

Chapter 2

Biodiversity of Lactic Acid Bacteria

Wenjun Liu, Huili Pang, Heping Zhang and Yimin Cai

Abstract Lactic acid bacteria (LAB) are regarded the most important bacteria concerning food fermentation, pharmaceutical and special dietary applications. The most commonly used strains of different LAB species in food including the genera of *Aerococcus*, *Carnobacterium*, *Enterococcus*, *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Pediococcus*, *Streptococcus* and *Bifidobacterium* are updated and described on taxonomy and description based on physiological and biochemical characteristics. Diversity of LAB in different traditional fermented foods (especially dairy products, fermented vegetable food and meat-based food) is reviewed in this chapter. The LAB variable component and predominated species in different foods and the same food products in different places is introduced briefly. Specifically, the biodiversity of lactic acid bacteria in silage is reviewed at the end of this chapter.

Keywords Lactic acid bacteria • Diversity • Fermented food • Silage

W. Liu (✉) · H. Zhang

Key Laboratory of Dairy Biotechnology and Engineering, Ministry of Education,
Inner Mongolia Agricultural University, Hohhot, China
e-mail: wjliu168@163.com

H. Zhang
e-mail: hepingdd@vip.sina.com

H. Pang
Zhengzhou University, Zhengzhou, People's Republic of China
e-mail: pang@zzu.edu.cn

Y. Cai
Crop, Livestock and Environment Division, Japan International Research Centre
for Agricultural Sciences, 1-1 Ohwashi, Ibaragi, Tsukuba 305-8686, Japan
e-mail: cai@affrc.go.jp

2.1 Introduction

2.1.1 General Background

The concept of lactic acid bacteria (LAB) as a group of organisms developed at the beginning of the 1900s. The first pure culture ('*Bacterium lactis*', now known as *Lactococcus lactis*') was isolated in 1873 by Lister (Fennema et al. 2004). LAB are historically defined as a ubiquitous and heterogeneous family of microbes that can ferment a variety of nutrients into, primarily, lactic acid although recent molecular evidence has challenged this definition (Brooijmans et al. 2009). They are found in environments rich in available carbohydrate substrates, such as food and feed, but also in human and animal cavities, and in sewage and plant material. Indeed, strains have been isolated from all these environments (Kandler and Weiss 1986). Besides lactic acid, other side products include acetate, ethanol, CO₂, formate and succinate (Hammes and Vogel 1995; Hammes and Hertel 2009).

The general characteristics of LAB are that they are gram-positive, catalase negative (although some strains can produce pseudocatalase), anaerobic or microaerophilic, acid-tolerant and non-sporulating rods and cocci (Orla-Jensen 1919). Traditionally, LAB were called 'milk-souring organisms', and often negatively associated with loss of food and feed due to fermentation. However, LAB are increasingly considered as beneficial microorganisms; some strains are even thought to be health promoting (probiotic). Of all the bacteria exploited for domestic use, the LAB are the most widely studied and are exploited in numerous industrial applications ranging from starter cultures in the dairy industry to probiotics in dietary (Konigs et al. 2000) supplements and bio-conversion agents (Adams 1999).

LAB are found in two distinct phyla, namely *Firmicutes* and *Actinobacteria*. Within the *Firmicutes*, LAB belong to the order *Lactobacillales* and include the following genera: *Aerococcus*, *Alloiococcus*, *Carnobacterium*, *Enterococcus*, *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Oenococcus*, *Pediococcus*, *Streptococcus*, *Symbiobacterium*, *Tetragenococcus*, *Vagococcus* and *Weissella*, which are all low guanine–cytosine content organisms (31–49 %) (Horvath et al. 2009). LAB in *Actinobacteria* phylum only includes species of *Bifidobacterium* genus.

LAB obtain their energy by substrate-level phosphorylation because they do not possess a functional respiratory system. Two basic hexose fermentative pathways are used. The homofermentative pathway is based on the Embden–Meyerhof–Parnas pathway and produces virtually only lactic acid as the end product. The heterofermentative or heterolactic pathway (also known as the pentose phosphoketolase pathway, the hexose monophosphate shunt, or the 6-phosphogluconate pathway) produces not only lactic acid as the end product, but also significant amounts of CO₂ and ethanol or acetate (Kandler 1983; Lahtinen et al. 2011). Historically, the mode of fermentation in combination with physiological characteristics such as temperature ranges for growth and sugar utilisation patterns

were used as classification criteria to allocate LAB to genera and species. With the application of modern taxonomic tools (especially molecular methods) to LAB identification and classification some flaws in taxonomy based on physiology have been identified although these attributes still remain very important for the classification and ultimate exploitation of LAB.

2.1.2 Sources of LAB

LAB are found in diverse habitats wherever carbohydrate substrates are available. These include food and feed (dairy products, grain products, meat and fish products, beer, wine, fruits and fruit juices, pickled vegetables, mash, sauerkraut, silage and sourdough), water, soil, sewage and the oral (mucous membranes), respiratory, gastrointestinal and genital tracts of humans and animals (Horvath et al. 2009; Klaenhammer et al. 2002, 2005; Kleerebezem and Hugenholtz 2003).

The largest genus, *Lactobacillus*, includes over 100 species that are ubiquitous wherever substances rich in carbohydrates are available. They are closely associated with terrestrial and marine animals, their environment (plants, materials of plant origin, manure) and their food (cheese, yogurt) and most commonly found in the body cavities of humans and animals (Ring and Gatesoupe 1998; Tailliez 2001). In humans they are present in the oral cavity (1×10^3 to 1×10^7 colony forming units (CFU)/g), the ileum (1×10^3 to 1×10^7 CFU/g) and the colon (1×10^4 to 1×10^8 CFU/g) and are the dominant microorganism in the vagina (Hill et al. 1984; Forsum et al. 2005; Merk et al. 2005). *Lactobacillus* spp. have been found in the gastrointestinal tract of humans, pigs, chickens, cattle, dogs, mice, rats and hamsters (Hammes and Hertel 2009).

To date, 154 species from the genus *Lactobacillus* have been validly published isolated from different sources (<http://www.bacterio.net/lactobacillus.html>). Here we classify these sources into 11 major types (Fig. 2.1). The majority of species (almost a third of those described) were isolated from human and animal intestinal tracts and faeces (shown in Fig. 2.1). Vegetables and their associated fermentation products (including pickle and kimchi, sourdough etc.) provided the second largest number of *Lactobacillus* species isolated.

Species from other genera such as *Enterococcus* and *Bifidobacterium* were also mainly isolated from the intestinal tracts, faeces and skin of animals or humans (Felis and Dellaglio 2007). Species from the genus *Leuconostoc* were mainly isolated from chill-stored meats or clinical sources, although they were also found in association with plant material, fermented dairy products and wines (Thunell 1995). Species from the genus *Pediococcus* have long been associated with spoilage of beer as they produce diacetyl during fermentation and are most often isolated from spoiled beer, distilled material, or from cellars used for fermenting (Stiles and Holzapfel 1997). Other *Pediococcus* species, particularly *Pediococcus pentosaceus*, have also been isolated from dairy products (Tzanetakis and Litopoulou-Tzanetaki 1989).

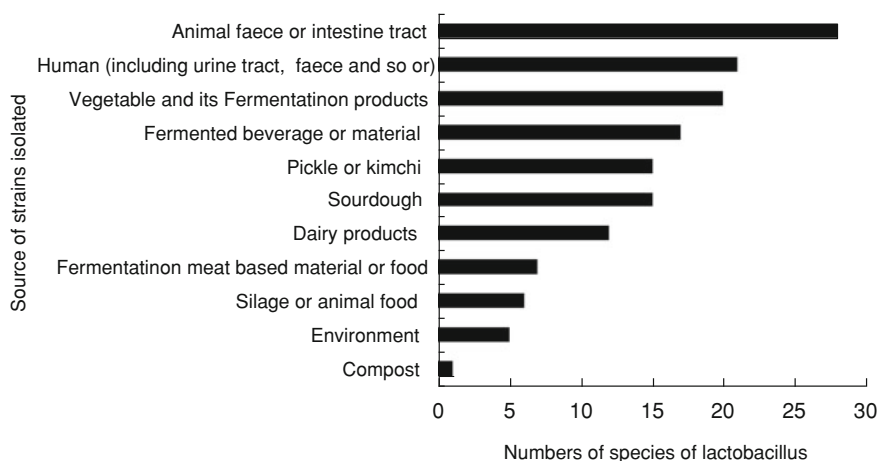


Fig. 2.1 Original source of the type specimens of *Lactobacillus* species that have been isolated

Species from the genus *Lactococcus* have been isolated from plant material (Cai et al. 2011; Chen et al. 2012), but are most commonly associated with dairy products (Teuber 1995).

2.2 Diversity in LAB

Early in the twentieth century, the term ‘Lactic acid bacteria’, or LAB, was first coined in the monograph of Orla-Jensen (1919) and this still forms the basis of our current classification system. The criteria for description of bacteria used by Orla-Jensen (1919) include cellular morphology, mode of glucose fermentation, temperature ranges for growth and sugar utilisation patterns (Table 2.1). According to the current taxonomic classification LAB belong to the phylum *Firmicutes*, class *Bacilli* and order *Lactobacillales* (Lahtinen et al. 2011); the different families include *Aerococcaceae*, *Carnobacteriaceae*, *Enterococcaceae*, *Lactobacillaceae*, *Leuconostocaceae* and *Streptococcaceae* (<http://www.uniprot.org/taxonomy/186826>). The genera of LAB that are associated with food are *Aerococcus*, *Carnobacterium*, *Enterococcus*, *Tetragenococcus*, *Vagococcus*, *Pediococcus*, *Lactobacillus*, *Leuconostoc*, *Oenococcus*, *Weissella*, *Lactococcus* and *Streptococcus*. Phylogenetically, all the above-mentioned genera form a clade belonging to the clostridial branch of Gram-positive bacteria with low guanine–cystine content (<50 %). This property distanced these ‘traditional’ LABs from the bifidobacteria which have greater than 55 % guanine–cystine content and belong to the ‘Actinomyces’ branch of bacteria (Schleifer and Ludwig 1995a, b). Nevertheless, the genus *Bifidobacterium* is still regarded as a LAB by some researchers, because of its similar physiological and biochemical properties and because it shares some common ecological niches such as the gastrointestinal tract (Klein et al. 1998).

Table 2.1 Genera of LAB associated with food and their physiological characteristics

Family	Genera	Characteristics									
		Shape	CO ₂ from glucose	Growth at 10 °C	Growth at 45 °C	Growth in 6.5 % NaCl	Growth in 18 % NaCl	Growth at pH 4.4	Growth at pH 9.6	Type of lactic acid	
<i>Aerococcaceae</i>	<i>Aerococcus</i>	Cocci (tetrads)	—	+	—	+	—	—	+	L	
	<i>Carnobacteriaceae</i>	Rods	—	+	—	ND	—	ND	—	L	
<i>Enterococcaceae</i>	<i>Enterococcus</i>	Cocci	—	+	+	+	—	+	—	L	
	<i>Tetragenococcus</i>	Cocci (tetrads)		+	—	+	+	Variable	+	L	
	<i>Vagococcus</i>	Cocci		+	—	—	—	ND	—	ND	
	<i>Pediococcus</i>	Cocci (tetrads)	—	Variable	Variable	Variable	—	+	—	D, L, DL	
<i>Lactobacillaceae</i>	<i>Lactobacillus</i>	Rods	Variable	Variable	Variable	Variable	—	ND	L	D, L, DL	
<i>Leuconostocaceae</i>	<i>Leuconostoc</i>	Cocci	+	+	—	Variable	—	Variable	—	D	
	<i>Oenococcus</i>	Cocci	+	+	—	Variable	—	Variable	—	D	
<i>Streptococcaceae</i>	<i>Weissella</i>	Cocci ^a	+	+	—	Variable	—	Variable	—	D, DL	
	<i>Lactococcus</i> ^b	Cocci	—	+	—	—	—	Variable	—	L	
	<i>Streptococcus</i>	Cocci	—	—	Variable	—	—	—	—	L	

The table is compiled from the work of Lahtinen et al. (2011) and Fennema et al.(2004)

Note ND Not Determined

^a Some *Weissella* strains are rod shaped

^b In the old literature, *Lactococcus* species are referred to as Group *N Streptococci*

2.2.1 Description and Taxonomy of LAB Genera

2.2.1.1 The Genus *Aerococcus*

The genus *Aerococcus* was created by Williams et al. (1953) to accommodate some species that were Gram-positive, microaerophilic and catalase negative (although some display weak nonheme pseudocatalase activity); these coccoid organisms differed from *Streptococcus* species primarily by their characteristic tetrad cellular arrangement. *Aerococcus* species have been found from a wide range of environments including air, dust, vegetation, meat-curing brines, soil, human respiratory tracts and marine sources. For a long time, the genus contained only a single species, *Aerococcus viridans* and historically, this species was thought to resemble *Pediococcus* species more than *Streptococcus* species on account of the cellular morphology. However, more recently, six other *Aerococcus* species have been described from human sources: *Aerococcus christensenii*, *Aerococcus sanguinicola*, *Aerococcus suis*, *Aerococcus urinae*, *Aerococcus urinaehominis* and *Aerococcus viridans* (Garvie 1988; Aguirre and Collins 1992; Collins et al. 1999; Lawson et al. 2001a, b; Felis et al. 1934). Comparative 16S rRNA gene sequences studies showed that this expanded *Aerococcus* genus formed a robust group among the catalase negative, Gram-positive cocci (Collins et al. 1999; Lawson et al. 2001a, b). Phylogenetically, *Aerococcus* is distinct from other genera such as *Streptococcus* and *Pediococcus*. A phylogenetic tree depicting the interrelationships between *Aerococcus* spp. and their close relatives can be found in Bergey's Manual of Systematic Bacteriology (Hammes and Hertel 2009).

Although the genus *Aerococcus* is phylogenetically distinct, using phenotypic traits, it is difficult to distinguish it from related genera that have a coccoid shape. In contrast, the species within the genus *Aerococcus* are very easily distinguished from each other using conventional and miniaturised API test systems (Hammes and Hertel 2009) (Table 2.2).

2.2.1.2 The Genus *Carnobacterium*

The genus *Carnobacterium* was first proposed by Collins et al. (1987) to accommodate the group of 'atypical lactobacilli' strains isolated from vacuum-packed meat that are also unable to grow on acetate agar (Collins et al. 1987). This description included two group strains that were rod shaped, Gram-positive, catalase negative and non-spore forming that had been isolated from poultry meat stored at low temperatures (Thornley 1957) and vacuum packed, chilled stored meat (Shaw and Harding 1984). The strains in these groups had previously been referred to as 'non-aciduric *Lactobacillus*'. Previously, two groups of non-aciduric *Lactobacillus* had also been described and proposed as being new species, specifically *Lb. divergens* (Holzapfel and Gerber 1983) and *Lb. carnis*

Table 2.2 Conventional and API system tests for distinguishing between species in the genus *Aerococcus*

Characteristics	<i>A. viridans</i>	<i>A. christensenii</i>	<i>A. sanguinicola</i>	<i>A. urinae</i>	<i>A. urinaequi</i>	<i>A. suis</i>	<i>A. urinaehominis</i>
<i>Conventional tests</i>							
PYRA	+	–	+	–	–	–	+
LAP	–	+	+	+	ND	ND	–
BE	v	–	d	–	ND	ND	–
NaCl 6.5 %	+	–	+	+	ND	+	+
Hippurate	v	+	+	+	ND	–	+
VP	–	+	–	–	ND	ND	–
<i>Sugar fermentation</i>							
Maltose	v	–	–	+	+	–	–
Mannitol	v	–	+	d	v	–	d
Ribose	v	–	+	+	–	–	+
Sucrose	v	–	+	–	+	–	–
Trehalose	v	–	+	d	+	–	+
Esculin	+	–	+	–	–	–	–
D-Arabitol	–	–	–	d	ND	–	–
Lactose	+	–	–	+	v	–	–
Mannitol	v	–	–	+	ND	ND	–
Maltose	+	–	+	–	+	–	+
MBDG	v	–	d	–	ND	+	+
Ribose	v	–	–	v	ND	+	–
Sorbitol	v	–	–	v	+	–	–
Sucrose	+	–	+	–	+	–	–
Trehalose	+	–	+	–	+	–	–
<i>Production during fermentation of:</i>							
β-GLUR	–	–	–	+	ND	ND	+
PYR	v	–	+	–	ND	+	–

Note Symbols + >85 % positive; v variable between strains (16–84 % positive); – 0–15 % positive. ND no data available. Abbreviations PYRA pyrrolidonyl arylamidase; LAP leucine amine peptidase; BE Bile-esculin; MBDG methyl β-D-glucopyranoside; β-GLUR β-glucuronidase; PYR pyroglutamic acid arylamidase; VP Voges-Proskauer; for conventional tests see Facklam and Elliott (1995) and for API rapid ID32 Strep system tests see (Hammes and Hertel 2009)

(Shaw and Harding 1985). However, comparative 16S rRNA gene sequence analysis of these species and the genus *Carnobacterium* (Wallbanks et al. 1990) confirmed their similarity with *Carnobacterium* species and their distinction from all other LAB. Although *Carnobacterium* species were originally isolated with *Lactobacillus* species, phylogenetically, the genus is more closely related to the genera *Enterococcus* and *Vagococcus*. *Carnobacterium piscicola* [previously *Lb. piscicolu*, (Hiu 1984)] showed 100 % rRNA sequence homology with *Lb. mul-fuomicus* (Miller et al. 1974), hence Collins et al. (1991) proposed that the correct name for both these organisms should be amended to *C. armltarornicus*. Currently, the genus *Carnobacterium* comprises 11 species with a variety of distinguishing physiological characteristics (Table 2.3).

Application in Food. Within the genera of LAB, *Carnobacterium* species are one of the most frequently isolated from natural environments and food and play a major role in biopreservation of food products. *Carnobacterium maltaromaticum* strains are widely found in foods including dairy products (Afzal et al. 2010) and have the potential to be applied as a protective culture in foods. Most research has focused on the production of bacteriocins by *C. maltaromaticum* and their roles in inhibition of *Listeria monocytogenes* and regulation of metabolic pathways of sensory importance (Leisner et al. 2007).

2.2.1.3 The Genus *Enterococcus*

Although species in the genus *Enterococcus* have been recognised since Thiercelin (1899) who described them as ‘entérocoque’ to emphasise their intestinal origin (Thiercelin 1899), the genus was not formally established until it was distinguished from the genus *Streptococcus* based on DNA–DNA and DNA–rDNA hybridisation studies (Collins et al. 1984). The first *Enterococcus*-type organism was described by Andrewes and Horder (1906) as *Streptococcus faecalis*, which was isolated from a patient with endocarditis (Andrewes and Horder 1906). Because there are no phenotypic characteristics to separate the genus from other genera of Gram-positive, catalase negative cocci, the taxonomy of this group of bacteria was vague until molecular tools became available. Application of molecular techniques for differentiation has resolved many of the uncertainties about these bacteria. However, the physical and chemical characteristics of growth at different temperatures, carbohydrate fermentation type and cell wall peptidoglycan type remain effective for distinguishing between *Enterococcus* species (Table 2.4).

Application in Food. Strains of *Enterococcus* species are mainly used in pig and poultry nutrition. However, there are pharmaceutical products that contain *Enterococcus* species as a probiotic. The genus *Enterococcus* contains 46 species (Table 2.4), but only *E. faecalis* and *E. faecium* are used as probiotics for animals and humans, of which *E. faecalis* is primarily used as a human probiotic.

