environments, together with milk, natural starter cultures and cheese curds [31-33]. Strains of *S. thermophilus* have additionally

been detected within the teats of cows, cowsheds and farm facilities [34, 35].

Leuconostoc

The genus *Leuconostoc* consists of twenty-three species and four subspecies (www.bacterio.cict.fr). *Leuconostoc* spp. are often related to material, but some, and specifically the species *mesenteroides* and *pseudomesenteroides*, are found in milk. However, it's potential that this is often because of their introduction throughout the gathering of milk or subsequent storage and process. Notably, during this regard, *Leuconostoc* spp. have the power to survive on surfaces, tools and pasteurisers for long periods of your time and to resist heat treatments and refrigeration temperatures [36].

CONCLUSION

The microbial community at intervals milk is advanced. The dominant, and tone, microorganisms gift in milk will have a spread a spread on the flavour, style and texture of raw milk-derived product. Variety of those microorganisms even have the potential to contribute to health through the assembly of antimicrobials or possessing different probiotic-associated traits. Through trendy genomics-based analysis, it's been established that several of those microorganisms became custom-made to

take advantage of niches from varied sources, as well as plant and gut environments, through genomic evolution and cistron gain and/or loss. Despite the beneficial impact of the many milk-associated microorganisms from a flavour, technological or health-related perspective, it's clear that there may be may be related to the consumption of milk and raw milk-derived product or, additional additional, of the pathogens that may be found in this. whereas several of those microorganisms gain entry to the milk from instrumentality and/or personnel, animal disease pathogens may also be introduced into milk from unhealthy animals. As a consequence of this risk, sterilization or different treatments square measure utilized to get rid of disease-causing microorganisms. Within the food trade, the negative impact of removing science lab and different bacterium on resultant food fermentations has been self-addressed for a few time through their re-introduction within the kind of starter and adjunct cultures.

ACKNOWLEDGEMENT

It's our privilege and honour to express our sincerest gratitude to the Parul University, Vadodara, Gujarat for providing me all the necessary support and facilities including state of the art infrastructural facilities with advanced technological scientific laboratories

and everything else that was required to carry out this work.

REFERENCE

- [1] Prajapati JB. Fundamentals of Dairy Microbiology Aktaparakashal Nadiad Gujarat, India, 1995, 2(4) 4-45.
- [2] Schmidt GH and Van Vlerck LD. Principles of Dairy Science Surjeet Publication, New Delhi, 1982, 2(4) 3-5.
- [3] Frank JF (1997) Milk and dairy products. Food Microbiology – Fundamental and Frontiers (Doyle P, Beuchat R & Montville J, eds), pp. 169–186. ASM Press, Washington, DC.
- [4] Quigley L, O’Sullivan O, Beresford TP, Ross RP, Fitzgerald GF & Cotter PD (2011) Molecular approaches to analysing the microbial composition of raw milk and raw milk cheese. Int J Food Microbiol 150:81-94.
- [5] Martin R, Heilig HG, Zoetendal EG, Jimenez E, Fernandez L, Smidt H & Rodriguez JM (2007) Cultivation-independent assessment of the bacterial diversity of breast milk among healthy women. Res Microbiol 158: 31-37.
- [6] Tambekar, D.H. and Bhutada, S.A. (2010). An evaluation of probiotic potential of *Lactobacillus sp.* from milk of domestic animals and commercial available probiotic preparations in prevention of enteric bacterial infections. Recent Research in Science and Technology, 2(10): 82-88.6.
- [7] Lavanya, B., Sowmiya, S., Balaji, S. and Muthuvelan, B. (2011). Screening and characterization of lactic acid bacteria from fermented milk, British Journal of Dairy Sciences, 2(1): 5-10.
- [8] Raats D, Offek M, Minz D & Halpern M (2011) Molecular analysis of bacterial communities in raw cow milk and the impact of refrigeration on its structure and dynamics. Food Microbiol, 28 37(2013): 465–471.
- [9] Masoud W, Vogensen FK, Lillevang S, Abu Al-Soud W, Sorensen SJ & Jakobsen M (2012) The fate of indigenous microbiota, starter cultures, *Escherichia coli*, *Listeria innocua* and *Staphylococcus aureus* in Danish raw milk and cheeses determined by pyrosequencing and quantitative real time (qRT)-PCR. Int J Food Microbiol, 37(2013) 153: 192–202.