Table 2.3 Physiological properties of species in the genus *Carnobacterium*^a used for identification and differentiation

Characteristic	<i>C. alternifundium</i> ^b	<i>C. divergens</i> ^b	<i>C. funditum</i> ^b	<i>C. gallinarum</i> ^b	<i>C. iners</i> ^b	<i>C. inhibens</i> ^b	<i>C. jeikei</i> ^b	<i>C. maltaromaticum</i> ^b	<i>C. mobile</i> ^b	<i>C. pleistocenium</i> ^c	<i>C. vindans</i> ^d
<i>Growth at different temperatures</i>											
Growth at 0 °C	+	+	—	+	+	+	ND	v	+	+	2 °C(+)
Growth at 30 °C	—	+	—	ND	—	—	+	+	+	—	+
Growth at 40 °C	—(+)	+	—(+)	ND	—	—	+	v	—	—	—
Motility	+	—	+	—	ND	+	ND	—	+	+	—
Arginine hydrolysis	+	+	—	+	ND	+	—	—	+	ND	—
Voges-Proskauer test	ND	+	ND	+	ND	ND	ND	+	—	ND	—
<i>Sugar fermentation</i>											
Amygdalin	+	+	—	+	ND	+	—	v	—	ND	—
Arabinose	—	—	—	—	w	—	—	—	—	+	—
Galactose	w	—	w	+	ND	ND	—	+	+	ND	+
Gluconate	—	+	d	+	ND	—	—	+	—	ND	—
Glycerol	W	ND	w	ND	—	—	—	+	+/-	—	—
Inulin	—	—	—	—	ND	w	—	+	+	ND	—
Lactose	—	—	—	+	+	w	—	—	—	+	+
Mannitol	—	—	+	—	+	+	+	+	—	+	—
Melezitose	—	d	—	+	ND	—	—	v	—	ND	—
Melibiose	—	—	—	—	ND	—	—	+	—	ND	—
Methyl D-Glucoside	d	—	—	+	ND	—	ND	+	—	ND	—
Ribose	+	+	+	+	+	+	—	+	+	+	+
D-Tagatose	ND	—	ND	+	ND	—	—	—	v	ND	+
Trehalose	—	+	+	+	+	+	—	+	+	+	+
D-Turanose	—	—	—	+	ND	—	ND	v	—	ND	—
Xylose	—	—	—	+	ND	—	—	—	—	ND	—
Esculin hydrolysis	+	ND	—	+	+	+	+	+	—	—	ND

Note ^a Symbols + positive; — negative; v variable (11–89 % positive); w weak; ND no data available

^b The table is compiled from the studies of Second edition of Bergey's Manual of Systematic Bacteriology 2 rmd, Vol (3) Hammes and Hertel (2009)

^c Data from Kim et al. (2009)

^d Data from Pikuta et al. (2005)

Table 2.4 Physiological characteristics of species in the genus *Enterococcus* used for identification and differentiation

Characteristics	<i>E. avium</i>	<i>E. alcedinis</i>	<i>E. asini</i>	<i>E. aquimarinus</i>	<i>E. cacciae</i>	<i>E. camelliae</i>	<i>E. canis</i>	<i>E. canintestini</i>	<i>E. casseliflavus</i>	<i>E. cecorum</i>	<i>E. columbae</i>	<i>E. devriesei</i>
Motility	-	-	-	-	-	-	-	-	+	-	-	-
Growth at different temperatures												
45 °C	+	-	±	+	+	+	+	ND	+	+	ND	-
50 °C	-	ND	ND	ND	ND	ND	ND	ND	-	ND	ND	ND
Growth in												
6.5 % NaCl	+	-	-	(+)	+	+	+	+	+	-	-	+
0.04 % nitrite	-	ND	ND	ND	-	ND	ND	ND	+	ND	ND	ND
0.01 % tetrazole	ND	ND	ND	ND	ND	ND	+	ND	ND	ND	ND	ND
Methylene blue (0.1 % milk) test:	d	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Pigment production	-	ND	-	ND	-	ND	ND	-	+	d	ND	ND
Haemolysis	α	ND	ND	+	ND	Weak	ND	ND	ND	α	-	ND
H2S	+	ND	ND	ND	ND	ND	ND	ND	-	ND	ND	ND
NH3 from arginine	ND	-	ND	-	-	-	+	ND	+	-	ND	-
Arginine dehydrolase	-	-	-	-	-	-	+	ND	+	-	ND	-
Hippurate hydrolysis	d	-	+	-	-	ND	+	ND	-	-	ND	-
Voges-Proskauer test	-	+	ND	-	+	ND	+	ND	+	+	-	+
Sugar fermentation												
D-xylose	-	+	+	+	ND	-	ND	-	+	-	+	-
L-rhamnose	+	-	+	-	ND	-	ND	-	(+)	+	+	-
Sucrose	+	+	-	+	+	+	+	+	+	+	-	+
Lactose	+	-	+	+	-	-	-	+	+	+	+	+
Melibiose	-	-	-	+	-	-	-	-	+	+	+	-
Raffinose	-	-	-	+	-	-	-	-	+	+	+	-
Melzitose	+	ND	-	-	ND	-	-	-	+	+	ND	-
Glycerol	+	-	-	-	+	-	+	-w	-	-	-	-

(continued)

Table 2.4 (continued)

Characteristics	<i>E. avium</i>	<i>E. alcedinis</i>	<i>E. asini</i>	<i>E. aquimarinus</i>	<i>E. cacciae</i>	<i>E. camelliae</i>	<i>E. canis</i>	<i>E. canintestini</i>	<i>E. caseiliflavus</i>	<i>E. cecorum</i>	<i>E. columbae</i>	<i>E. devriesei</i>
Adonite	+	ND	ND	ND	ND	ND	ND	ND	-	-	ND	-
Sorbitol	+	-	-	-	-	-	-	-	-	-	+	-
Mannitol	+	+	-	-	-	+	-	-	+	+	+	-
Lancefield Reference	Q (D)	D	D	-	D	ND	D	Non-D	D	Non-D	D	-
	Collins et al. (1984)	Frolkova et al. (2013)	De vaux (1998)	Švec et al. (2005a)	Carvalho et al. (2006)	Sukontasing et al. (2007)	De graef et al. (2001)	Naser et al. (2005)	Collins et al. (1984)	Williams et al. (1989)	Devriese et al. (1990)	Švec et al. (2005b)
Characteristics	<i>E. dispar</i>	<i>E. durans</i>	<i>E. eurekaensis</i>	<i>E. faecalis</i>	<i>E. faecium</i>	<i>E. gallinarum</i>	<i>E. glyvus</i>	<i>E. haemoperoxidus</i>	<i>E. hermanniensis</i>	<i>E. hirae</i>	<i>E. italicus</i>	
Motility	-	-	-	(-)	-	-	-	-	-	-	-	-
<i>Growth at different temperatures</i>												
<i>Growth in</i>	45 °C	+	+	+	+	+	+	ND	-	+	+	v
	50 °C	-	-	ND	(-)	+	ND	ND	ND	+	+	ND
	6.5 % NaCl	+	+	+	+	+	+	ND	+	+	+	-
	0.04 % nitrite	ND	-	ND	+	(+)	ND	ND	ND	-	-	ND
	0.01 % tetrazole	ND	-	ND	+	+	+	ND	ND	ND	ND	ND
Methylene blue (0.1 % milk) test:	ND	+	ND	ND	ND	v	ND	ND	ND	ND	ND	ND
Pigment production	-	-	ND	ND	-	-	+	ND	-	-	ND	-
Haemolysis	ND	α , β	ND	(β)	(α)	α , β	ND	ND	α	-	-	α
H2S	-	-	ND	ND	ND	-	ND	ND	ND	ND	ND	ND
NH3 from arginine	-	ND	+	+	+	+	ND	ND	ND	ND	ND	ND
Arginine dehydrolyase	+	+	+	+	+	+	ND	-	ND	+	+	-
Hippurate hydrolysis	d	d	-	-	+	+	ND	-	+	+	+	+
Voges-Proskauer test	ND	ND	-	-	ND	ND	ND	ND	ND	+	+	ND

(continued)

Table 2.4 (continued)

Characteristics	<i>E. dispar</i>	<i>E. durans</i>	<i>E. eurekaensis</i>	<i>E. faecalis</i>	<i>E. faecium</i>	<i>E. gallinarum</i>	<i>E. glyvus</i>	<i>E. haemoperoxidus</i>	<i>E. hermanniensis</i>	<i>E. hirae</i>	<i>E. italicus</i>
<i>Sugar fermentation</i>											
D-xylose	-	-	-	-	-	+	-	-	-	-	-
L-rhamnose	-	ND	ND	d	-	-	+	-	-w	-	-
Sucrose	+	-	ND	+	v	+	+	+	+	+	+
Lactose	+	+	ND	+	+	+	+	+	-	+	+
Melibiose	+	-	ND	-	v	+	+	-	ND	+	-
Raffinose	+	-	ND	-	-	+	+	-	ND	+	-
Melzitose	ND	-	ND	(+)	-	+	ND	ND	ND	(-)	-
Glycerol	+	-	ND	+	+	-	+	+	ND	(-)	-
Adonite	ND	-	ND	-	-	-	ND	ND	ND	-	ND
Sorbitol	+	-	ND	(+)	-	-	+	-	-	-	-
Mannitol	-	(-)	ND	+	(+)	+	+	v	+	-	v
<i>Lancefield Reference</i>											
Collins et al. (1991)	Collins et al. (1991)	Collins et al. (1984)	Cotta et al. (2013)	Collins et al. (1984)	Collins et al. (1984)	Collins et al. (1984)	Tyrrell et al. (2002)	Švec et al. (2001)	Koort et al. (2004)	Farrow and Collins (1985)	Fortina et al. (2004)
Collins et al. (1991)	Collins et al. (1984)	Collins et al. (1984)	Collins et al. (1984)	Collins et al. (1984)	Collins et al. (1984)	Collins et al. (1984)	Tyrrell et al. (2002)	Švec et al. (2001)	Koort et al. (2004)	Farrow and Collins (1985)	Fortina et al. (2004)
<i>Characteristics</i>											
<i>E. lactis</i>	<i>E. lactis</i>	<i>E. leuconii</i>	<i>E. malodoratus</i>	<i>E. moraviensis</i>	<i>E. mundtii</i>	<i>E. pallens</i>	<i>E. phenicalicola</i>	<i>E. plantarum</i>	<i>E. pseudocaulum</i>	<i>E. quebecensis</i>	<i>E. raffinosus</i>
-	-	-	-	-	-	-	-	-	-	-	-
<i>Motility</i>											
<i>Growth at different temperatures</i>											
45 °C	+	+	-	-	+	+	-	+	+	-	+
50 °C	ND	ND	-	-	-	ND	-	ND	ND	ND	ND
<i>Growth in</i>											
6.5 % NaCl	+	+	+	+	+	+	-	+	-	-	+
0.04 % Nitrite	ND	ND	-	-	-	ND	ND	ND	ND	ND	ND
0.01 % Tetrazole	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Methylene blue (0.1 % milk) test	+	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

(continued)

Table 2.4 (continued)

Characteristics	<i>E. lactis</i>	<i>E. lenanti</i>	<i>E. malodoratus</i>	<i>E. moraviensis</i>	<i>E. mundtii</i>	<i>E. pallens</i>	<i>E. phoenicicola</i>	<i>E. plantarum</i>	<i>E. pseudocaulum</i>	<i>E. quebecensis</i>	<i>E. raffinosus</i>
Pigment production											
Haemolysis	α	-	ND	ND	-	ND	ND	ND	ND	ND	ND
H ₂ S	ND		+	+	-	ND	-	ND	α	ND	ND
NH ₃ from arginine	ND	ND		ND	ND	+	-	-	ND		ND
Arginine dehydroase	+	-		-	ND	-	ND	-			
Hippurate hydrolysis	v	d		d	ND	+	-	-		+	+
Voges-Proskauer test	+	-		-	ND	ND	ND	+		-	-
Sugar fermentation											
D-xylose	-		d	d	ND	+	+	-	ND	ND	ND
L-rhamnose	-	+w	+	+	(+)	ND	+	+	ND	ND	ND
Sucrose	-	+w	+	+	+	+	+	-	-	+	+
Lactose	+	+w	+	+	+	+	+	+	+	+	+
Melibiose	+	+	+	+	+	+	-	-	-	+	+
Raffinose	-	+	+	+	+	+	-	-	-	-	+
Melzitiose	-	ND	-	-	-	ND	-	ND	-	-	ND
Glycerol	-		d	d	d	+	+	-	-	ND	+
Adonite	ND		+	+	-	ND	ND	ND	ND	ND	ND
Sorbitol	-		+	+	v	+	+	-	+	-	+
Mannitol	+		+	+	+	+	-	-	+	+	+
<i>Lancefield</i>											
Reference	Morandi et al. (2012)	Cotta et al. (2013)	Collins et al. (1984)	Švec et al. (2001)	Collins et al. (1986)	Tyrell et al. (2002)	Law-Brown and Meyers (2003)	Švec et al. (2012)	Hammes and Hertel (2009)	Sistek et al. (2012)	Collins et al. (1989)

Characteristics	<i>E. ratti</i>	<i>E. rivorum</i>	<i>E. rotai</i>	<i>E. saccharolyticus</i>	<i>E. seriolide</i>	<i>E. sulfureus</i>	<i>E. termitis</i>	<i>E. thailandicus</i>	<i>E. urealyticus</i>	<i>E. viktkiensis</i>	<i>E. villorum</i>
Motility	-	-	-	-	-	-	-	-	-	-	-
Growth at different temperatures											
45 °C	+	-	-	+	+	+	+	+	+	-	+
50 °C	ND	ND	ND	-	-	ND	ND	ND	ND	ND	ND

(continued)

Table 2.4 (continued)

Characteristics	<i>E. ratti</i>	<i>E. rivorum</i>	<i>E. rotai</i>	<i>E. saccharolyticus</i>	<i>E. serotolide</i>	<i>E. sulfureus</i>	<i>E. termitis</i>	<i>E. thailandicus</i>	<i>E. urelyticus</i>	<i>E. vikkiensis</i>	<i>E. villorum</i>
<i>Growth in</i>											
6.5 % NaCl	+	-	-	+	+	+	+	+	-	+	+
0.04 % Nitrite	ND	ND	ND	ND	+	ND	+	ND	ND	ND	ND
0.01 % Tetrazole	ND	ND	ND	ND	+	ND	-	ND	ND	ND	ND
Methylene blue (0.1 % milk) test	-	ND	ND	+	ND	+	ND	ND	ND	ND	
Pigment production	-	ND	ND	-	ND	+	-	ND	-	-	
Haemolysis	α	ND	ND	-	α	ND	-	+	α	α	α
H ₂ S	ND	ND	ND	ND	-	ND	ND	-	ND	ND	ND
NH ₃ from arginine	+	+	+	-	ND	ND	ND	+	ND	ND	
Arginine dehydrolase	+	-	+	-	ND	-	-	ND	ND	-	
Hippurate hydrolysis	-	-	+	+	ND	-	-	ND	ND	-	
Voges-Proskauer test	ND	+	+	+	ND	ND	-	ND	ND	ND	
<i>Sugar fermentation</i>											
D-xylose	+	v	-	-	-	+	+	ND	ND	-	D-
L-rhamnose	ND	-	-	-	-	+	-	-	-	-	+
Sucrose	-	+	+	+	-	+	-	+	-	ND	-
Lactose	-	v	+	+	-	-	-	+	+	+	+
Melibiose	-	-	+	+	-	-	-	-	-	-	+
Raffinose	-	-	+	+	-	+	-	-	-	-	-
Melzitose	-	-	+	+	-	-	-	ND	ND	-	ND
Glycerol	-	+	+	+	-	-	+	+	+	+	+
Adonite	ND	ND	ND	-	-	ND	ND	ND	ND	ND	ND

(continued)

Table 2.4 (continued)

Characteristics	<i>E. ratti</i>	<i>E. rivorum</i>	<i>E. roiai</i>	<i>E. saccharolyticus</i>	<i>E. serotolide</i>	<i>E. sulfureus</i>	<i>E. termitis</i>	<i>E. thailandicus</i>	<i>E. urelyticus</i>	<i>E. vikkiensis</i>	<i>E. villorum</i>
Sorbitol	-	+	-	+	+	-	-	-	-	-	+
Mannitol	+	+	+	+	+	+	+	+	+	+	-
<i>Lancefield</i>	D	Non-D	D	Non-D	Non-D	ND	ND	ND	D	D	ND
Reference	Teixeira et al. (2001)	Nieni et al. (2012)	Sedláček et al. (2013)	Chen et al. (2013)	Kusuda et al. (1991)	Martinez-Murcia and Collins (1991b)	Švec et al. (2006)	Tanasupawat et al. (2008)	Sedláček et al. (2013)	Rahkila et al. (2011)	De graef et al. (2001)

Note Symbols + positive; - negative; v variable (11–89 % positive); w, weak; ND, no data available

2.2.1.4 The Genus *Lactobacillus*

The genus *Lactobacillus* is most closely related to the genera *Paralactobacillus* and *Pediococcus*, being grouped within the same family (Release 5.0, Garrity et al. 2004). The genus was first described by Beijerinck (1901). Then Orla-Jensen (1919) divided it into three subgenera, *Thermobacterium*, *Streptobacterium* and *Betabacterium* according to their optimal growth temperatures and hexose fermentation pathways. In the 2nd edition of Bergey's Manual of Systematic Bacteriology (Kandler and Weiss 1986), numerous *Lactobacillus* species were listed, and the nomenclature reorganised into three groups: group I (obligate homofermentative species), group II (facultative heterofermentative species) and group III (obligate heterofermentative species). This division suited the interests of food microbiologists; several species in groups I and II, and also some species in group III are used in fermented foods, although group III species are actually most commonly associated with food spoilage. Based on 16S rRNA the principal groupings are: (1) *Lb. delbrueckii* group including primarily the homofermentative species; (2) the *Lb. case-Pediococcus* group, comprised of obligate homofermentative species as well as facultative and obligate heterofermentative species; (3) the *Leuconostoc* group that includes some obligate heterofermentative species and has subsequently been subdivided into three genera: *Leuconostoc*, *Oenococcus* and *Weissella* (Collins et al. 1991). More recently the smaller groups have been split again according to their metabolic characteristics, phylogenetic groupings, guanine–cytosine content and the type of peptidoglycan present in the cell wall (Hammes and Hertel 2003). These detailed grouping of species was again updated by Felis and Dellaglio (2007) resulting in 106 validly described species separated into 15 groups some of which contained only single species (Felis and Dellaglio 2007). These species groups are *Lb. delbrueckii* group (delb), *Lb. salivarius* group (sal), *Lb. reuteri* group (reu), *Lb. buchneri* group (buch), *Lb. alimentarius*–*Lb. farciminis* group (al-far), *Lb. casei* group (casei), *Lb. sakei* group (sakei), *Lb. fructivorans* group (fru), *Lb. coryniformis* group (cor), *Lb. plantarum* group (plan), *Lb. perolens* group (per), *Lb. brevis* group (bre), *Pediococcus dextrinicus* group (Pdex) (Felis and Dellaglio 2007). In 2012, the taxonomy of the genus *Lactobacillus* was further updated and species within the genus were further clustered from a taxonomic point of view (Elisa et al. 2012). This updated phylogenetic analysis, also based on 16S rRNA gene sequencing, revealed 152 validly described species divided into 15 groups that contained three or more species, 4 groups that contained only two species and 10 single lines of descent (Elisa et al. 2012) (Table 2.5).

2.2.1.5 The Genus *Lactococcus*

The phylogenetic position of the genus *Lactococcus* within the *Firmicutes* was established by comparison of 16S rRNA gene sequences (Schleifer and Ludwig 1995a, b) and in the second edition of Bergey's Manual of Systematic Bacteriology

Table 2.5 Physiological characteristics of species in the genus *Lactobacillus* (validly published from 2012 to 2013) used for identification and differentiation

Characteristics	<i>Lb. backii</i>	<i>Lb. brantae</i>	<i>Lb. curteae</i>	<i>Lb. delbrueckii</i> subsp. jacobsonii	<i>Lb. delbrueckii</i> subsp. sunkii	<i>Lb. futsaii</i>	<i>Lb. heilongjiangensis</i>	<i>Lb. gigerionum</i>	<i>Lb. kankeei</i>	<i>Lb. hokkaidonensis</i>	<i>Lb. hominis</i>
<i>Growth at</i>											
15 °C	+	ND	+	+	-	+	ND	ND	+	-	-
45 °C	-	-	+	+	+	-	ND	+	-	-	+
PH 4.0	+		+	+	+	+	ND	+	-	+	-
PH 8.5	ND		w	ND	ND	+	ND	-	-	-	-
Salt tolerance 5 %	+	ND	+	ND	ND	ND	ND	-	ND	ND	+
Enzyme activity											
Alkaline phosphatase	-		ND	ND	ND		ND	+	ND	-	w
C4 esterase	+	ND	ND	ND	ND		ND	-	ND	+	-
C8 esterase	-	ND	ND	ND	ND		ND	-	ND	ND	-
Cysteine aminopeptidase	-	ND	ND	ND	ND		ND	-	ND	ND	-
Naphthol-AS-BI-phosphohydrolase	-	ND	ND	ND	ND		ND	ND	ND	+	w
β -Galactosidase	-	-	ND	ND	ND		ND	-	ND	+	+
α -Galactosidase	-	ND	ND	ND	ND		ND	-	ND	+	+
β -Galactosidase	-	-	ND	ND	ND		ND	-	ND	+	+
N-Acetyl- β -glucosaminidase		ND	ND	ND	ND		ND	-	ND	+	-
Voges-Proskauer	ND	-	ND	ND	ND		ND	ND	ND	-	+
Isomers of Lactic acid	DL	ND	DL	DL	DL	DL	ND	L	DL		DL
<i>Sugar fermentation</i>											
Aesculin	-	-	w	ND	ND	+	+	+	-	-	+
Amylose	ND	-	ND	ND	ND	ND	ND	ND	ND	ND	ND
D-Arabitol	-	-	-	ND	ND	-	-	-	-	+	-
Arbutin	-	-	-	-	-	+	-	+	-	-	-
L-Arabinose	-	-	+	ND	ND	-	-	-	-	+	-
Cellobiose	-	+	-	+	-	+	+	+	-	-	+
D-Galactose	-	+	+	-	-	+	+	+	+	-	+
D-fructose		+	+	+	ND	+	+	ND	+	-	+

(continued)

Table 2.5 (continued)

Characteristics	<i>Lb. buckii</i>	<i>Lb. bruntiae</i>	<i>Lb. curvatae</i>	<i>Lb. delbrueckii</i> subsp. jacobsonii	<i>Lb. delbrueckii</i> subsp. <i>sunkii</i>	<i>Lb. futsui</i>	<i>Lb. heilongjiangensis</i>	<i>Lb. gigerionum</i>	<i>Lb. kunzei</i>	<i>Lb. hokkaidonensis</i>	<i>Lb. hominis</i>
D-glucose	+	—	+	+	+	+	+	+	+	+	+
2-ketogluconate	—	ND	—	—	ND	ND	—	—	—	—	—
Lactose	—	—	w	—	—	+	+	—	—	—	+
Maltose	—	—(+)	+	+	+	+	+	+	—	+	+
D-Mannose	+	+	w	+	+	+	+	+	—	—	+
D-Mannitol	+	—	—	—	ND	—	—	—	+	—	—
Melezitose	—	—	+	ND	ND	—	—	—	—	—	—
D-Ribose	—	—	+	ND	ND	—	—	—	—	+	—
L-Rhamnose	—	—	—	ND	ND	—	—	—	—	—	—
Raffinose	—	—	+	—	—	—	—	—(—)	—	—	+
D-sorbitol	—	—	—	—	—	—	—	—	—	—	—
Salicin	—	—	—	—	+	+	+	+	—	—	+
Sucrose	—	—	+	+	+	+	+	+	+	—	+
D-xylose	—	—	—	—	ND	—	—	—	—	+	—
Xylitol	—	—	—	ND	ND	—	—	—	—	—	—
G+C mol%	41.3	48.2 ± 2.6	44.1	50.2	50.9	36.3	38.9	41.9	36–37	39.4 ± 0.4	42.8
References	Tohno et al. (2013)	Dmitriy et al. (2012)	Lei et al. (2013)	David B et al. (2013)	Kudo et al. (2012)	Chao et al. (2012)	Gu et al. (2012)	Cousin et al. (2012)	Endo et al. (2012)	Tohno et al. (2013)	Cousin et al. (2013)
Characteristics	<i>Lb. ivatensis</i>	<i>Lb. kinchintensis</i>	<i>Lb. nasuensis</i>	<i>Lb. oryzae</i>	<i>Lb. pasteurii</i>	<i>Lb. porcinae</i>	<i>Lb. seniviri</i>	<i>Lb. shenzhenensis</i>	<i>Lb. senioris</i>	<i>Lb. xiangfangensis</i>	<i>Lb. yonginensis</i>
Growth at											
15 °C	+	+	ND	+	ND	+	ND	+	+	ND	+
45 °C	—	—	+	+	+	—	—	+	—	ND	—
PH 4.0	+	ND	w	+	+	+	+	+	—	ND	+
PH 8.5	—	+	ND	—	ND	ND	+	+	—	ND	—
Salt tolerance 5 %	+	+	—	+	ND	+	+	+	w	ND	+
Enzyme activity											
Alkaline	—	ND	ND	+	+	ND	ND	ND	ND	ND	ND
phosphatase											
C4 esterase	+	ND	ND	+	ND	ND	ND	ND	ND	ND	ND
C8 esterase	+	ND	ND	+	ND	ND	ND	ND	ND	ND	ND

(continued)

Table 2.5 (continued)

Characteristics	<i>Lb. ivatensis</i>	<i>Lb. kimchiensis</i>	<i>Lb. nasuensis</i>	<i>Lb. oryzae</i>	<i>Lb. pasteurii</i>	<i>Lb. porcinae</i>	<i>Lb. sanviri</i>	<i>Lb. shenzhenensis</i>	<i>Lb. senioris</i>	<i>Lb. xiangfangensis</i>	<i>Lb. yonginensis</i>
Cystine aminopeptidase	—	ND	ND	+	ND	ND	ND	ND	ND	ND	ND
Naphthol-AS-BI-phosphohydrolase	—	ND	ND	+	w	ND	ND	ND	ND	ND	ND
β -Galactosidase	—	ND	—	—	+	ND	ND	ND	ND	ND	ND
α -Galactosidase	—	ND	w	—	—	ND	ND	ND	ND	ND	ND
β -Galactosidase	—	ND	+	—	—	ND	ND	ND	ND	ND	ND
N-Acetyl- β -glucosaminidase	—	ND	ND	—	—	ND	ND	ND	ND	ND	ND
Voges-Proskauer	ND	ND	ND	ND	+	ND	ND	ND	ND	ND	ND
Isomers of Lactic acid	DL	D/L	D/L	D/L	D	DL	DL	ND	D/L	ND	D/L
<i>Sugar fermentation</i>											
Aesculin	—	—	—	—	+	+	+	+	—	D	ND
Amylose	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
D-Arabitol	—	ND	—	—	—	—	ND	—	—	—	+
Arbutin	—	w	—	—	+	—	+	+	+	—	—
L-Arabinose	—	w	w	—	—	—	—	+	+	—	+
Cellobiose	+	+	—	—	+	+	+	+	+	+	—
D-Galactose	—	+	+	+	—	—	+	+	—	+	+
D-fructose	—	+	+	—	+	+	+	+	+	ND	+
D-glucose	+	+	—	—	+	+	+	+	+	ND	+
2-ketogluconate	—	—	w	ND	ND	—	w	w	+	—	—
Lactose	—	+	—	+	+	—	—	w	—	—	ND

(continued)

Table 2.5 (continued)

Characteristics	<i>Lb. ivatensis</i>	<i>Lb. kinchitensis</i>	<i>Lb. nasutensis</i>	<i>Lb. oryzae</i>	<i>Lb. pasteurii</i>	<i>Lb. porcinae</i>	<i>Lb. saniviri</i>	<i>Lb. shenzhenensis</i>	<i>Lb. senioris</i>	<i>Lb. xiangfangensis</i>	<i>Lb. yonginensis</i>
Maltose	+	+	w		+	+	+	+	—	ND	+
D-Mannose	+	+	—	—	+	+	+	+	+	+	—
D-Mannitol	+	—	—	—	+	—	+	—	+	+	—
Melezitose	+	—	—	—	—	—	+	W	—	—	—
D-Ribose	—	—	+	—	+	—	+	W	+	ND	+
L-Rhamnose	—	—	—	—	—	—	—	+	+	—	ND
Raffinose	—	—	—	—	—	—	+	+	—	—	ND
D-sorbitol	—	—	—	—	—	—	—	—	—	+	ND
Salicin	—	+	—	—	+	+	+	+	+	+	+
Sucrose	—	+	—	—	+	+	+	+	+	+	—
D-xylose	—	—	w	—	—	—	ND	—	+	+	+
Xylitol	—	—	ND	—	—	—	+	—	ND	—	ND
G+C mol%	41.3	35.7	58.5–59.2	43.4	45.4	47.6	48.1	56.1–56.5	39.8	46.6	47.8
References	Tohno et al. (2013)	Kim et al. (2013)	Cai et al. (2012)	Tohmo et al. (2013)	Cousin et al. (2013)	Nguyen et al. (2013)	Okamoto et al. (2012)	Zou et al. (2013)	Okamoto et al. (2012)	Gu et al. (2012)	Yi et al. (2013)

Note: + 90 % or more strains positive; — 90 % or more strains negative; d 11–89 % of strains positive; D delayed reaction (positive after incubating at 30 °C for 4 days); w weak; ND no data available

(Hammes and Hertel 2009) *Lactococcus* was described as a member of the family *Streptococcaceae*, along with *Streptococcus* and *Lactovum*, in the order *Lactobacillales*. However, *Lactococcus* species are clearly separated from *Streptococcus* spp. which are pathogenic (Stackebrandt and Teuber 1988). To date, the genus *Lactococcus* comprises 12 species, amongst which, *Lactococcus lactis* including 3 subspecies. The species can be differentiated based on physiological characteristics (Table 2.6).

Application in Food. *Lactococcus lactis* subsp. *lactis* and *cremoris* are the species traditionally used in dairy applications. The main differences between the subspecies are their salt tolerance and ability to hydrolyse arginine. Both these are typical for subsp. *lactis* but absent in *cremoris*. The diacetyl-producing variants of *Lc. lactis* subsp. *lactis* are often referred to as biovar diacetylactis (Batt 2000).

2.2.1.6 The Genus *Leuconostoc*

Leuconostoc is the most economically important genus of LAB, and *Leuc. mesenteroides* subsp. *mesenteroides* is the principle species isolated from plants (Mundt 1970). The *Leuconostoc* genus was considered close to the genus *Streptococcus* based on morphological classification criteria. Phenotypically, species from the *Leuconostoc*, *Lactobacillus* and *Pediococcus* genera share many characteristics and are often isolated from the same habitat (Garvie 1976; Sharpe 1972). Physiological properties can be used for identification and differentiation between species in *Leuconostoc* (Table 2.7). Phylogenetically, the genus *Leuconostoc* is closely related to the genera *Fructobacillus*, *Oenococcus* and *Weissella*, and together they are commonly known as the ‘*Leuconostoc* group’ of LAB. Originally, the LAB included in the ‘*Leuconostoc* group’ were all classified as *Leuconostoc* species. However, in the early 1990s, molecular phylogenetic analyses led to a subdivision of the group into three distinct lineages: the genus *Leuconostoc* sensu stricto, the *Leuconostoc paramesenteroides* group, and the *Leuconostoc oenos* group (Martinez-Murcia and Collins 1990; Martinez-Murcia et al. 1993). In the past 10 years some *Leuconostoc* species have been reclassified as *Oenococcus oeni* (Dicks et al. 1995) or moved to the genera *Weissella* (Collins et al. 1993) or *Fructobacillus* (Endo and Okada 2008) based on a combination of genetic and phenotypic characteristics. To date there are 16 validly described species (Table 2.6) with *Leuc. mesenteroides* being the type species (Euzéby 2009).

Application in Food. The role of *Leuconostoc* species in fermented food can be both positive and negative. The positive effects on dairy products were recognised early in the twentieth century when researchers found that during the fermentation process *Leuconostoc* species were responsible for a buttery aroma, which was a desirable characteristic for many dairy products (Thunell 1995; Dessart and Steenson 1995; Vedamuthu 1994). Currently, *Leuconostoc* species are used as starter cultures in the manufacture of fermented dairy, vegetable and cereal foods in conjunction with the acid-producing species *Lc. lactis*. The negative effects of

Table 2.6 Physiological properties of species in the genus *Lactococcus* used for identification and differentiation

Characteristics	<i>Lc.</i> <i>chungensis</i>	<i>Lc.</i> <i>garvieae</i>	<i>Lc.</i> <i>fuijensis</i>	<i>Lc. lactis</i>			<i>Lc.</i> <i>raffinolactis</i>	<i>Lc.</i> <i>piscium</i>	<i>Lc.</i> <i>plantarum</i>	<i>Lc.</i> <i>taiwanensis</i>
				<i>cremoris</i>	<i>hordniae</i>	<i>lactis</i>				
Growth at 4 °C	+	+	ND	—	+	+	—	+	—	ND
Growth at 10 °C	+	+	ND	+	+	+	+	ND	+	+
Growth at 45 °C	—	—	+	—	—	—	—	—	—	+
Growth at 4 % NaCl	—	+	—	—	—	+	—	+	+	+
Growth at 6.5 % NaCl	ND		ND	ND	—	ND	ND	ND	ND	+
Growth at pH 9.2	ND		ND	—	—	+	ND	ND	ND	ND
Methylene blue (0.1 % milk)	ND	+	ND		—	ND	ND	—	—	ND
Growth in Bile (40 %)	ND		ND	—	+	+	ND	ND	ND	ND
NH ₃ from arginine	+	+	ND	—	—	+	—	ND	ND	ND
CO ₂ from citrate	ND		ND	—	+	—	ND	ND	ND	ND
Diacetyl and acetoin	ND		ND	—		—	ND	ND	ND	ND
Serological group ^b	ND		ND	N		N	ND	ND	ND	ND

Sugar fermentation

(continued)

Table 2.6 (continued)

Characteristics	<i>Lc. chungensis</i>	<i>Lc. garvieae</i>	<i>Lc. fujiensis</i>	<i>Lc. lactis</i>			<i>Lc. raffinolactis</i>	<i>Lc. piscium</i>	<i>Lc. plantarum</i>	<i>Lc. taiwanensis</i>
				<i>cremoris</i>	<i>hordniae</i>	<i>lactis</i>				
Galactose	-	+	+	+	-	+	+	-	-	+
Lactose	-	+	-	-	-	+	+	+	-	+
Mannitol	ND		+	-		-	ND	ND	+	+
Raffinose	-	-	ND	-	-	-	+	-	-	-
aesculin	+		ND	ND		-	-	ND	+	ND
Maltose	+		ND	-	-	+	+	+	+	+
Melibiose	-		ND	-	-	-	+	+	+	-
Ribose	ND		+	-	-	+	ND	-	-	+
Starch	ND	-	+	-		-	-w	ND	-	-w
DNA G+C (%)	ND	38.3-38.7	42.1-42.5	35.0-36.0	35.2	33.8-36.8	40-43	ND	36.9-38.9	39.6
References	Cho et al. (2008)	Schleifer et al. (1985)	Cai et al. (2011)	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Schleifer et al. (1985)	Williams et al. (1990)	Schleifer et al. (1985)	Chen et al. (2013)

Note Symbols + positive; - negative; w weakly positive; v variable reaction; ND no data available

Table 2.7 Physiological properties of species in the genus *Leuconostoc* used for identification and differentiation

Characteristics	<i>Leuc. mesenteroides</i> subsp.				<i>Leu.camosum</i>	<i>Leu.citreum</i>	<i>Leu.durionis</i>	<i>Leu.fallax</i>
	<i>mesenteroides</i>	<i>dextranum</i>	<i>cremoris</i>	<i>Leu.argentinum</i>				
Cell morphology	Coccoid or elongation of cocci	Coccoid or elongation of cocci	Coccoid or elongation of cocci	Coccoid or elongation of cocci	Coccoid or elongation of cocci	Coccoid or elongation of cocci	Coccoid	Coccoid
Ammonia from arginine	–	–	–	–	–	–	–	–
Lactic acid configuration	D	D	D	D	D	D	D	D
Hydrolysis of esculin	+	+	–	–	v	+	–	ND
Dextran production	+	+	–	–	+	ND	ND	ND
Growth at Ph 4.8	–	–	–	ND	ND	ND	+	+
Growth in 10 % ethanol	–	–	–	ND	ND	ND	ND	ND
Growth at 37 °C	d	+	–	+	–	d	+	+
Requirement for TJE	–	–	–	–	–	–	–	–
G6PDH presente	+	+	+	ND	ND	ND	ND	ND
<i>Sugar fermentation</i>								
Amygdalin	ND	ND	ND	ND	ND	ND	–	ND
Arabinose	+	–	–	v	–	+	–	–
Arbutin	v	–	–	–	–	–	–	–
Cellulose	v	d	–	ND	ND	ND	ND	ND

(continued)

Table 2.7 (continued)

Characteristics	<i>Leuc. mesenteroides</i> subsp.				<i>Leu.camosum</i>	<i>Leu.citream</i>	<i>Leu.durionis</i>	<i>Leu.fallax</i>
	<i>mesenteroides</i>	<i>dextranica</i>	<i>cremoris</i>	<i>Leu.argentinum</i>				
Cellobiose	v	—	—	v	v	—	—	—
Lactose	v	+	d	+	—	—	—	—
Maltose	+	+	—	+	—	+	—	—
Mannitol	v	—	—	v	—	d	+	(d)
Mannose	v	v	—	+	—	d	+	—
Raffinose	v	v	—	+	—	—	—	—
Ribose	v	+	—	—	d	—	+	+
Salicin	v	—	—	—	d	+	—	—
Sucrose	+	+	—	+	+	+	+	(+)
Trehalose	+	+	—	v	+	+	+	(+)
Xylose	v	d	—	v	—	—	—	—
Reference	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Dicks et al. (1993)	Shaw and Harding (1989)	Farrow et al. (1989)	Leisner et al. (2005)	Martinez-Murcia and Collins (1991a)
Characteristics	<i>Leu. ficulneum</i>	<i>Leu. fructosum</i>	<i>Leu. gasicomitatum</i>	<i>Leuc. gelidum</i>	<i>Leu. inhae</i>	<i>Leu. kimchii</i>	<i>Leu. lactis</i>	<i>Leuc. pseudomesenteroides</i>
Cell morphology	Cocci	Cocci or elongation of cocci	Cocci or elongation of cocci	Cocci or elongation of cocci	Cocci or elongation of cocci	Cocci or elongation of cocci	Cocci or elongation of cocci	Cocci or elongation of cocci
Ammonia from arginine	—	—	—	—	—	—	—	—
Lactic acid configuration	D	D	D	D	D	D	D	D
Hydrolysis of esculin	—	—	+	+	+	ND	—	d
Dextran production	+	—	+	+	v	+	—	ND

(continued)

Table 2.7 (continued)

Characteristics	<i>Leu. ficulneum</i>	<i>Leu. fructosum</i>	<i>Leu. gasicomitatum</i>	<i>Leuc. gelidum</i>	<i>Leu. inhae</i>	<i>Leu. kimchii</i>	<i>Leu. lactis</i>	<i>Leuc. pseudomesenteroides</i>
Growth at Ph 4.8	–	ND	ND	ND	+	ND	–	ND
Growth in 10 % ethanol	ND	ND	ND	ND	ND	ND	–	ND
Growth at 37 °C	–	+	–	–	–	+	+	+
Requirement for TJE	–	–	–	–	–	–	–	–+
G6PDH presente	ND	ND	ND	ND	ND	ND	+	ND
<i>Sugar fermentation</i>								
Amygdalin	ND	ND	–	ND	v	+	ND	ND
Arabinose	–	–	+	ND	v	+	ND	ND
Arbutin	ND	ND	–	–	–	ND	–	ND
Cellulose	ND	ND	ND	ND	ND	ND	–	ND
Cellobiose	–	–	+	+	+	+	–	v
Lactose	–	–	–	–	–	+	+	v
Maltose	+	d	+	+	+	+	+	+
Mannitol	+	+	–	–	+	+	–	–
Mannose	+	–	–	+	+	+	d	+
Raffinose	–	–	+	+	–	+	d	v
Ribose	–	–	+	–	–	+	–	v
Salicin	ND	ND	–	+	d	+	d	v
Sucrose	–	+	+	+	+	+	+	v
Trehalose	+	–	+	+	+	+	–	+
Xylose	–	–	–	+	–	–	–	v
Reference	Antunes et al. (2002)	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Hammes and Hertel (2009)	Hammes and Hertel (2009)

Note + positive; – negative; w weakly positive; v variable reaction; ND no data available

some *Leuconostoc* species is food spoilage. In 1878, a French natural scientist, Philippe van Tieghem studied slime-forming bacteria and described them as *Leuconostoc mesenteroides* (Euzeby 2009) and to date, *Leuconostoc* species are still implicated in the spoilage of packaged, refrigerated foods, particularly meat and meat products.

2.2.1.7 The Genus *Pediococcus*

Species in the genus *Pediococcus* were among the first bacteria to be studied by Louis Pasteur in relation to their role in the spoilage of beer. Their spherical shape and tetrad formation served as key characteristics in their early recognition. Initially, they were the only LAB that were divided in two planes to produce tetrads or pairs. However, more recent taxonomic changes have increased the number of tetrad forming genera to three. In Bergey's Manual of Systematic Bacteriology (Kandler and Weiss 1986) only 8 species were recognised in this genus but now there are 11 species that can be distinguished from each other based on physiological characteristics (Table 2.8). The species commonly referred to as *P. cerevisiae* was very variable and on subsequent study has been lost and the strains within it redistributed amongst the species *P. damnosus*, *P. acidilactici* and *P. pentosaceus*.

Application in Food. Most of the strains originally designated as *P. cerevisiae* that were used as meat starters have been reclassified as *P. acidilactici*. Among the known *Pediococcus* species, *P. acidilactici*, *P. pentosaceus* and *P. halophilus* are most commonly associated with food fermentation.