- [10] Tsakalidou E & Odos I (2012) Microbiota of Goat's Milk and Goat's Milk Cheese. Proceedings of First Asia Dairy Goat Conference, pp. 40–41. University Putra Malaysia and the Food and Agricultural Organisation on the United Nations (FAO), Kuala Lumpur, Malaysia, 37(2013).
- [11] Boyazoglu J & Morand-Fehr P (2001) Mediterranean dairy sheep and goat products and their quality: a critical review. *Small Rum Res*, 40 37(2013):1–11.
- [12] Klinger I & Rosenthal I (1997) Public health and the safety of milk and milk products from sheep and goats. *Rev Sci Tech* 16 37(2013): 482.
- [13] Callon C, Duthoit F, Delbes C, Ferrand M, Le Frileux Y, De Cremoux R & Montel MC (2007) Stability of microbial communities in goat milk during a lactation year: molecular approaches. *Syst Appl Microbiol* 30 37(2013): 547–560.13.
- [14] Fotou K, Tzora A, Voidarou C et al. (2011) Isolation of microbial pathogens of subclinical mastitis from raw sheep's milk of Epirus (Greece) and their role in its hygiene. *Anaerobe* 17 37(2013): 315–319.
- [15] Yabrir B, Hakem A, Laoun A, Labiad M, Nazek E-G, Hamadi A & Abderrahmane M (2013) Does the aridity of Algerian Steppe affect the Ewe's raw milk quality? *Bull Univ Agric Sci Vet Med Cluj Napoca* 69 37(2013):1–9.
- [16] Alegria A, Szczesny P, Mayo B, Bardowski J & Kowalczyk M (2012) Biodiversity in Oscypek, a traditional Polish cheese, determined by culture-dependent and -independent approaches. *Appl Environ Microbiol* 78 37(2013): 1890–1898.
- [17] Ercolinic D, Russo F, Ferrocino I & Villani F (2009) Molecular identification of mesophilic and psychrotrophic bacteria from raw cow's milk. *Food Microbiol* 26 37(2013): 228–231.
- [18] Ercolini D, De Filippis F, La Stora A & Iacono M (2012) "Remake" by high-throughput sequencing of the microbiota involved in the production of water buffalo mozzarella cheese. *Appl Environ Microbiol* 78 37(2013): 8142–8145.

- [19] Hugenholtz J & Starrenburg MJ (1992) Diacetyl production by different strains of *Lactococcus lactis* subsp. *lactis* var. *diacetylactis* and *Leuconostoc spp.* Appl Microbiol Biotechnol 38 37(2013): 17-22.
- [20] Bolotin A, Quinquis B, Renault P et al. (2004) Complete sequence and comparative genome analysis of the dairy bacterium *Streptococcus thermophilus*. Nat Biotechnol 22 37(2013): 1554–1558.9.
- [21] Bolotin A, Wincker P, Mauger S et al. (2001) The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp. *lactis* IL1403. Genome Res 11 37(2013): 731–753.10.
- [22] Bernardeau M, Vernoux JP, Henri-Dubernet S & Gueguen M (2008) Safety assessment of dairy microorganisms: the *Lactobacillus* genus. Int J Food Microbiol 126 37(2013): 278–285.
- [23] Quigley L, O’Sullivan O, Beresford TP, Ross RP, Fitzgerald GF & Cotter PD (2011) Molecular approaches to analysing the microbial composition of raw milk and raw milk cheese. Int J Food Microbiol 150 37(2013):81-84.
- [24] Broadbent J, Cai H, Larsen R et al. (2011) Genetic diversity in proteolytic enzymes and amino acid metabolism among *Lactobacillus helveticus* strains. J Dairy Sci 94 37(2013): 4313–4328.
- [25] Kiernan RC, Beresford TP, O’Cuinn G & Jordan KN (2000) Autolysis of lactobacilli during Cheddar cheese ripening. Irish J Agric Food Res 39 37(2013): 95-106.
- [26] Hannon JA, Wilkinson MG, Delahunty CM, Wallace JM, Morrissey PA & Beresford TP (2003) Use of autolytic starter systems to accelerate the ripening of Cheddar cheese. Int Dairy J 13 37(2013): 313–323.
- [27] Hickey DK, Kilcawley KN, Beresford TP & Wilkinson MG (2007) Lipolysis in cheddar cheese made from raw, thermized, and pasteurized milks. J Dairy Sci 90 37(2013): 47–56.
- [28] Callanan M, Kaleta P, O’Callaghan J et al. (2008) Genome sequence of *Lactobacillus helveticus*, an organism distinguished by selective gene loss and insertion sequence

- element expansion. *J Bacteriol* 190 37(2013): 727–735.28.
- [29] Christensen JE, Dudley EG, Pederson JA & Steele JL (1999) Peptidases and amino acid catabolism in lactic acid bacteria. *Anton Leeuw Int JG* 76 37(2013): 217–246.
- [30] Facklam R (2002) What happened to the streptococci: overview of taxonomic and nomenclature changes. *Clin Microbiol Rev* 15 37(2013): 613.13.
- [31] Duthoit F, Callon C, Tessier L & Montel MC (2005) Relationships between sensorial characteristics and microbial dynamics in ‘Registered Designation of Origie’ Salers cheese. *Int J Food Microbiol* 103 37(2013): 259–270.14.
- [32] Randazzo CL, Vaughan EE & Caggia C (2006) Artisanal and experimental Pecorino Siciliano cheese: microbial dynamics during manufacture assessed by culturing and PCR-DGGE analyses. *Int J Food Microbiol* 109 37(2013): 1-8.15.
- [33] Santarelli M, Gatti M, Lazzi C, Bernini V, Zapparoli GA & Neviani E (2008) Whey starter for Grana Padano cheese: effect of technological parameters on viability and composition of the microbial community. *J Dairy Sci* 91 37(2013): 883–891.16.
- [34] Vacheyrou M, Normand A-C, Guyot P, Cassagne C, Piarroux R & Bouton Y (2011) Cultivable microbial communities in raw cow milk and potential transfers from stables of sixteen French farms. *Int J Food Microbiol* 146 37(2013): 253–262.17.
- [35] Braem G, De Vliegher S, Verbist B, Heyndrickx M, Leroy F & De Vuyst L (2012) Culture-independent exploration of the teat apex microbiota of dairy cows reveals a wide bacterial species diversity. *Vet Microbiol* 157 37(2013): 383–390.18.
- [36] Hemme D & Foucaud-Scheunemann C (2004) *Leuconostoc*, characteristics, use in dairy technology and prospects in functional foods. *Int Dairy J* 14: 467–494.