2.2.1.8 The Genus *Streptococcus*

Species in the genus *Streptococcus* were amongst the earliest bacteria to be recognised by microbiologists because of their involvement in a large number of human and animal diseases. The generic name *Streptococcus* was first used by Rosenbach (1884) to describe the chain-forming, coccus-shaped bacteria associated with wound infections (Rosenbach 1884). The genus *Streptococcus* was originally described based on morphological, serological, physiological and biochemical characteristics and it comprised a wide range of organisms including the highly pathogenic bacteria *S. pneumoniae*, *S. pyogenes* and *S. agalactiae*; the intestinal group D *Streptococci* *S. faecalis* and *S. faecium*; and the economically important group N starter bacteria *S. cremoris* and *S. lactis* (these latter two species were subsequently placed in the genus of *Lactococcus*). There are more than 50 species in the *Streptococcus* genus and most are associated with human and animal disease, and therefore not of relevance to this chapter. Jones (1978) reviewed the composition and differentiation of the genus *Streptococcus* and proposed seven groups, including the strict anaerobes and pneumococci, based on pathogenicity, habitat and oxygen tolerance criteria (Jones 1978). However, based on molecular

Table 2.8 Physiological properties of species in the genus *Pediococcus* used for identification and differentiation

Characteristics	<i>P. acidilactici</i>	<i>P. damnosus</i>	<i>P. dextrinicus</i>	<i>P. halophilus</i>	<i>P. inopinatus</i>	<i>P. lotii</i> Doi et al. (2009)	<i>P. parvulus</i>	<i>P. pentosaceus</i>	<i>P. pentosaceus</i> subsp. <i>intermedius</i>	<i>P. stillessii</i>	<i>P. stiamensis</i>	<i>P. urinaeque</i>
Growth temperature												
35 °C	+	—	+	+	+	+	+	+	+	+	ND	+
40 °C	+	—	±(weak)	±(weak)	±(weak)	—	—	±(weak)	±(weak)	+	ND	±(weak)
45 °C	+	—	±(weak)	—	—	—	—	±(weak)	±(weak)	+	+	±(weak)
50 °C	+	—	—	—	—	—	—	—	—	ND	ND	—
Tolerance of NaCl	10 %	5 %	6 %	>18 %	8 %	ND	8 %	10 %	10 %	8 %	8 %	10 %
Growth at different pH												
4.5	+	+	±	—	+	+	+	+	+	+	—	—
5.0	+	+	+	—	+	+	+	+	+	+	+	—
7.5	+	—	+	±	±	+	±	+	+	+	+	+
8.0	+	—	—	+	—	+	—	+	+	+	+	+
8.5	±	—	—	+	—	—	—	±	±	+	+	+
Catalase	—	—	—	—	—	—	—	—	—	—	—	±
CO ₂ from glucose	—	+	—	—	—	—	—	—	—	—	—	—
Ammonia	—	—	—	—	—	ND	—	+	+	ND	—	—
from arginine												
Hippurate hydrolysis	—	—	—	—	—	ND	—	—	—	ND	ND	+
Formation of acetoin	±	±	—	±	—	ND	—	±	±	ND	ND	—
Configuration of Lactic acid	DL	DL	L(+)	L(+)	DL	DL	DL	DL	DL	DL	DL	L(—)
Litmus milk reaction (0.1 % milk)	±	—	±	—	±	ND	—	+	+	ND	—	ND
Reduction	±	—	±	—	±	—	—	+	+	—	—	ND
Clotting	±	—	±	—	±	—	—	±	+	—	—	ND
Sugar fermentation												
Arabinose	±	—	—	+	—	+	—	+	—	—	+	±
Ribose	+	—	—	—	—	+	—	+	—	+	—	±
Fructose	+	+	+	+	+	+	+	+	+	+	+	+
Rhamnose	±	—	—	—	—	+	—	—	—	—	—	ND
Glucose	+	+	+	+	+	ND	+	+	+	+	+	+
Mannose	+	+	+	+	+	ND	+	+	+	+	+	+

(continued)

Table 2.8 (continued)

Characteristics	<i>P. acidilactici</i>	<i>P. damnosus</i>	<i>P. dextrinicus</i>	<i>P. halophilus</i>	<i>P. inopinatus</i>	<i>P. lotii</i> Doi et al. (2009)	<i>P. parvulus</i>	<i>P. pentosaceus</i>	<i>P. pentosaceus</i> subsp. <i>intermedius</i>	<i>P. stilesii</i>	<i>P. siamensis</i>	<i>P. urinaeque</i>
Galactose	+	±	+	±	+	+	±	+	+	+	+	+
Maltose	-	±	+	+	+	-	±	-	+	+	-	+
Trehalose	±	±	±	+	+	-	+	+	±	+	+	±
Cellobiose	+	+	±	+	+	-	+	±	+	+	+	ND
Sucrose	±	±	±	-	-	-	-	-	+	-	-	+
Lactose	±	-	±	-	+	-	-	±	+	-	+	±
Melibiose	-	-	-	+	-	ND	-	±	±	-	ND	ND
Melezitose	±	±	-	±	-	-	-	-	-	ND	-	ND
Raffinose	±	-	-	-	-	-	-	-	±	-	-	+
Maltotriose	-	±	+	-	±	ND	±	±	±	ND	ND	ND
Dextrin	±	-	+	±	±	ND	±	±	-	ND	ND	±
Starch	-	-	+	-	-	ND	-	-	-	-	ND	-
Inulin	-	-	±	-	-	ND	-	-	±	-	ND	-
Glycerol	±	-	-	±	-	ND	-	-	±	+	-	-
Mannitol	±	-	-	-	-	ND	-	-	-	-	-	±
Sorbitol	-	-	-	+	-	ND	-	+	-	-	-	±
Salicin	-	±	±	+	±	+	-	-	-	+	+	ND
Amygdaloside	±	±	+	+	±	ND	+	-	±	ND	ND	+

Note + positive; - negative; ± weakly positive; v variable reaction; ND no data available

studies, the genus has subsequently undergone major revisions. Similarities in 16S rRNA sequences from the Clostridium branch of gram-positive bacteria indicated that it was appropriate to separate the genus into three genetically distinct groups that were each genera in their own right: *Streptococcus* sensu stricto, *Enterococcus* and *Lactococcus* (Stackebrandt and Teuber 1988; Schleifer and Kilpper-Bälz 1984, 1987). The species remaining in the genus *Streptococcus* include all the pathogenic and the oral (Sherman's Viridans group) species. *Streptococcus thermophilus* is an exception in this genus because it is the only one that is not a pathogen and is an important starter organism for yogurt and cheese manufacture.

Application in Food. *Streptococcus thermophilus* is widely used in combination with *Lb. delbrueckii* subsp. *bulgaricus*, *Lb. lactis* and/or *Lb. helveticus*, as a starter culture for yogurt and related fermented milk products as well as Swiss and Italian-type cheeses (Smit et al. 2005). It has an optimum incubation temperature above 40 °C. There is a special relationship between *S. thermophilus* and *Lb. delbrueckii* subsp. *bulgaricus* in which *S. thermophilus* produces formic acid that promotes the growth of the other species which, in turn, provides flavour compounds (acetaldehyde) and the proteolytic activity to ensure that the *S. thermophilus* can grow in milk.

2.2.1.9 The Genus *Bifidobacterium*

According to the Taxonomic Outline of the Prokaryotes (Garrity et al. 2004), the genus *Bifidobacterium* belongs to the phylum *Actinobacteria*, class *Actinobacteria*, subclass *Actinobacteridae*, order *Bifidobacteriales*, family *Bifidobacteriaceae*. The other genera in this family are: *Aeriscardovia*, *Falcivibrio*, *Gardnerella*, *Parascardovia* and *Scardovia*. Although, the genus *Bifidobacterium* is only poorly phylogenetically related to LAB and its species exploit a different metabolic pathway for the degradation of hexoses to the 'genuine' LAB, it has been listed amongst LAB in much of the traditional literature. In addition, species in the genus *Bifidobacterium* are as important as species in the genus *Lactobacillus* for food microbiology and human nutrition due to their role in food and feed production and preservation. Many species also exhibit probiotic properties. For these reasons, we include the genus *Bifidobacterium* in this chapter. The genus *Bifidobacterium* is comprised of 44 species and 9 subspecies (Table 2.9). Using a number of different methods and models for phylogenetic analyses, Felis and Dellaglio (2007) affirmed that, within the genus *Bifidobacterium*, there were distinct groups, each containing several associated species (Felis and Dellaglio 2007). These groups are: *B. adolescentis* group, *B. pullorum* group, *B. boum* group and *B. pseudolongum* group.

Table 2.9 Physical properties of species in the genus *Bifidobacterium* used for species identification and differentiation

Species	Sugar fermentation												
	Sor- bitol	L- arabinos	Raf- finose	D- Ribose	Starch	Lactose	Inulin	Cello- biose	Mel- zitose	Gluc- onate	Xylose	Man- nose	Fruc- tose
<i>B. actinocoloniiforme</i> ^a	-	+	-	+	-	ND	-	+	-	-	+	-	+
<i>B. adolascensis</i> ^b	v	+	+	+	+	+	v	+	+	+	+	v	+
<i>B. angulatum</i> ^b	d	+	+	+	-	+	+	-	-	v	+	-	+
<i>B. animalis</i> ^b	-	-	+	-	+	+	-	v	-	-	+	-	-
<i>B. asteroides</i> ^b	-	-	+	+	-	-	ND	+	-	v	+	+	+
<i>B. biavatii</i>	-	-	+	-	-	+	-	-	+	ND	+	-	+
<i>B. bifidum</i> ^b	-	-	-	-	-	+	-	-	-	-	-	-	-
<i>B. bifenitum</i> ^c	-	+	+	+	-ND	-	-	-	-	+	-	+	+
<i>B. bohemianum</i> ^c	-	-	+	-	+	ND	+	-	-	ND	-	-	+
<i>B. bombi</i> ^b	-	+	+	-	+	d	v	ND	v	ND	-	-	-
<i>B. boum</i> ^b	-	+	+	+	+	+	v	v	v	-	-	+	v
<i>B. breve</i> ^b	+	+	+	-	-	ND	-	+	+	ND	+	+	+
<i>B. callitrichos</i> ^d	+	+	+	+	+	+	+	+	+	+	+	+	+
<i>B. catenulatum</i> ^b	+	+	+	+	+	+	v	+	+	v	+	+	+
<i>B. choerinum</i> ^b	-	+	-	-	+	-	+	ND	-	-	-	-	-
<i>B. coryneforme</i> ^b	-	+	+	+	+	-	v	+	+	+	+	+	+
<i>B. cuniculi</i> ^b	-	+	+	+	+	v	-	v	v	+	+	+	v
<i>B. dentium</i> ^b	-	+	+	+	+	+	-	+	+	+	+	+	-
<i>B. gallinarum</i> ^b	-	-	+	+	+	-	-	-	-	-	+	+	+
<i>B. galinarum</i> ^b	-	+	+	+	+	-	+	-	-	-	+	+	+
<i>B. indicum</i> ^b	+	+	+	+	-	+	-	+	-	ND	+	+	+
<i>B. kashiwanohensis</i> ^e	+	+	+	+	-	+	-	+	-	+	+	+	+
<i>B. longum</i> ^b	-	+	+	+	-	+	-	-	+	-	v	+	-
<i>B. longum</i> subsp. <i>infantis</i> ^b	-	+	+	+	-	+	v	-	-	-	v	v	-
<i>B. longum</i> subsp. <i>suis</i> ^b	-	+	+	+	-	+	+	v	v	+	+	+	+
<i>B. magnum</i> ^b	-	-	+	-	-	v	+	-	-	ND	+	-	+
<i>B. merycicum</i> ^b	-	+	+	+	+	+	-	v	-	-	+	-	+
<i>B. minimum</i> ^b	-	+	+	-	+	+	-	ND	-	-	-	v	-

(continued)

Table 2.9 (continued)

Species	Sugar fermentation																			
	Sor- bitol	L- arabinos	Raf- fiose	D- Ribose	Starch	Lactose	Inulin	Cello- biose	Mel- ezitose	Gluc- onat	Xylose	Man- nose	Fruic- tose	Galaet- ose	Sucrose	Malt- ose	Treha- lose	Meli- biose	Manni- tol	Saltcin
<i>B. mongoliense</i> ^b	—	+	+	+	+	+	—	+	—	w	—	—	—	+	ND	—	ND	ND	—	+
<i>B. pseudocatenulatum</i> ^b	—	+	+	+	+	+	—	v	—	v	+	+	+	+	+	+	v	—	+	—
<i>B. pseudolongum</i> ^b	—	+	+	+	+	+	—	+	—	—	+	—	+	+	+	+	ND	ND	ND	±
<i>B. pseudolongum</i> subsp. <i>Globosom</i> ^b	—	v	+	+	+	+	—	—	—	—	+	—	+	+	+	+	—	+	—	—
<i>B. psychraerophilum</i> ^f	—	+	—	+	—	+	—	+	+	w	+	—	+	+	+	+	ND	ND	—	+
<i>B. pullorum</i> ^b	—	—	+	—	—	—	—	—	—	—	—	—	+	+	+	+	—	+	—	—
<i>B. reuteri</i> ^d	—	—	+	—	+	ND	—	w	w	ND	+	—	ND	—	ND	+	ND	w	—	+
<i>B. ruminantium</i> ^b	—	—	—	+	+	—	—	—	—	—	—	—	+	+	+	+	—	—	+	+
<i>B. saeculare</i> ^b	—	+	+	+	—	+	+	—	—	—	+	—	+	+	+	+	+	+	—	—
<i>B. sagittatus</i> ^d	—	+	+	+	—	+	—	+	—	w	+	—	+	+	+	+	ND	+	—	+
<i>B. scardovii</i> ^b	—	+	+	+	ND	ND	ND	ND	w	ND	ND	+	ND	—	ND	+	ND	—	—	ND
<i>B. stellerboschense</i> ^d	+	+	+	+	—	ND	—	—	+	ND	+	—	+	+	+	+	ND	ND	+	+
<i>B. subtilis</i> ^b	+	+	—	—	+	—	—	—	—	+	—	—	+	+	+	+	—	ND	—	—
<i>B. thermophilum</i> ^b	—	—	+	+	+	+	—	v	v	—	—	v	+	+	+	+	v	+	—	+
<i>B. thermacidophilum</i> ^b	+	+	+	v	+	ND	v	ND	+	ND	v	—	ND	+	ND	ND	ND	+	—	+
<i>B. tsurumense</i> ^b	—	+	+	+	+	+	—	+	—	+	+	+	+	+	+	+	ND	ND	+	+

Note: + positive; — negative; w weakly positive; v variable reaction; ND no data available; ^a data from the references Killer et al. (2011); ^b data from the references Goodfellow (2012); ^c data from the references (Killer et al. 2011); ^d data from the references (Endo et al. 2012); ^e data from the references (Montia et al. 2011); ^f data from the references (Simpson et al. 2004)

2.2.2 Species of Lactic Acid Bacteria

Although more than 50 genera of LAB have been validly published till now, a considerable number of species have been described and increased sharply. The most important genera are described above, among which (alphabetically) *Enterococcus*, *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Pediococcus* and *Streptococcus* are regarded as the most important food microorganisms. Thus, the most important species in these genera are described in more detail in this section.

Species of *Enterococcus*. Bacteria from the genus *Enterococcus* were first observed by Thiercelin (1899) and Andrews and Horder (1906) used the name *S. faecalis* for the *Enterococcus*-type organism that they isolated from a patient with endocarditis. In 1937, Sherman first described those organisms from physiological and biochemical and serological characteristics (Devriese et al. 1993; Seegers 2002). To date, there were 45 validly described species in the genus *Enterococcus* from a range of different sources (Table 2.10).

Species of *Lactobacillus*. *Lactobacillus* is the largest group of LAB and includes some of the most important species involved in food microbiology and human nutrition; several *Lactobacillus* species are essential in fermented food production and are used as starter cultures or food preservatives. Moreover, certain species of human origin are being exploited as probiotics or vaccine carriers (Seegers 2002). This genus includes a large number of GRAS species (Generally Recognised As Safe). The number of species described has increased sharply in recent years (Fig 2.2). There were 74 new species of *Lactobacillus* described between the year of 2001 and 2010. This is the same number of new *Lactobacillus* species described in the whole of the twentieth century. This amazing increase in the number of *Lactobacillus* species identified has a strong relationship with advances in the development of innovative molecular techniques and their application to microbial taxonomy and identification. This was particularly evident in the 1980s when a large number of new species were identified using 16S rRNA gene sequence analysis and then again in the last 10 years due to the advent of polyphasic taxonomic methods.

Species of *Lactococcus* On the basis of exhaustive reinvestigations, N streptococci (Lancefield 1933) were separated from the oral streptococci, enterococci and hemolytic streptococci, and placed in a new genus, *Lactococcus*, by Schleifer et al. (1985, Lancefield (1933). In recent years, molecules have allowed detection and differentiation of a number of new species. However, the genus remains relatively compact and comprises only 12 species (Table 2.5). Of these, *Lactococcus lactis* is the most important in industrial fermentation and especially for the manufacture of dairy products. There are four subspecies of *Lc. lactis*: *Lc. lactis* subsp. *lactis*, *Lc. lactis* subsp. *cremoris*, *Lc. lactis* subsp. *hordniae*, *Lc. lactis* subsp. *tructae*. Subsp. *lactis* is the most important commercially used LAB.

Species of *Pediococcus* This genus was one of the first LAB to be studied intensively by food microbiologists because of their association with beer spoilage. Species in *Pediococcus* can be confused with micrococci and aerococci because of

Table 2.10 Detailed information of species of *Enterococcus*

Species	Source	Principal habitats	References
<i>E. alcedinis</i>	New	Common kingfisher	Frolkova (2013)
<i>E. aquimarinus</i>	New	Sea water	Švec et al. (2005a)
<i>E. asini</i>	New	Caecum of donkeys	De vaux (1998)
<i>E. avium</i>	Transfer	Poultry and mammalian intestines	Collins et al. (1984)
<i>E. cacciae</i>	New	Human stools	Carvalho et al. (2006)
<i>E. canintestini</i>	New	Fermented tea leaves in	Naser et al. (2005)
<i>E. canis</i>	New	Faecal samples of healthy dogs	De graef et al. (2001)
<i>E. casseliflavus</i>	Transfer	Grass, silage, plants, soil	Collins et al. (1984)
<i>E. cecorum</i>	Transfer	Clinical origin, animals	Williams et al. (1989)
<i>E. columbae</i>	New	Pigeon intestines	Devriese et al. (1990)
<i>E. devriesei</i>	New	Animal sources	Švec et al. (2005b)
<i>E. dispar</i>	New	Human sources	Collins et al. (1991)
<i>E. durans</i>	Transfer	Clinical origin, animals	Collins et al. (1984)
<i>E. eurekaensis</i>	New	Swine-manure storage pit	Cotta et al. (2013)
<i>E. faecalis</i>	Transfer	Human and other animal intestines	Schleifer and Kilpper-Bhlz (1984)
<i>E. faecium</i>	Transfer	Human and other animal intestines, including poultry	Schleifer and Kilpper-Bhlz (1984)
<i>E. gallinarum</i>	Transfer	Poultry intestines	Collins et al. (1984)
<i>E. gilvus</i>	New	Human clinical specimens	Tyrrell et al. (2002)
<i>E. haemoperoxidus</i>	New	Water	Švec et al. (2001)
<i>E. hermanniensis</i>	New	Modified-atmosphere-packaged broiler meat and canine tonsils	Koort et al. (2004)
<i>E. hirae</i>	New	Young chickens	Farrow and Collins (1985)
<i>E. italicus</i>	New	Italian cheeses	Fortina et al. (2004)
<i>E. lactis</i>	New	Italian raw milk cheeses	Morandi et al. (2012)
<i>E. lenanii</i>	New	Swine-manure storage pit	Cotta et al. (2013)
<i>E. malodoratus</i>	Transfer	Originally from Gouda cheese	Collins et al. (1984)
<i>E. moraviensis</i>	New	Water	Švec et al. (2001)

(continued)

Table 2.10 (continued)

Species	Source	Principal habitats	References
<i>E. mundtii</i>	New	Grass, silage, plants, soil	Collins et al. (1986)
<i>E. pallens</i>	New	Human clinical specimens	Tyrrell et al. (2002)
<i>E. phoeniculicola</i>	New	Uropygial gland of the Red-billed Woodhoopoe	Law-Brown and Meyers (2003)
<i>E. plantarum</i>	New	Plants	Švec et al. (2012)
<i>E. pseudoavium</i>	New		Collins et al. (1989)
<i>E. quebecensis</i>	New	Water	Sistek et al. (2012)
<i>E. raffinosus</i>	New	Clinical isolates, endocarditis	Collins et al. (1989)
<i>E. ratti</i>	New	Associated with enteric disorders in animals	Teixeira et al. (2001)
<i>E. rivorium</i>	New	Water of pristine brooks	Niemi et al. (2012)
<i>E. rotai</i>	New	Environment	Sedláček et al. (2013)
<i>E. saccharolyticus</i>	Transfer	Bedding and skin of cattle	Chen et al. (2013)
<i>E. silesiacus</i>	New	The gut of a termite	Švec et al. (2006)
<i>E. solitarius</i>	New		Collins et al. (1989)
<i>E. sulfurous</i>		Yellow-pigmented <i>E. species</i>	Martinez-Murcia and Collins (1991b)
<i>E. termites</i>	New		Švec et al. (2006)
<i>E. thailandicus</i>	New	Fermented sausage in Thailand	Tanasupawat et al. (2008)
<i>E. ureasiticus</i>	New	Water	Sistek et al. (2012)
<i>E. urelyticus</i>	New	Environment	Sedláček et al. (2013)
<i>E. viikkiensis</i>	New	Broiler products	Rahkila et al. (2011)

Note new new species; transfer transfer from group D streptococci from Devriese and Pot (1995)

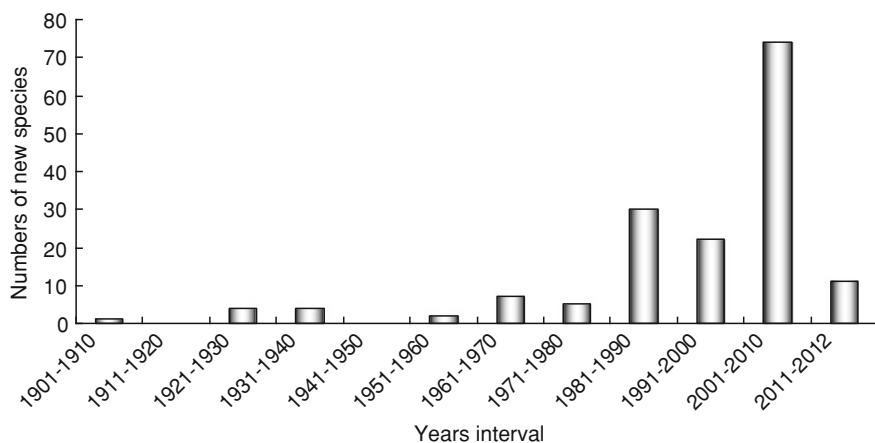


Fig. 2.2 Number of new species of *Lactobacillus* found between 1901 and 2012

morphological similarities, pseudocatalase production and salt tolerance (Garvie 1986). In Bergey's Manual of Systematic Bacteriology (Garvie 1986) eight species were recognised but the number of species has now increased to nine (Hammes and Hertel 2009). To date, there were 15 validly described species in the genus (<http://www.bacterio.net/p/pediococcus.html>).

Species of *Leuconostoc* *Leuconostoc* is the predominant genus among the LAB on plants, with *Leuc. mesenteroides* subsp. *mesenteroides* as the principal species (Mundt 1970). *Leuconostocs* are traditionally found in association with plant matter, fermented dairy products and wines. The first species was isolated in 1878 by Cienkowski. There were four species listed in the Bergey's Manual of Systematic Bacteriology (Garvie 1986) but, at the time of writing, there are now 12 species in the genus (Table 2.7).

Species of *Streptococcus* The genus *Streptococcus* is large, containing numerous clinically significant species that are responsible for a wide variety of infections in man and in animals. To date there are 82 approved listed species (<http://www.bacterio.net/s/streptococcus.html>).

2.3 Genetic Diversity of Lactic Acid Bacteria

2.3.1 Biodiversity of Lactic Acid Bacteria as Identified by Culture-Dependent Approaches

LAB have often been isolated and identified from traditionally fermented dairy products in the last 20 years. These fermented dairy products include busa (Turkestan), cieddu (Italy), dadhi (India), kefir (Balkans), kumiss (Steppes), kurut

(Himalayan regions), laban zabadi (Egypt), mazun (Armenia), taette (N. Europe), skyr (Iceland), masl (Iran), crowdies (Scotland), kuban and yogurt (Miyazaki and Matsuzaki 2008). Studies of the different types of raw milk used (including cow, goat, ewe, mare, camel, buffalo and yak) show a great diversity of LAB at the genus and species level. For example, 12 different species of LAB were isolated and identified during the manufacture and storage of Anevato cheese, a traditional spreadable Greek cheese made from raw goat's or ewe's milk: three species were from the genus *Lactococcus* (*Lc. lactis*, *Lc. garviae*, *Lc. raffinolactis*), three species were from the genus *Leuconostoc* (*Leuc. mesenteroides*, including the subspecies *mesenteroides* and *dextranicum*, *Ln. paramesenteroides* and *Leuc. lactis*) and six species were from the genus *Lactobacillus* (*Lb. plantarum*, *Lb. coryneformis*, *Lb. paracasei*, *Lb. brevis*, *Lb. bifementans* and *Lb. viridens*).

2.3.1.1 LAB in Koumiss

Koumiss (also known as koumiss, kumiss, kumys, kumyz, kimiz or coomys) is a very popular drink consumed in countries from the Cancasus region of Kazakhstan, Azerbaijan, Turkey (kumye) and in China and Mongolia (Tooner 1994). In the seventh century, koumiss became an everyday drink of the Mongolian tribes where, today, the product is known as airag, arrag, irag, chige or chigo (in the Mongolian language) (Zhang and Zhang 2012). Traditional koumiss is produced from mare's milk and in Mongolia it is also produced from camel's milk. In Europe and North America, a koumiss-like product is made from full or skimmed cow's milk (Mann 1989; Di Cagno et al. 2004).

The microflora isolated from koumiss has not been well defined, but consist mainly of LAB and yeast. Indeed, *Saccharomyces unisporus* was identified as the principal microorganism from traditional koumiss in Kazakhstan (Montanari and Grazia 1997; Park et al. 2006). Sometimes, acetic acid bacteria have also been found (Zhang and Zhang 2012; Park et al. 2006). In recent years, numerous studies have been published clarifying the diversity of LAB isolated and grown in pure culture from traditional koumiss in China and Mongolia (Table 2.11).

2.3.1.2 LAB in Traditional Fermented Camel's Milk and Related Products

Camels (*Camelidae*) mainly inhabit desert and semi-desert regions, with major populations distributed within Sudan and other African countries, Arab countries, India, Mongolia and the northwest region of China (Jiri et al. 2009). Raw camel milk products, fresh unpasteurised milk or spontaneously fermented milk (such as suusac) are also an important component of the daily diet of pastoralists in East African countries such as Kenya and Somalia (Farah et al. 2007). In Sudan, fresh unpasteurised camel's milk and fermented camel's milk (gariss) are widely consumed by pastoralist communities living in the arid and semi-arid regions of the

Table 2.11 Composition and distribution of lactic acid bacteria in koumiss of different regions of Mongolia

Country/ Regions	Number of samples	Number of isolates	Species of LAB	Total	Predominant species	References
Mongolia	3	–	<i>Lb. helveticus</i>	–	<i>Lb. helveticus</i>	Uchida et al. (2007)
			<i>Lb. kefir</i>			
			<i>Lb. paracasei</i>			
			<i>Lb. plantarum</i>			
			<i>Lb. farcininis</i>			
			<i>Lb. curvatus</i>			
	22	367	<i>Lb. helveticus</i>	93	<i>Lb. helveticus</i>	Watanabe et al. (2008)
			<i>Lb. kefiranoferiens</i>	35	<i>Lb. kefiranoferiens</i>	
			<i>Lb. casei</i>	13		
			<i>Lb. diolivorans</i>	1		
			<i>Lb. farcininis</i>	1		
			<i>Lb. higardii</i>	1		
			<i>Lb. kefir</i>	4		
			<i>Lb. parafarranginis</i>	1		
			<i>Lb. plantarum</i>	8		
			<i>Lc. lactis</i> subsp. <i>lactis</i>	7		
	5	30	<i>Leuc. mesenteroides</i>	13		Menghebilige et al. (2004)
			<i>Leuc. pseudomesenteroides</i>	2		
			<i>Lb. fermentum</i>	1		
			<i>Lactococcus</i>	2		
			<i>S. thermophilus</i>	1		
			<i>E. faecium</i>	1		
			<i>Lb. acidophilus</i> group	20	<i>Lb. acidophilus</i> group	
			<i>Lb. casei</i>	1		

(continued)

Table 2.11 (continued)

Country/ Regions	Number of samples	Number of isolates	Species of LAB	Total	Predominant species	References
			<i>Lb. plantarum</i>	9		
			<i>Lb. paracase</i> subsp. <i>paracase</i>	–		Burentegusi et al. (2002)
			<i>Lb. coryniformis</i>	–		
			subsp. <i>coryniformis</i>			
			<i>Lb. curvatus</i>			
			<i>Lb. kefiranoferiens</i>			

country (Ashmaig et al. 2009). Traditionally, fermented camel's milk and are also popular in China (*shubat* in the Hazakh language) (and Mongolia (*hogormag* in the Mongolian language) (Shuangquan and Miyamoto 2004). Early reports indicated that the bacterial component of the microflora of traditional fermented camel milk products was dominated by LAB species belonging to several different genera. In recent years, in order to improve the spontaneous traditional fermentation and develop suitable starter cultures for safer production of traditional food, many species of LAB have been isolated and identified from camel's milk by different research institutes and in different countries and regions (Table 2.12).

2.3.1.3 LAB in Traditional Fermented Cow's Milk and Related Products

Historically, fermented dairy products were developed by nomadic tribes people to preserve the valuable nutrients from fresh raw milk. With the advancement of human civilization and changes in life style, the role of these foods as the sole source of nutrition for nomadic people has ceased. However, the process of making these traditional fermented dairy products continues to be developed and handed down through the generations in the minority ethnic populations of China. Nowadays, many different fermented dairy products are consumed by minority ethnic people living in Mongolia, Xinjiang, Tibet and other provinces of China. However, as cows are currently the main domestic livestock variety in China, cow's milk is the major raw material for making a variety of these dairy products, including *dairy fan*, *yogurt*, *Eedsen Su Aarchi* and *wurum*. The Key Laboratory of Dairy Biotechnology and Engineering, Ministry of Education P.R.China have long been engaged in isolating and identifying LAB from products traditionally fermented from cow's milk in China. From 2001 to the present, a wide variety have been isolated and identified in a selection of different ethnic minority areas of China, Mongolia and Tibet (<http://www.bio149.cn/html/labcc.html>) (Table 2.13).

2.3.1.4 LAB in Kurut and Other Fermented Yak's Milk Products

Yaks are one of the most ancient bovine species in China and mainly distributed in the Qing-Tibetan plateau at an average altitude of 4,000 m. China has approximately 13 million yaks which is the largest number for any country in the world (Zhang et al. 2008). China has both the largest number of yak herds and the highest associated milk production in the world (Zhu and Zhang 2005). Many varieties of dairy products including kurut, qula, butter and cheese are prepared from yak's milk and consumed by Tibetan people in the Qing-Tibetan plateau regions of China. Kurut is one of the most important fermented products and is made using traditional production methods as reported by Chen et al. (2009). The high altitude and special climate of the Tibetan plateau represents a distinct ecological with a wide biodiversity. Such diversity of species, including a diversity of LAB, results

Table 2.12 Diversity of LAB in naturally fermented camel's milk products

Species of LAB	Number of isolates	Predominant species	Type of samples and country of origin
<i>E. avium</i>	1 ^d	—	Fermented milk, China
<i>E. durans</i>	2 ^d	—	Fermented milk, China
<i>E. faecalis</i>	— ^b ; 2 ^d	—	Shubat, India; fermented milk, China
<i>E. faecium</i>	— ^b ; — ^e	<i>E. faecium</i>	Shubat, India; fermented milk, China
<i>Lb. casei</i> , subsp. <i>pseudoplanatarum</i>	1 ^d	—	Fermented milk, China
<i>Lb. acidophilus</i>	1 ^d ; — ^e	—	Fermented milk, China
<i>Lb. brevis</i>	1 ^a ; — ^b	—	Gariss, Sudan; Shubat India
<i>Lb. casei</i> subsp. <i>casei</i>	5 ^d	—	Fermented milk, China
<i>Lb. casei</i>	— ^e	—	Fermented milk, China
<i>Lb. curvatus</i>	1 ^d	—	Fermented milk, China
<i>Lb. divergens</i>	1 ^a	—	Gariss, Sudan
<i>Lb. farcinini</i>	1 ^d	—	Fermented milk, China
<i>Lb. fermentum</i>	1 ^a ; 7 ^c ; 1 ^d	—	Gariss, Sudan
<i>Lb. gasseri</i>	1 ^a	—	Gariss, Sudan
<i>Lb. helveticus</i>	— ^b ; — ^e	—	Shubat, India; fermented milk, China
<i>Lb. paracasei</i> subsp. <i>paracasei</i>	64 ^e	<i>Lb. paracasei</i> subsp. <i>paracasei</i>	Gariss, Sudan
<i>Lb. paracasei</i>	1 ^a	—	Gariss, Sudan
<i>Lb. plantarum</i>	7 ^a ; 3 ^c ; 4 ^d	<i>Lb. plantarum</i>^a	Gariss, Sudan; fermented milk, China
<i>Lb. rhamnosus</i>	1 ^a	—	Gariss, Sudan

(continued)

Table 2.12 (continued)

Species of LAB	Number of isolates	Predominant species	Type of samples and country of origin
<i>Lb. sakei</i>	— ^b	<i>Lb. sakei</i>	Shubat India
<i>Lc. alimentarium</i>	1 ^a	—	Gariss, Sudan
<i>Lc. lactis</i>	— ^b ; 2 ^d	—	Shubat, India; fermented milk, China
<i>Lc. raffinolactis</i>	6 ^a	—	Gariss, Sudan
<i>Lc. subsp.cremoris</i>	— ^e	—	Fermented milk, China
<i>Leuc. lactis</i>	— ^b ; — ^e	—	Shubat, India; fermented milk, China
<i>Leuc. mesenteroides</i> subsp. <i>dextranum</i>	2 ^d	—	Fermented milk, China
<i>Leuc. mesenteroides</i> subsp. <i>mesenteroides</i>	1 ^d	—	Fermented milk, China
<i>W. hellenica</i>	— ^b	—	Shubat, India

Note ^a Represent data from Ashmaig et al. (2009); ^b represent data from Rahman et al. (2009); ^c represent data from Sulieman et al. (2006); ^d represent data from Menghebilige et al. (2004); ^e represent data from Shuangquan et al. (2004)

Table 2.13 The species and number of isolations of LAB from traditionally fermented cow's milk products in different regions

Species of LAB	Inner Mongolia	Tibet	Yunnan Province, China	Tibetan regions of Gansu and Sichuan Provinces, China	Mongolia
<i>E. durans</i>	10	7	1	9	3
<i>E. faecalis</i>	6	2	–	–	1
<i>E. faecium</i>	5			1	
<i>E. italicus</i>	1				
<i>Lb. acetotolerans</i>	1				
<i>Lb. brevis</i>	4			4	3
<i>Lb. casei</i>	106			31	16
<i>Lb. crispatus</i>	1				
<i>Lb. crustorum</i>		1			
<i>Lb. curvatus</i>	1				
<i>Lb. delbrueckii</i> subsp. <i>bulgaricus</i>	4			11	129
<i>Lb. diolivorans</i>	68			1	15
<i>Lb. fermentum</i>	5	1	10	10	42
<i>Lb. helveticus</i>	153	2	56	88	169
<i>Lb. hilgardii</i>	4		1	1	
<i>Lb. kefiranofaciens</i> subsp. <i>kefiranofaciens</i>	3				
<i>Lb. kefiranofaciens</i> subsp. <i>kefirgranum</i>	9		5		
<i>Lb. kefirgranum</i>	10		8		
<i>Lb. kefiri</i>	27		1		7
<i>Lb. parabuchneri</i>	15				
<i>Lb. plantarum</i>	68	8	1	4	7
<i>Lb. pontis</i>	5				
<i>Lb. reuteri</i>	11				
<i>Lb. rhamnosus</i>	4				
<i>Lc. garvieae</i>		1	2		
<i>Lc. lactis</i> subsp. <i>cremoris</i>	6	3		6	
<i>Lc. lactis</i> subsp. <i>lactis</i>	132	9	4		6
<i>Lc. raffinolactis</i>	3			13	
<i>Leuc. lactis</i>	2	1		1	22
<i>Leuc. mesenteroides</i>	6				38
<i>Leuc. mesenteroides</i> subsp. <i>mesenteroides</i>	97	3		49	16
<i>Leuc. pseudomesenteroides</i>	5				
<i>S. thermophilus</i>	18			38	182

in a very specific microflora associated with yak's milk and its products (Li et al. 2002; Luo et al. 2005). These differences in biodiversity of bacteria are very important in forming the typical features of traditional fermented dairy products in different regions. Several studies have reported the species composition and biodiversity of LAB in yak's milk products from different regions of China including Tibet (Zhang et al. 2008; Airidengcaিকে et al. 2010; Duan et al. 2008) and the provinces of Qihai (Sun et al. 2010), Gansun (Bao et al. 2012a) and Sichuan (Bao et al. 2012b). It was described in Table 2.14. A predominance of *L. helveticus* was recorded in qula and whey products from Gansu and Sichuan provinces, respectively. It also predominated in kurut from Gansu province. However, the predominated species in kurut from Sichuan, Qinghai and Tibet were *Lb. helveticus*, *S. thermophilus* and *Lb. fermentum*, respectively. Other species from the genera *Lactobacillus*, *Enterococcus*, *Lactococcus*, and *Leuconostoc* were also isolated at a low frequency. The number of identified species ranged from one to over 20 depending on the product. The overall distribution pattern showed that the predominant species and biodiversity of LAB in yak's milk products from the four geographically distant regions varied substantially.

2.3.2 Biodiversity of Lactic Acid Bacteria as Determined by Culture-Independent Approaches

Before 1990, isolation and growth of microorganisms in pure culture was the only method for their identification and characterisation. For this reason, early species composition studies and biodiversity analyses were mainly achieved based on culture-dependent methods. However, it is well known that less than 1 % of microorganisms can be cultivated in the laboratory (Ward et al. 1990; Engelen et al. 1998). Furthermore, the in vitro growth step can lead to underestimates in biodiversity analysis because slow-growing species or species present in low numbers may be out-competed by faster growing or more prevalent species (Hugenholtz et al. 1998). The emergence of cultivation-independent approaches has overcome these issues and provides unique opportunities to reveal the diversity of previously unculturable prokaryotic species by analysis of the ribosomal RNA (rRNA) genes of mixed microbial populations from environmental samples (Hugenholtz et al. 1998). This is far more representative of the real spectrum of microorganisms and their genes that are active in the habitat of choice. To comprehensively assess the microbial composition of dairy products and other fermented food, studies on the microbial composition of LAB have been clarified using culture-independent approaches.

Table 2.14 Species and numbers of isolates of LAB from fermented yak's milk and related products in regions where Tibetan tribes people live regions

Species of LAB	Sichuan province ^a			Gansu province ^b			Tibet ^c Qinghai ^c province					
	Kurut	Raw milk	Qula	Whey	Butter	Kurut	Raw milk	Qula	Whey	Butter	Kurut	Kurut
<i>E. hormaechei</i> subsp. <i>steigerwaltii</i>			1									
<i>E. durans</i>	1							1		2	8	7
<i>E. faecalis</i>												5
<i>E. faecium</i>	1		1								4	1
<i>Lb. brevis</i>						1						
<i>Lb. buchneri</i>		1										
<i>Lb. casei</i>	7	1	7	1		17					24	
<i>Lb. coryniformis</i> subsp. <i>torquens</i>					2 *							
<i>Lb. delbrueckii</i> subsp. <i>bulgaricus</i>	5		4	2		11						23
<i>Lb. diolivorans</i>									1			
<i>Lb. fermentum</i>	1		5	2	1	6	1	1	1		51 *	3
<i>Lb. helveticus</i>	7	4	22 *	8 *		50 *	4	23 *	10 *		4	13
<i>Lb. hilgardii</i>					1				1			
<i>Lb. kefir</i>	4								2			
<i>Lb. plantarum</i>		5						2				12
<i>Lb. rari</i>	1											

(continued)

Table 2.14 (continued)

Species of LAB	Sichuan province ^a				Gansu province ^b				Tibet ^c Qinghai ^c province			
	Kurut	Raw milk	Qula	Whey	Butter	Kurut	Raw milk	Qula	Whey	Butter	Kurut	Kurut
<i>Lb. ivanum</i>	4			1								
<i>Lc. lactis</i> subsp. <i>cremoris</i>	4	1						2			4	5
<i>Lc. lactis</i> subsp. <i>lactis</i>	5	1	1	1				8			3	15
<i>Lc. raffinolactis</i>	5	1	1	1				8				
<i>Leuc. citreum</i>	6	2	6	1			4	1	2			5
<i>Leuc. lactis</i>	5	13	3	2							1	8
<i>Leuc. mesenteroides</i> subsp. <i>mesenteroides</i>	4	29 [*]	19	8	1	21	2	1	5	1	3	4
<i>S. thermophilus</i>	20 [*]	1	7					4	7	4 [*]		51 [*]
<i>W. cibaria</i>			1									

* Represent the predominant species in a given product by region. **Bold** means the species is the predominated species in this samples or region
Note ^a Represented the data from Bao et al. (2012a); ^b Represented the data from Bao et al., 2012a) ^c represented the data from Sun et al. (2010)

2.3.2.1 Microbial Diversity in Traditionally Fermented Dairy Products as Determined by Metagenomic Sequence Analysis

Culture-independent approaches have been used increasingly to determine the composition of complex microbial communities. These procedures have enabled the simultaneous characterisation of whole ecosystems and the identification of many species from these sources (Quigley et al. 2011). There is a vast amount of information held within the genomes of microorganisms that cannot be cultured in conventional ways and metagenomics techniques are one of the key technologies now used to access and investigate this potential. These techniques have detected all of the commonly cultured species, as well as some previously undetected microorganisms. In recent years, pyrosequencing has been used increasingly to study the diversity and dynamics of the bacterial populations of an Irish kefir grain and its corresponding fermented products (Dobson et al. 2011) and other fermented food (Humblot and Guyot 2009; Roh et al. 2010; Jung et al. 2011). Biodiversity of LAB in traditionally fermented dairy products (including fermented cow's milk, koumiss and kurut) in China, Mongolia and Russia are also currently being investigated using pyrosequencing technology in the Key Laboratory of Dairy Biotechnology and Engineering, Ministry of Education, China (Inner Mongolia Agricultural University) to complement our previous extensive culture-dependent studies (Bao et al. 2012a, b). Although these data are not published a summary will be provided in the following sections.

Microbial Diversity in Traditionally Fermented Cow's Milk

Samples of fermented cow's milk were collected from the Xinjiang Uygur Autonomous Region, China ($n = 10$ from Zhaosu County and 12 from Tekesi County) and subjected to microbial diversity studies using 454 pyrosequencing (unpublished data). This resulted in a total of 245,423 high quality 16S rRNA sequences with each sample producing an average of 13,062 sequences (range = 7913–16476, SD = 3096). After PyNAST alignment and 100 % sequence identity clustering analysis, 11,790 representative sequences were obtained. RDP combined with the BLAST homology sequence alignment cluster method were then used to identify the sequences to phylum and genus level. The sequences were distributed amongst seven phyla (Fig. 2.3), four of which were the bacterial phyla *Firmicutes*, *Proteobacteria*, *Bacteroides* and *Actinobacteria* which together accounted for 99 % of the sequences. A further two of the phyla were also bacteria, TM7 and *Verrucomicrobia*, but they were represented by only 0.01 and 0.007 % of the total sequences, respectively.

All the sequences were also identified to genus level (Fig. 2.4). There were 11 genera represented in these samples (at a level of at least 0.03 % of sequences/sample), of which XX were LAB and, of those, *Lactobacillus* was regarded as the most abundant. In some five samples 99 % of sequences could be attributed to

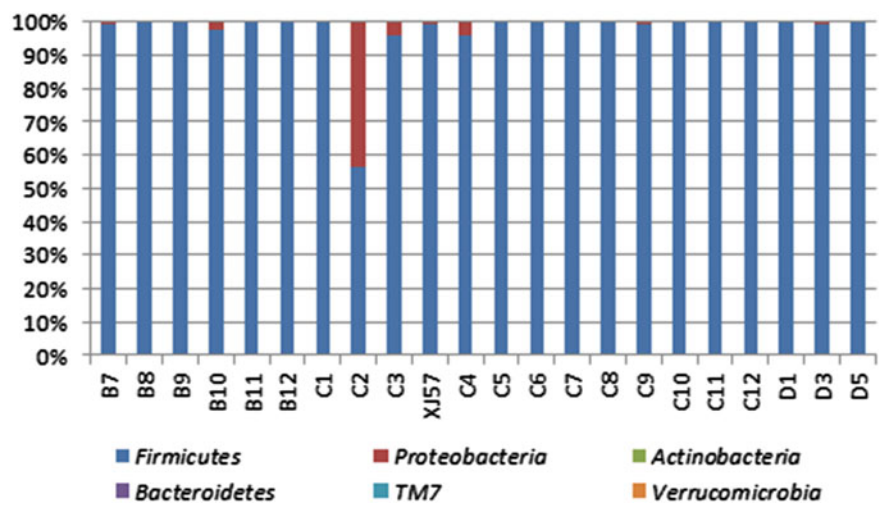


Fig. 2.3 The proportion of 16S rRNA sequences from samples of traditionally fermented cow's milk attributable to phyla of microorganisms

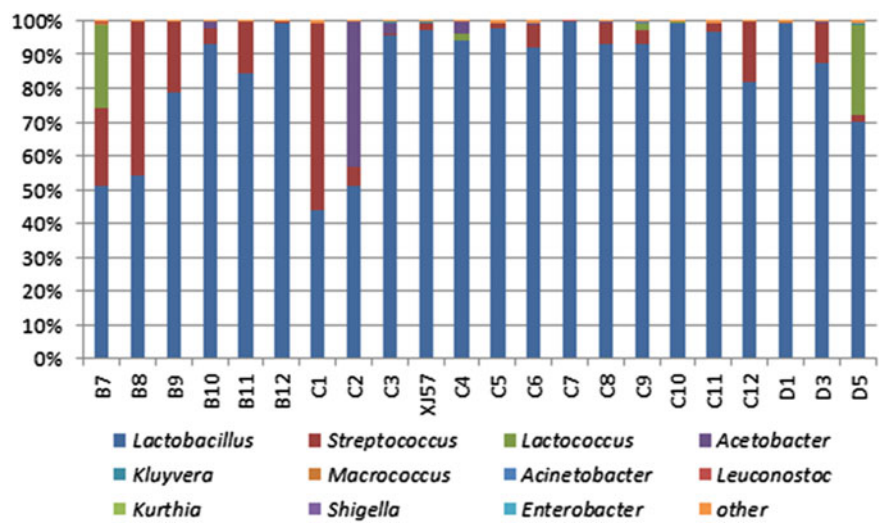


Fig. 2.4 The proportion of 16S rRNA sequences from samples of traditionally fermented bovine milk attributable to genera of microorganisms

Lactobacillus. The next most abundant genus was *Streptococcus* which, at its maximum in sample one sample represented 55 % of sequences. The highest proportion of sequences attributable to *Lactococcus* was 26.85 and 24.77 % in two samples, respectively.

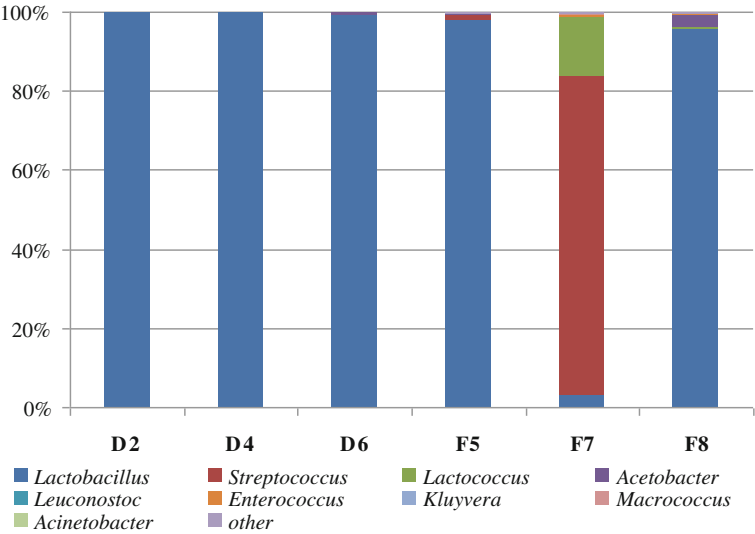


Fig. 2.5 Bacterial relative content (16S rRNA sequence proportion) in traditional koumiss based on the level of genera

Microbial Diversity of Traditional Koumiss

Microbial diversity in traditional koumiss were also studied by using the pyrosequencing technology (these data has not been published). For example, six koumiss samples (three samples from Xinjiang of China, three samples from Russia) collected from the Xinjiang Uygur Autonomous Region and Kalmuckia region of Russia. All the sequences were identified to genus level shown in Fig. 2.5, which represented the relative content of the bacteria on the genus level (greater than 0.3 %) in these samples. There were 9 genus presented these samples, of which *Lactobacillus* was regarded as the most abundant bacteria. Its content got to more than 98 %, especially in four of samples. Followed by the *Streptococcus* genus, the maximum content of these bacteria got to 81 % in one sample. Moreover, the highest content of *Lactococcus* was 14.83 % in one of samples. The other genus resented these samples were less than 10 %. All the sequences were identified to 11 phyla, Firmicuters are the predominated microflora in most samples (Fig 2.6).

Microbial Diversity in Traditional Kurut

Samples of kurut (traditionally fermented yak’s milk) were collected from the Tibet Autonomous Region, China ($n = 8$ samples from Geda County, and 8 from Ningzhong County) and subjected to microbial diversity studies using 454 pyrosequencing analysis (unpublished data). The samples for sequencing were allocated to the different regions of two County. This resulted in 112,173 high

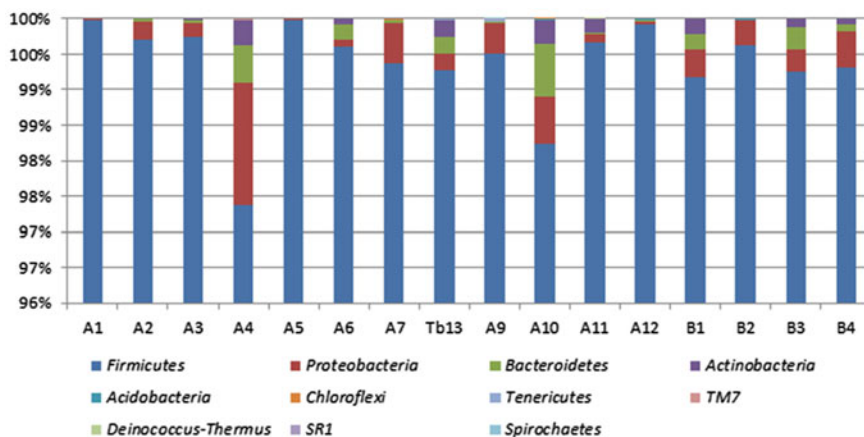


Fig. 2.6 The proportion of 16S rRNA sequences from samples of kurut attributable to phyla of microorganisms

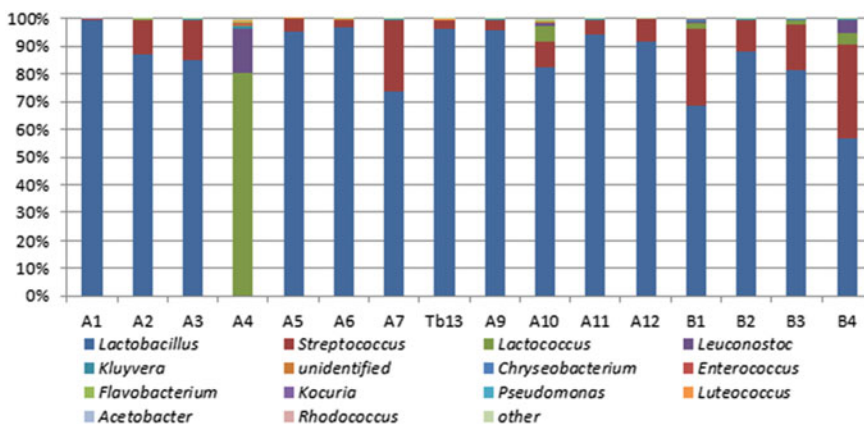


Fig. 2.7 The proportion of 16S rRNA sequences from samples of kurut attributable to genera of microorganisms

quality 16S rRNA sequences with each sample producing an average of 13062 sequences (range = 6274–7765, SD = 482). Following PyNASt alignment and 100 % sequence identity clustering analysis, 6530 representative sequences were obtained. RDP combined with the BLAST homology sequence alignment cluster method were then used to identify the sequences to phylum and genus level. The sequences were distributed amongst 11 phyla (Fig. 2.7) of which four were the bacterial phyla *Firmicutes*, *Proteobacteria*, *Bacteroidetes* and *Actinobacteria* which together accounted for 99 % of the sequences. The remaining seven phyla were also bacteria (*Acidobacteria*, *Chloroflexi*, *Tenericutes*, *TM7*, *Deinococcus-Thermus*, *Spirochaetes* and *SR1*) each accounting for between 0.013 and 0.015 % of the sequences.

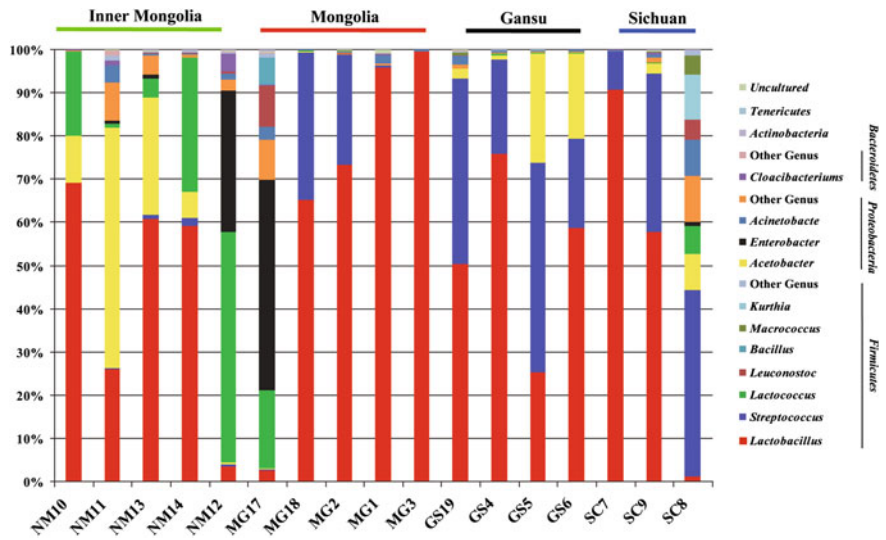


Fig. 2.8 Relative abundances (percentage of sequences) of the bacteria in naturally fermented dairy products in different regions

The sequences were also identified to genus level (Fig. 2.8). There were 13 genera identified in these samples (each at a level of at least 0.01 % of the sequences present), of which XX were LAB and, of those, *Lactobacillus* was regarded as the most abundant, representing 99 % or more of the sequences in a number of the samples. The second most abundant was *Streptococcus* genus, which was at its highest levels (33.89 % of sequences) in sample B4. In sample A4 *Lactococcus* reached its highest levels (80.20 % of sequences).

Microbial Diversity in Traditional Dairy Products in Different Places

The bacterial community diversity in fermented dairy products from Mongolia, Gansu Province, China; Sichuan Province, China and Inner Mongolia Autonomous Region, China were also examined using a metagenomic approach involving high-throughput 454 pyrosequencing (unpublished data) (Fig. 2.8). The sequences were distributed among four bacterial phyla, namely Firmicutes, Proteobacteria, Bacteroidetes and Actinobacteria. Of the four bacterial phyla, *Firmicutes* dominated in all samples from all locations. The second most dominant bacterial phyla was Proteobacteria, representing on average 17 % (± 9 %) of the sequences. Bacteroidetes (0.53 % \pm 0.59 %), Actinobacteria (0.11 % \pm 0.05 %) and unclassified bacteria (0.11 % \pm 0.07 %) were at low levels in all samples. At the genus level, a total of 95 bacterial genera were identified from the four phyla, of which *Lactobacillus* was the most abundant. At the depth of analysis carried out, 14 genera were found to be common in all the naturally fermented dairy product samples

from the four different sampling locations (Mongolia, Gansu Province, Sichuan Province and Inner Mongolia Autonomous Region). In addition to *Lactobacillus* (67.22, 52.51, 49.91 and 43.70 % for each region respectively) these were *Streptococcus* (12.07, 33.55, 29.51 and 0.71 %), *Lactococcus* (3.66, 0.17, 2.26 and 21.86 %), *Leuconostoc* (1.92, 0.02, 1.60 and 0.16 %) species of LAB.

Simultaneously, *Acinetobacter* (1.13, 0.75, 3.09 and 1.31 %), *Enhydrobacter* (0.15, 0.16, 0.42 and 0.37 %), *Cloacibacterium* (0.15, 0.09, 0.18 and 1.09 %), *Acetobacter* (0.10, 12.09, 3.57 and 20.06 %), *Macroccoccus* (0.05, 0.17, 1.52 and 0.02 %), *Chryseobacterium* (0.05, 0.03, 0.02 and 0.12 %), *Delftia* (0.03, 0.01, 0.03 and 0.12 %), *Escherichia* (0.02, 0.05, 0.06 and 0.04 %), *Rhizobium* (0.02, 0.01, 0.16 and 0.09 %) and *Roseomonas* (0.02, 0.01, 0.03 and 0.06 %) were identified.

2.3.2.2 LAB Diversity in Traditionally Fermented Dairy Products as Determined by Other Molecular Techniques, Particularly Denaturing Gradient Gel Electrophoresis

In addition to metagenomic sequence analysis, there are other molecular techniques that allow culture-independent identification and monitoring of microbial diversity. Most of these techniques are based on polymerase chain reaction (PCR) amplification and detection of the predominant nucleic acids present in a sample (Yang et al. 2001). Compared to conventional methods these molecular methods are generally faster, more specific, more sensitive and more accurate, allowing a precise study of microbial populations and their diversity in given ecosystems. These have been useful to monitor changes in microbial communities.

Culture-independent studies based on molecular fingerprinting techniques such as denaturing gradient gel electrophoresis (DGGE) (Ercolini et al. 2004; Lafarge et al. 2004), temporal temperature gradient electrophoresis (TTGE) (Lafarge et al. 2004; Ogier et al. 2002), single strand conformation polymorphism (SSCP) (Duthoit et al. 2003) have been used to characterise bacterial diversity in raw milk and other dairy products and fermented food (Table 2.14). These culture-independent methods can not only fully characterise the primary LAB from milk such as *Lactobacillus*, *Streptococcus*, *Enterococcus*, *Lactococcus*, *Leuconostoc*, *Weissella* and *Pediococcus*, but can also detect the large spectrum of other microbes that occur less frequently or cannot be detected by culture-dependent methods (Table 2.15).

2.4 Review of Biodiversity of Lactic Acid Bacteria in Fermented Foods

2.4.1 Summary

Globally, in the past century, many microorganisms have been isolated and characterised from traditionally fermented food. LAB have received considerable

attention from the pharmaceutical and /or food fermentation industries because of their biotechnology potential. LAB have an essential role in the dairy industry because of the high levels of human consumption of several important fermented food products, mainly cheese and fermented milks. The most important LAB belong to the nonpathogenic genera *Lactococcus*, *Lactobacillus*, *Leuconostoc*, *Oenococcus* and *Streptococcus* which have been used traditionally in the food industry. Numerous strains of these genera have been isolated and identified from dairy products, grain products, meat and fish products, beer, wine, fruit and fruit juices, pickled vegetables, mash, sauerkraut, silage, sourdough, etc. from various regions including Europe, Asia, Africa and Latin America. In this section, we review and list the predominant species of LAB from different fermented food.

2.4.2 History of LAB in Fermented Food

The definition of ‘fermentation’ is ‘a process in which chemical changes are brought about in an organic substrate through the action of enzymes produced by microorganisms’ (Prescott and Dunn 1957; Psoni et al. 2003). Although it is extremely difficult to pinpoint the precise beginnings of human awareness of the presence and role of microorganisms in foods, the available evidence indicates that this knowledge preceded the establishment of bacteriology or microbiology as fields within science. The exploitation of fermentation in human society has a long history. The first evidence of beer manufacture has been traced to 7000 BC in ancient Babylon (Pederson 1971). At around 3000 BC, the Sumerians are believed to have been the first great livestock breeders and dairymen and were among the first to make butter (Tamime 2002). Milk, butter and cheese were also used by the Egyptians as early as 3000 BC (Jay et al. 1996). In China, koumiss has a long history of use as a popular drink among traditional nomadic people. The earliest records of koumiss appeared during the Han dynasty (202 BC–202 AD) and it attained widespread popularity during the Yuan dynasty (1271 AD–1368 AD).

Kircher (1659) first demonstrated the occurrence of bacteria in milk and this was confirmed by Bondeau (1846) two centuries later. Leeuwenhoek (1680) was the first to observe yeast cells in milk but it was Pasteur (1857) who was the first scientist to show that souring of milk was caused by the growth of microorganisms within it. By the turn of the twentieth century, the term lactic acid bacterium or LAB was used to mean ‘milk-souring organisms’. Significantly, the first pure culture of a bacterium was *Bacterium lactis* (likely to be what we now call *Lc. lactis*) (Lister 1873) and Metchnikoff et al. (1907) isolated and named a bacterium from, *Lb. delbrueckii* subsp. *bulgaricus*.

Table 2.15 Species composition of LAB and other microorganism from fermented dairy products as determined by culture-dependent and culture-independent molecular fingerprinting approaches used simultaneously against the same samples

Country/ region	Dairy Product	Microorganisms detected by culture-dependent methods	Microorganisms detected by culture-independent molecular fingerprinting methods	Culture-independent method used	References
Italy	Cow's milk cheese	<i>E. sulfurans/faecalis</i>	<i>Enterococcus sulfurans/faecalis</i>	DGGE	Randazzo et al. (2002)
		<i>E. hiraea</i>	<i>Lb. fermentum/plantarum/</i>		
		<i>Lb. fermentum/plantarum/casei</i>	<i>casei/delbrueckii</i> subsp. <i>bulgaricus</i>		
		<i>Lc. lactis</i>	<i>Lc. lactis</i>		
		<i>Leuc. mesenteroides</i>	<i>Leuconostoc mesenteroides</i>		
		<i>P. acidilactici</i>	<i>Pediococcus acidilactici</i>		
		<i>S. thermophilus</i>	<i>Streptococcus thermophilus/</i> <i>bovis</i>		
		A further other microorganism species that were not LAB	<i>Candida pseudorugosa/kefyr/</i>		
		<i>Candida catenulata/pararugosa/</i>	<i>pseudointermedia/humilis/rugosa</i>		
		<i>parapsilosis/zyllanoides/pseudointermedia/</i> <i>rugosa</i>	<i>Galactomyces</i> spp.		
North East of Italy	Cow's milk	<i>Cryptococcus curvatus</i>	<i>Kluyveromyces marxianus/lactis</i>	DGGE	Cocolin et al. (2002)
		<i>Kluyveromyces marxianus/lactis</i>	<i>Macrococcus caseolyticus</i>		
		<i>Pichia guilliermondii</i>	<i>Saccharomyces bayanus/cerevisiae</i>		
		<i>Saccharomyces cerevisiae</i>			
		<i>Trichosporon mucoides</i>			
		<i>Lb. paracasei</i> subsp. <i>paracasei/</i> <i>delbrueckii</i>	<i>Lactobacillus paracasei</i> subsp. <i>paracasei/</i>		
		subsp. <i>bulgaricus/delbrueckii</i> subsp. <i>lactis/</i>	<i>plantarum</i>		
		<i>casei</i>			
Germany	Cow's milk cheese			TTGE	Henri-Dubernet et al. (2008)

(continued)

Table 2.15 (continued)

Country/ region	Dairy Product	Microorganisms detected by culture-dependent methods	Microorganisms detected by culture- independent molecular fingerprinting methods	Culture-independent method used	References
France	Cow's milk cheese	<i>Lactobacillus curvatus</i> subsp. <i>curvatus</i> <i>Lactococcus lactis</i> subsp. <i>lactis</i> <i>S. thermophilus</i> A further other microorganism species that were not LAB'	<i>Lactobacillus curvatus</i> subsp. <i>curvatus</i> <i>Lactococcus lactis</i> subsp. <i>lactis/cremoris</i> <i>Streptococcus thermophilus</i>	SSCP	Feurer et al. (2004)
		<i>Brevibacterium linens</i> <i>Brachybacterium species</i> <i>Carnobacterium maltaromaticum</i> <i>Corynebacterium casei</i> <i>Marine bacterium</i> <i>Marinolactibacillus psychrotolerans</i> <i>Microbacterium gubbeenense</i>	<i>Brevibacterium linens</i> <i>Brachybacterium species</i> <i>Carnobacterium maltaromaticum</i> <i>Corynebacterium casei</i> <i>Marine bacterium</i> <i>Marinolactibacillus psychrotolerans</i> <i>Microbacterium gubbeenense</i> <i>Pseudalteromonas species</i> Uncultured Flavobacterium <i>Kluyveromyces lactis/marxianus</i> <i>Kluyveromyces</i> <i>Candida</i> <i>zeylanoides/parapsilosis/silvae/intermedia</i>	SSCP	Callon et al. (2006)
		<i>Kluyveromyces lactis/marxianus</i> <i>Kluyveromyces</i> <i>Candida</i> <i>zeylanoides/parapsilosis/silvae/intermedia/</i> <i>tropicalis/rugosa</i> <i>Enterococcus faecalis</i> <i>Lactobacillus casei</i> <i>Lactococcus lactis</i> <i>Lactococcus garvieae</i> <i>S. thermophilus/dysgalactiae</i> Plus a further 29 species that were not LAB	<i>E. faecalis</i> <i>Lb. casei/kefiranoferiens</i> <i>Lc. lactis</i> <i>S. dysgalactiae/thermophilus</i> Plus a further 23 species that were not LAB	SSCP	Delbes et al. (2007)
France	Cow's milk cheese				

(continued)

Table 2.15 (continued)

Country/ region	Dairy Product	Microorganisms detected by culture-dependent methods	Microorganisms detected by culture- independent molecular fingerprinting methods	Culture-independent method used	References
France	Goat's milk	<i>E. faecalis</i> <i>E. saccharominimus</i> <i>Lb. casei</i> <i>Lc. lactis/garvieae</i> <i>Leuc. mesenteroides</i> <i>S. mitis</i> Plus a further 35 species that were not LAB	<i>E. faecalis/saccharominimus</i> <i>Lb. lactis/garvieae/casei</i> <i>Leuc. mesenteroides</i> <i>S. mitis</i> Plus a further 34 species that were not LAB	SSCP	Callon et al. (2007)
Belgium	Cow's milk cheese	<i>Lb. paracasei/plantarum/brevis/curvatus/rhannosus/perolens</i> <i>Lc. lactis</i> subsp. <i>lactis</i> <i>P. pentosaceus</i> <i>S. salivarius</i> <i>Weissella paramesenteroides</i>	<i>E. faecalis</i> <i>Lb. paracasei/plantarum/brevis/curvatus/rhannosus/parabuchneri/gallinarum</i> <i>Lc. lactis</i> subsp. <i>lactis</i> <i>P. pentosaceus</i>	DGGE	Van Hoorde et al. (2008)
Serbia	Goat milk cheese	<i>E. faecalis</i> <i>Lb. paracasei</i> subsp. <i>paracasei</i> <i>Lc. lactis</i> subsp. <i>lactis</i>	<i>Lb. paracasei</i> subsp. <i>paracasei</i> <i>Lc. lactis</i> subsp. <i>lactis</i> <i>Leuc. mesenteroides</i>	DGGE	Nikolic et al. (2008)
	Goat's milk cheese	<i>Lb. casei/buchneria/paracasei</i> subsp. <i>paracasei/tolerans/rhannosus</i> <i>P. acidilactia</i>	<i>Lb. casei/delbrueckii</i> subsp.	DGGE	Gala et al. (2008)
Italy	Cow's milk cheese	<i>E. faecium</i> <i>E. faecalis</i> <i>Lb. plantarum/paracasei/casei/coryneformis</i> subsp. <i>torquens/delbrueckii</i> subsp. <i>lactis</i> <i>Lc. lactis</i> subsp. <i>lactis</i> /subsp. <i>cremoris</i>	<i>lactis/parabuchneri/fermentum/rhannosus</i> <i>Lb. plantarum/kefirifaciens</i> <i>Lc. lactis</i> subsp. <i>lactis</i> /subsp. <i>cremoris</i> <i>Streptococcus agalactiae</i> Other microorganism species that were not LAB <i>Macrococcus caseolyticus</i>	DGGE	Dolci et al. (2008)

(continued)

Table 2.15 (continued)

Country/ region	Dairy Product	Microorganisms detected by culture-dependent methods	Microorganisms detected by culture- independent molecular fingerprinting methods	Culture-independent method used	References
France	Cow's milk cheese	<i>Lb. paracasei/helveticus/rhamnosus/parabuchneri/fermentum/perlens/acidophilus/brevis/kefiri/delbrueckii</i> subsp. <i>Lb. helveticus/delbrueckii</i> subsp. <i>E. faecalis/durans/faecium</i> <i>Lb.</i> subsp. <i>bulgarius/delbrueckii</i> subsp. <i>delbrueckii/delbrueckii</i> subsp. <i>indicus/fermentum</i> <i>Lb. paracasei/rhamnosus</i> <i>Lc. Garvieae/lactis</i> <i>Leuc. mesenteroides</i> subsp. <i>lactisa</i>	<i>Lb. paracasei/plantarum/acidophilus/rhamnosus</i>	TTGE	Henri-Dubernet et al. (2008)
Italy	Cow's milk cheese	<i>Lb. helveticus/delbrueckii</i> subsp. <i>E. faecalis/durans/faecium</i> <i>Lb.</i> subsp. <i>bulgarius/delbrueckii</i> subsp. <i>delbrueckii/delbrueckii</i> subsp. <i>indicus/fermentum</i> <i>Lb. paracasei/rhamnosus</i> <i>Lc. Garvieae/lactis</i> <i>Leuc. mesenteroides</i> subsp. <i>lactisa</i>	<i>Lb. helveticus/delbrueckii</i> subsp. <i>lactis</i> <i>Lc. lactis</i> <i>S.thermophilus</i> <i>Weissella species</i> Other microorganism species that were not LAB	DGGE	Aponte et al. (2008)
Spanish	Goat and sheep's milk cheese	<i>P. acidilacticia</i> <i>S. thermophilus/paraburberis/haemolyticus/croceolyticus/warneri/pasteuria</i> Other microorganism species that were not LAB <i>Macrococcus caseolyticus</i> <i>E. devriesei/faecium</i> <i>Lb.s paracasei/plantarum/brevis</i> <i>Lc. lactis</i> <i>Leuc.c mesenteroides/pseudomesenteroides</i> <i>P. urinaequi</i> Other microorganism species that were not LAB <i>Hafnia alvei</i> <i>Escherichia coli</i> <i>Obesumbacterium proteus</i> <i>Shigella flexneri</i>	<i>Macrococcus caseolyticus</i> <i>Morexella osloensis</i> <i>Rahnella species</i> <i>Aeromonas simiae</i> <i>E. species</i> <i>Lactobacillus plantarum/brevis/acidophilus/paracasei</i> <i>Lc. Lactis</i> Other microorganism species that were not LAB <i>Escherichia coli</i> <i>Nitrogen-fixing bacterium</i>	TTGE	Abriouel et al. (2008)

(continued)

Table 2.15 (continued)

Country/ region	Dairy Product	Microorganisms detected by culture-dependent methods	Microorganisms detected by culture- independent molecular fingerprinting methods	Culture-independent method used	References
Italy	Sheep and goat's milk cheese	<i>Lb. plantarum/brevis/coryneformis/ paraplantarum</i> LAB	<i>Lb. delbrueckii</i> subsp. <i>bulgaricus /plantarum/helveticus/ suntoryeus/gallinarum</i> <i>Lc. lactis</i> <i>S. thermophilus</i> Other microorganism species that were not LAB	DGGE	Rantsiou et al. (2008)
		<i>Kluyveromyces lactis</i> <i>Pichia membranifaciens/fermentans</i> <i>Candida kristii/zeilanoideis</i>			
Italy	Goat's milk cheese	<i>E. faecium/durans/faecalis/ malodoratus</i> <i>Lb. curvatus/plantarum</i> <i>Lactococcus lactis</i> subsp. <i>lactis</i> <i>Streptococcus thermophilus</i>	<i>Kluyveromyces lactis</i> <i>Pichia membranifaciens/fermentans</i> <i>Candida zeylanoides</i> <i>Lb. plantarum</i> <i>E. faecium/durans/faecalis/ malodoratus</i> <i>Lc. lactis</i> subsp. <i>Lactis</i> <i>Streptococcus species</i> Other microorganism species that were not LAB	DGGE	Serhan et al. (2009)
Italy	Sheep's milk cheese	<i>E. faecalis</i> <i>Lb. rhamnosus/brevis</i> <i>Leuc. mesenteroides</i> <i>Lc.lactis</i> <i>S. thermophilus</i>	<i>Staphylococcus haemolyticus</i> <i>Escherichia coli</i> <i>Clostridium bifermetans/Eubacterium tenue</i> Unidentified bands <i>E. faecalis</i> <i>Lb. rhamnosus/brevis/ plantarum/pentosus/fermentum/ buchneri/delbrueckii</i> <i>Leuc. mesenteroides</i> <i>Lc. lactis</i> <i>S. thermophilus</i>	DGGE	Randazzo et al. (2009)

(continued)

Table 2.15 (continued)

Country/ region	Dairy Product	Microorganisms detected by culture-dependent methods	Microorganisms detected by culture- independent molecular fingerprinting methods	Culture-independent method used	References
Lebanon	Cow's milk cheese	<i>Lb. plantarum</i> <i>Lactococcus lactis/garvieae</i> <i>Leuc. mesenteroides</i> Other microorganism species that were not LAB <i>Staphylococcus saprophyticus/pasteuri</i> <i>Klebsiella</i> sp. <i>Escherichia coli</i> <i>Micrococcus luteus</i> <i>Corynebacterium variable</i> <i>Flavobacterium species</i> <i>Microbacterium oxydans</i> <i>Musa acuminata</i>	<i>E. faecium</i> <i>Lb. plantarum/casei/paracasei</i> <i>Lc. lactis/garvieae</i> <i>S. thermophilus/paraberis/uberis/finiae</i> Other microorganism species that were not LAB <i>Corynebacterium variable</i> <i>Macrococcus caseolyticus</i> <i>Geotrichum candidum</i> <i>Kluyveromyces</i> sp. <i>Saccharomyces</i> sp. <i>Trichosporon gracile</i>	DGGE	Alegria et al. (2009)
Italy	Goat's milk cheese	<i>Lb. pentosus/brevis/plantarum</i> <i>Lc. subsp. lactis/garvieae</i> <i>E. faecium/casseliflavus/faecalis/italicus/</i> <i>durans</i> <i>Leuc. citreum/mesenteroides</i> <i>P. pentosaceus</i> <i>Weissella paramesenteroides</i> <i>Aerobasidium pullulans</i> <i>Candida paraugosa/zeylanoides/parapsilosis</i>	<i>Lc. lactis subsp. lactis</i> <i>Lb. helveticus</i> <i>Leuc. pseudomesenteroides</i> Other microorganism species that were not LAB <i>Candida paraugosa</i> <i>Rhizomucor miehei</i> <i>Alternaria alternata</i>	DGGE	Alessandria et al. (2010)

(continued)

Table 2.15 (continued)

Country/ region	Dairy Product	Microorganisms detected by culture-dependent methods	Microorganisms detected by culture- independent molecular fingerprinting methods	Culture-independent method used	References
Spain	Cow's milk cheese	<i>Lactococcus lactis</i> subsp. <i>lactis</i> / subsp. <i>cremoris</i>	<i>Lb. casei/helveticus</i>	DGGE	Dolci et al. (2010)
		<i>Lb. casei/plantarum</i> / <i>coryneformis</i> subsp. <i>torquens/acidipiscis</i>	<i>Lc. lactis</i> subsp. <i>lactis</i> /subsp. <i>cremoris</i> <i>S. agalactiae</i> Other microorganism species that were not LAB		
Turkey	Fermented dry sausage	<i>Streptococcus thermophilus/agalactiae</i> <i>Lb. Alimentarius/brevis/farcinini/sakei</i> / <i>curvatus/plantarum</i> <i>W. halotolerans</i>	<i>Spingomonas</i> sp. <i>Lb. brevis/curvatus/farcinini/sakei</i>	16S rRNA V ₃ Sequencing Rep-PCR DGGE	Kesmena et al. (2012)
			<i>Lc. piscium</i> <i>Leuc. mesenteroides/citream</i> <i>W. viridescens</i>		
Spain	Rioja wine	<i>Lb.mali/Lb.plantarum</i> <i>Leuc. fallax/mesenteroides</i> <i>O. oeni</i> <i>P. pentosaceus</i>	<i>Lb. Buchneri/plantarum</i> <i>Lc.lactis</i> <i>Leuc. mesenteroides</i> <i>O. kitaharae/oeni</i> <i>P. parvulus/pentosaceus</i>	DGGE	González-Arenzana et al. (2013)

2.4.3 LAB in Dairy Products

Milk is one of the most important components of human diet from infancy to old age (Elmagli and El-Zubeir 2006) and it can be fermented by LAB and yeast to produce other products that vary in their taste, constituents and shapes. It is likely that the origin of dairy products was the Middle East and the Balkans (Tamime 2002). Today, various types of fermented dairy products have been developed in all parts of the world including the Middle East, South Africa, Asia and Western Europe. There were approximately 400 generic names applied to traditional and industrialised products varying only in the kind of milk fermented (Kurmman et al. 1992). In recent years, with the advancement of study on dairy products, more and more species of LAB have been isolated and characterised from previously unknown natural fermented dairy products in remote rural areas. The most important varieties of dairy products worldwide, and the LAB within them are, alphabetically, as follows:

Amasi is a well-known sour cow milk drunk traditionally by the Zulu people of South Africa. It is produced in clay pots and gourds which are used repeatedly to ensure that spontaneous fermentation of the raw milk introduced to them occurs naturally at ambient temperature of $\pm 5^{\circ}\text{C}$ (Keller and Jordan 1990; Gadaga et al. 2001). Traditional preparation of amasi is similar in other countries where raw milk is poured into calabashes made from gourds or into stone jars. It is then left to ferment for several days. Amasi is now available in commercial outlets in South Africa. There were seven species of LAB isolated from Amasi by different researchers (Table 2.16). In a subsequent study by Feresu and Muzondo (1990), the predominant LAB isolated from amasi were identified as *Lb. helveticus*, *Lb. plantarum*, *Lb. delbrueckii* subsp. *lactis*, *Lb. paracasei* subsp. *paracasei* and *Lb. paracasei* subsp. *pseudoplanarum* (Feresu and Muzondo 1990).

Biruni is a cheese-like product made from XX's milk that is limited to the Nuba Mountains area of Sudan although it has recently spread into more areas inhabited by pastoralists who have named it laban-gadim (aged milk). It is similar to mish which is also produced in Sudan. Biruni has probably one of the longest shelf lives of any fermented milk product as it can be stored for at least 1 year and maybe as long as 10 years (Salih et al. 2011). Information on the product is scanty, however, because it comes from the region of the Nuba Mountains which is in the vicinity of the war-torn township of Dialing (Abdelgadira et al. 1998).

Branza dulce, telemea and urda are common names for Romanian artisan dairy products (Zamfir et al. 2006). The cows' or goats' or buffalos' milk is left overnight to ferment in a warm place (for instance, next to the oven in the farm house). In some cases the milk is first boiled for several minutes. On the second day, the upper layer is collected as fermented sour cream and the rest is used as fermented milk (sour milk) or for cheese production. For the latter, the sour milk is warmed up and rennet is added. Alternatively, rennet can be added to the milk before fermentation. The whey is then removed from the sour milk and the cheese curd is collected in a special cloth, pressed and drained. This so-called branza

Table 2.16 Species of LAB and yeast found in traditional fermented dairy products from around the world

Country/ Regions	Name of dairy product	Type of products	Raw material	Species of LAB present	Species of yeast present	Counts of microorganisms as CFU/g	References
South Africa	Amasi	Fermented milk	Cow's milk	3, 4, 9, 22, 27, 35, 38, 56	B, C, D, E	1.2×10^5 to 1.97×10^6	Salih et al. (2011)
Kenya	Sethemi	Fermented milk	Milk				Zamfir et al. (2006)
	Kule naoto	Fermented milk	Milk				Chelule et al. (2010)
Sudan	Gibna bayda	Cheese		4, 9, 35, 38, 42, 50, 55	B, D, F, G	1.0×10^6	Kebede et al. (2007)
	Gibna	White pickled cheese		19, 13, 66		1.0×10^7 to 1×10^9	Mathura et al. (2008)
	mudafifara					ND	Ahmed et al. (2009)
Ghana	Gariss	Fermented milk	Camel's milk	3 or 4, 9, 11, 13, 24, 38, 35, 51, 52	ND	ND	Sulteman et al. (2006), Abdel Moneim et al. (2006), Hassan et al. (2008), Ashmaig et al. (2009)
	Rob (Roub or Robe) also named kit, laben- rayeb	Fermented milk	Cow's, or sheep and goat's milk	13, 19, 24, 27, 37, 38, 42, 51	A, B, C	1×10^7 to 1×10^8 (for species of <i>Lactococcus</i> and <i>Lactobacillus</i>)	Saeed (1981), El Mardî (1988)
Netherlands	Zabadi	Fermented milk	Cow's milk	19, 65	H	ND	Abdelgadira et al. (1998)
	Nunu	Yogurt-like product	Cow's milk	<i>Lactobacillus</i> spp. <i>Leuconostoc</i> spp. <i>Enterococcus</i> spp. <i>Streptococcus</i> spp.	B, C, F	1×10^4 to 1×10^8 (for LAB)	Akabanda et al. (2010)
	Gouda	Dutch-type cheese	Cow's, sheep or goat's milk	3, 11, 18, 34, 35, 38, 42, 54, 62, 67		-1×10^6 (for yeasts)	Van Hoorde et al. (2008), Koenraad et al. (2008)
Italy	Parmigiano Reggiano	Cheese	Raw and partly skimmed cow's milk	13, 19, 22, 24, 34, 35, 42,		1×10^7 to 1×10^8	Gala et al. (2008)

(continued)

Table 2.16 (continued)

Country/ Regions	Name of dairy product	Type of products	Raw material	Species of LAB present	Species of yeast present	Counts of microorganisms as CFU/g	References
Morocco	Jben	Soft white cheese	Milk	1, 2, 3, 4, 11, 12, 38, (Park et al. 2006) Dewan S, Tamang 42, 49, 50, 52, 53, 55, 57, 65		1×10^8 to 1×10^9	Ouadghiri et al. (2005)
Greek	Batzos	Cheese	Goat's milk	18, 38, 35, 37, 44		ND	Psoni et al. (2003)
France	Emmental	Comté Camembert	Cow's milk	9, 13, 19, 22, 27, 35, 38		ND	Gagnaire et al. (2001), Bouton et al. (2002)
Caucasus	Kefir	Tart and mildly alcoholic effervescent fermented milk	Milk	11, 19, 27, 29, 32, 51, 65	B, D, E, F,	ND	Simova et al. (2002), Chen et al. (2008)
China	Qula	Yellow or white cheese	Yak's milk	3, 4, 38, 56, 57, 62		1×10^3 to 1×10^7 (for LAB) 0 to 1×10^5 for mould 1×10^5 to 1×10^6 for yeasts	Bao et al. (2012a), (b)
	Kurut	Fermented yak's milk	Yak's milk	2, 3, 4, 11, 13, 19, 24, 27, 32, 38, 50, 51, 52, 53, 54, 56, 65, 68		–	Sun et al. (2010), Bao et al. (2012a, b)
	Dairy fan	Cheese-like product	Goat's milk	2, 24, 25, 27, 28, 30, 31, 32, 38, 51, 53, 54		–	Liu et al. (2009)
	Milk cake	Cheese-like product	Cow's or goat's milk	2, 19, 27, 49, 50, 51, 65		8.32×10^{10} to 10^{16} $\times 10^{10}$ (for LAB) 1.6×10^{10} to 6.15×10^{10} (for yeasts)	Bao et al. (2011)
Romania	Chige Branza dulce/ Urda/ Telemea	Sweet cheese	Goat's and buffalo's milk	2, 3, 4, 11, 18, 31, 35, 49, 51, 52, 55, 57, 63, 65, 71		1×10^7 to 9×10^9 including commercial products	Zamfir et al. (2006)

(continued)

Table 2.16 (continued)

Country/ Regions	Name of dairy product	Type of products	Raw material	Species of LAB present	Species of yeast present	Counts of microorganisms as CFU/g	References
Egypt	Kishk						
	Laban zeer	Sour buttermilk	Milk				
	Domati cheese (Gbnah Beeda)	Soft white pickled cheese	Cow's or buffalo's milk	3, 9, 11, 13, 25, 38, 49, 50, 51, 52, 53, 55, 65		7.1 to 7.6×10^{10}	El-Baradei et al. (2007)
Senegal	M'Bannick	Kefir-like beverage					
Czech Republic	Zincica	Salted kefir-like beverage					
	Dahi	Curd milk or curd rice	Cow's milk or rice	10, 50, 51		1×10^7 to 1×10^8	Dewan and Tamang (2007)
India	Mohi	Buttermilk beverage	Milk	10, 50, 51		1×10^7 to 1×10^8	
	Chhutpi	Cottage cheese- like product	Fermented cow's milk	4, 10, 28, 32, 35, 38		1×10^7 to 1×10^8	
	Somar	Soft paste with bitter taste	Cow's milk	35		1×10^7 to 1×10^8	Dewan and Tamang (2007)
	Philu	Cream-like milk product	Cow's or yak's milk	35		1×10^7 to 1×10^8	
	Shyow	Thick-gel curd	Yak's milk	35		1×10^7 to 1×10^8	

(continued)

dulce (sweet cheese) can be consumed immediately. Alternatively, a salted cheese called telemea can be manufactured. This can be kept for several months in a mixture of water, whey and salt. Also, a soft whey cheese, called urda, can be prepared by warming up the whey to 80–90 °C, collecting the floating particles and drying them. LAB composition in these products was described by Zamfir et al. (2006) and included 15 species. The most frequent LAB found in Romanian raw milk and fermented dairy products (fermented milks, sour cream, cheese) was *Lc. lactis*.

Chhurpi is a cottage cheese-like fermented cows' or yaks' milk product from the Indian state of Sikkim and Nepal. It has a rubbery texture with a slightly sour taste. This traditional fermented dairy product is lesser known as dahi mohi, somar, philu and shyow because they are mainly restricted to the unorganised sector as well as individual households. During production, milk is boiled for about 15 minutes until a soft, white mass is formed which is sieved out and placed in a muslin cloth and allowed to drain thereby removing the remaining whey. This produces the soft variety of chhurpi which is eaten in curry or as a soup (Dewan and Tamang 2007). When chhurpi (Sherpas call it sherkam) is kept in a closed vessel for about 15 days or more, the fermented product is called somar which is a strong-flavoured, bitter but soft paste that is consumed as soup alongside cooked rice or finger millet by the Sherpas of Sikkim and Nepal. 128 isolates were identified to *Lb. bifementans*, *Lb. paracasei* subsp. *pseudoplantarum*, *Lb. kefir*, *Lb. hilgardii*, *Lb. alimentarius*, *Lb. paracasei* subsp. *paracasei*, *Lb. plantarum*, *Lc. lactis* subsp. *lactis*, *Lc. lactis* subsp. *cremoris* and *E. faecium* from these dairy product collected from different places of India, Nepal and Bhutan (Dewan and Tamang 2007).

Dairy fan is also called 'rusan' or 'ruxian' in the Chinese language because of its unique fan shape. It is a cheese-like product made from cows' milk and consumed by the Bais people, an ethnic minority from Yunnan Province and South-west China. The chemical composition and nutritional composition was evaluated by Liu et al. (2011). Dairy fan is produced by adding an 'acid juice' to the milk and heating it up (Zhang 2008). Liu et al. (2009) isolated 91 strains of LAB from 20 samples of dairy fan. These isolates could be attributed to 12 species or subspecies based on their physiological and biochemical characteristics, and 16S rRNA gene sequence analysis. *Lactobacillus helveticus* and *Lb. fermentum* were the predominant species in dairy fan from Yunnan.

Dahi is local Nepalese name for curd prepared from cow's milk and prepared in most rural households for direct consumption or for subsequent processing into other ethnic milk products like gheu, mohi and chhurpi (Dewan and Tamang 2007). For traditional dahi preparation, fresh cow's milk is first boiled in a vessel. After boiling, the milk is cooled to room temperature and a small quantity of previously prepared dahi is added and is left for 1–2 days in summer or for 2–4 days in winter at ambient room temperature for natural fermentation to occur. Dahi is also traditionally eaten with boiled rice or 'chewra' (beaten-rice) by Nepalese people.

Gariss is a unique Sudanese traditionally fermented camel's milk product. It is made in a semi-continuous fermentation process. The word Gariss means 'pinching' or 'stinging', denoting a high degree of sourness. Fermentation is done in two leather bags of tanned goat skin embedded in green or wet grass carried on the backs of camels. In this way, the milk is subjected to continuous shaking by the movement of the camels. Whenever part of the product is withdrawn for consumption, fresh camel's milk is added to make up the volume. This production process described by Salih et al. (2011) is similar to the procedure used for the traditional production of koumiss by the original nomadic Mongolian people in China. The LAB composition of Gariss includes more than 10 species isolated from the dairy products (Table 2.16). The most dominant species from the genus *Lactobacillus* were *Lb. paracasei* group, *Lb. fermentum*, *Lb. plantarum* and *Lb. raffinolactis*. The dominant coccoid species were *Lc. lactis*, *Enterococcus* spp. and *Leuconostoc* spp. (Suliman et al. 2006; Abdel Moneim et al. 2006; Hassan et al. 2008; Ashmaig et al. 2009).

Gibna (cheese) production from different raw milk (including cow's buffalo's milk) in Sudan began in the early eighteenth century by Greek families who had migrated to Sudan. Gibna making is the major preservation method for surplus milk in rural areas. The major types of cheese made are Gibna Bayda and Gibna Mudaffara (El-Sheikh 1997; Hamid and El-Owni 2007) and they vary in composition, texture, colour, taste and flavour, type of packaging and microbial activity during ripening (Salih 2011). Gibna bayda is unique in containing high concentrations of salt that are added to the milk before processing to prevent rapid deterioration before ripening can occur (Taormian 2010). The production process has been reviewed by Salih et al. (2011) mainly including some steps such as salting, coagulum fermentation, fitting, curd and so on. The LAB and other bacteria naturally present in the raw milk carry out the fermentation process and no starter is required (Abdel Gadir et al. 1998; El-Owni and Hanmid 2008). *Lb. delbrueckii* subsp. *bulgaricus*, *Lb. casei* and *S. mutans* was the most common microflora of the products (Ahmed 1997). Gibna Mudaffara is similar to Gibna bayda except even more salt is added to the milk. Rennet or a rennet extraction is also added to achieve firm coagulation into curds within 4–6 h. Ripening takes place while the curds are submerged in the whey. The curds are then transferred to wooden moulds lined with cheese cloth or muslin and the whey is allowed to drain out overnight. The drained whey is collected into a clean pan and boiled for 15 mins prior to removal of any fats and coagulated whey proteins. Then starter from previously fermented milk is added and left overnight to ferment. The next day the cheese is removed from the moulds and cut into 10 cm cubes that are then immersed in the whey. Giban Mudaffara remains preserved for a long time because it is immersed in the whey (Salih et al. 2011).

Gouda is a yellowish cheese named after the city of Gouda in the Netherlands, and is one of the primary Dutch-type cheese varieties produced worldwide (Walstra et al. 1993). It is a semi-hard cheese manufactured from cow's milk, although sheep and goat's milk can also be used (Van den Berg 2000). This type of cheese ripens for 1–20 months during which time the flavour changes from mild to

strong and it can be consumed at any stage of maturity depending on the product characteristics required, the flavour preferences of consumers and economic factors (Walstra et al. 1993). There were ten species of LAB were isolated and identified from this product (Table 2.16).

Kefir is an alcohol containing milk from Caucasian countries such as Russia, Armenia, etc., fermented by yeasts and LAB. The colour of these products is white or yellowish and the texture is rather thick, but not gluey, with an elastic consistency (Tamime 2006). According to Polish Standards, the microscopic composition should be 80 % *Lactobacillus* spp., 12 % yeasts and 8 % *Lactococcus* spp.. The LAB composition reported includes over 30 species or subsp. species of LAB and 24 species of yeasts (Tamime 2006). *Pseudomonas* spp. and *E. coli* have also been detected in kefir by DGGE (Chen et al. 2008).

Koumiss is produced from mare's milk that has been naturally fermented by LAB and yeasts and is made in the south of Russia, Mongolia and the northwestern regions of China. There have been 62 species or subspecies of LAB recorded from koumiss (Table 2.10) and in other sections of Chap. 7. Isolates of LAB reported include four species of *Enterococcus*, 45 species or subspecies of *Lactobacillus*, four species of *Lactococcus*, four species of *Leuconostoc*, two species of *Streptococcus* and three species of *Weissella* (Burentegusi 2002; Uchida et al. 2007; Watanabe et al. 2008).

Kule naoto is traditionally fermented milk produced by the Maasai tribespeople of Kenya. It is spontaneously fermented from raw cow's milk in traditionally prepared calabashes. The calabashes are first treated with burnt smoky twigs from a traditional plant. The milk is further pre-treated by adding fresh cow's blood, before initiating the fermentation process (Mathara et al. 2004, 2008). Seven species of LAB have been isolated from the fermented products (Table 2.4). Further studies have shown that the LAB composition of Kule naoto was 55 % from the genus *Lactobacillus*, 14 % from *Lactococcus*, 25 % from *Enterococcus* and 6 % from *Leuconostoc*. *Lactobacillus plantarum* was the predominant species and constituted 60 % of the *Lactobacillus* species present (Mathara et al. 2004).

Kurut is a traditional naturally fermented yak's milk product is one of the staple foods of the nomadic people from the Tibet Autonomous region of China. It is also consumed by people from Qinghai, Gansu and Sichuan Provinces of China. There have been 19 species of LAB isolated from kurut (Table 2.16) and the predominant species were *S. thermophilus*, *Lb. helveticus*, *Lb. fermentarium* and *S. thermophilus* in the Sichuan Province, Gansu Province, Tibet Autonomous Region and Qinghai Province of China, respectively (Sun et al. 2010; Bao et al. 2010, 2011; Liu et al. 2009).

Mish is a fermented cow's milk product from both the state of Darfur in western Sudan and from Egypt. Although most associated with Sudan mish is thought to have been introduced from Egypt (Abdelgadira et al. 1998). The preparation method of mish from Darfur is more similar to that of the product from Egypt than another Sudanese dairy product, biruni. Mish is produced by boiling the milk then cooling it and inoculating with a small quantity of material from a

previous batch as a starter. After souring, seeds of black cumin (*Nigella sativa*) and fenugreek (*Trigonella foenum graecum*) are added. Sometimes, a few pods of green or red pepper are also added. The product is fermented for a further two or more days before consumption (Dirar 1993).

Milk cake is a traditional fermented cheese-like product made from goat's milk and consumed by ethnic minority communities in the Yunnan province of China. The nutritional value of goat's milk is very high and includes vitamins and a diversity of trace elements (Chen et al. 2009). LAB (from 8.32×10^{10} CFU/g to 10.16×10^{10} CUF/g) and yeast (from 1.06×10^{10} CUF/g to 6.15×10^{10} CUF/g) were the predominant microorganisms in milk cake (Bao et al. 2011). Totally, 76 strains of LAB were isolated from 13 samples of milk cake and attributed to 9 species based on conventional and 16S rRNA gene sequence analysis methods (Bao et al. 2011). *Lactococcus lactis* subsp. *lactis* and *Lc. garvieae* were the most abundant species of LAB in Yunnan milk cake.

Nunu is yogurt-like product prepared and consumed by the Fulani people in Ghana. Nunu is processed from fresh cow's milk in calabashes or rubber buckets by spontaneous fermentation. The production method of this products was described in literature by Akabanda et al. (2010) The predominant LAB present included different species of *Lactobacillus*, *Leuconostoc*, *Enterococcus* and *Streptococcus*.

Philu is an indigenous cream-like milk product produced from cow's or yaks milk, and is typically cooked and eaten as a delicacy with boiled rice in Bhutan and the Indian state of Sikkim. During philu preparation, fresh milk is collected in cylindrical bamboo or wooden vessels and slowly swirled around the walls of the vessels for 5–10 min. During this time, a creamy mass begins to stick to the walls of the vessels. The remaining liquid is poured off and the vessels upturned to drain out the remaining liquid. This process is repeated daily for 6–7 days until a thick, white creamy layer is formed on the inside walls of the vessels. This soft mass is the philu and it is scraped off and stored in a dry place for consumption. Philu produced from cow's milk is white in colour with a butter-like texture and slightly bland taste, while philu produced from yak's milk has a more creamy-white colour and an inconsistent semi-solid texture. Philu is a high-priced traditional milk product sold in local markets of Sikkim and Bhutan. Chhu or sheden is a strong-flavoured indigenous cheese-like product prepared in a similar way from cow's milk or yak's milk in Sikkim, the Darjeeling hills, Arunachal Pradesh and Ladakh in India, Nepal, Bhutan and the Tibet Autonomous region of China (Dewan and Tamang 2007).

Qula is a grainy, hard, yellow or white cheese made from yak's milk in the Tibetan plateau of China. The process of making Qula cheese by traditional Tibetan methods has been described by Duan et al. (2008). LAB were the most important group of microorganisms in Qula (Table 2.16) and, of the 15 species or subspecies of LAB identified, *Lb. helveticus* was the predominant species.

Rob, also known as roub or robe, is produced in rural households of Sudan by fermentation of cow's milk or sheep and goat's milk. Surplus milk is collected in a container, inoculated with a starter culture from the previous day and left to

ferment overnight. The fermentation process usually starts in the evening when the animals return from grazing and the resulting sour product is churned in the morning when the herd leaves for grazing. Freshly produced rob has a pleasant taste with a pH of about 4.5. The early literature by Saeed (1981) and El Mardi (1988) revealed that *S. thermophilus*, *Lb. bulgaricus*, *Lb. helveticus*, *Lb. fermentum* and *Lc. lactis* were the most common LAB in rob. Hamza et al. (2009) also identified *Lb. delbreuckii* subsp. *bulgaricus*, *Lb. rhamnosus*, *Lb. plantarum*, *Lb. casei* and *Lb. pentosus* using API 50CHL and *A. viridians*, *E. faecium*, *E. gallinarum*, *Lc. lactis* sub sp. *lactis*, *Leuconostoc* sp., *S. acidominimus* and *S. bovis* by API 20 STREP. The results were confirmed by Random Amplified Polymorphic DNA (RAPD).

2.4.4 LAB in Fermented Vegetables and Beverages

2.4.4.1 LAB in Sourdough

Sourdough is an important modern fermentation method for cereal flours and water based upon an earlier spontaneous process (Vogel et al. 1999). The sourdough starter is used in the manufacture of a variety of products such as breads, cakes, Chinese steamed buns (mantou) and Chinese steamed stuffed buns (bao zi). Many sourdough wheat breads and cakes originate in Mediterranean countries, the San Francisco bay area of the United States and Southern America, whereas numerous sourdough products made with rye, wheat, barley or mixed flours originate in Germany, Central and Eastern Europe and Scandinavia (Stephan and Neumann 1999a, b). In Italy, wheat sourdough is used in more than 30 % of bakery products (Ottogalli et al. 1996). Baked (cake) and steamed products using wheat sourdough are staple foods in northern China. Due to their artisan and region-dependent preparation methods, sourdoughs have a very high diversity of LAB and yeast species and strains (Table 2.17). Recent studies suggest that more than 50 species of LAB, particularly species from the genus *Lactobacillus*, and more than 20 species of yeast, particularly from the genera *Saccharomyces* and *Candida*, can be in sourdough cultures used for making traditional/typical leavened baked goods worldwide (Corsetti et al. 2001; Minervini et al. 2012; Palomba et al. 2011; Venturi et al. 2012; Lattanzi et al. 2013).

2.4.4.2 LAB in Pickled Vegetables

Fermented vegetables play an important role in Asian family diet as a popular dish or as seasoning for food. Fermented vegetables have different names associated with the different materials and processes used to make them and the different countries and regions in which they are made. These include ‘kimchi’ (Korea and Japan), ‘suan cai’ or ‘suan-tsai’ (China or Taiwan) and ‘sauerkraut’ or ‘kraut’ (Germany).

Table 2.17 Species of LAB and yeasts found in sourdough products from around the world

Country	Product	Species of LAB present	Methods for isolation and identification	Reference
Belgium	Wheat and rye sourdoughs	11, 36, 38, 45	Polyphasic	Scheirlinck et al. (2009)
		36, 38, 39, 45		Scheirlinck et al. (2007)
		17, 27, 35, 36, 38, 39, 43, 45		Scheirlinck et al. (2008)
Denmark	Rye sourdough	39, 41, 45	Phenotypic	Rosenquist and Hansen (2000)
Finland	Rye sourdough	9, 13, 27, 38	Phenotypic	Salovaara and Katunpää (1984)
France	Wheat bread	11, 13, 18, 20, 22, 38, 56b, 62	Phenotypic	Infantes and Tourneur (1991)
Germany	Wheat sourdough	10b, 12, 13, 20, 24, 38	Phenotypic	Spicher (1959)
Greek	Traditional wheat sourdoughs	11, 39, 45, 68	SDS-whole cell protein/DNA-PCR 16 rRNA sequencing	Vuyst et al. (2002)
	Rye bread	9, 11, 13, 24, 38, 45	Phenotypic	Spicher (1979, 1987)
	Rye sourdough	9, 10, 11, 12, 13, 24, 38, 45	Phenotypic	Spicher (1984)
	Wheat sourdoughs (Panettone, wheat bread)	11, 13, 38, 28, 71	Phenotypic	Spicher (1987)
	Rye sourdough	10b, 24b, 39, 41	RAPD-PCR	Müller et al. (2001)
	Rye bran	10b, 33, 16, 39, 24, 24b, 25b, 41	PCR-DGGE	Meroth et al. (2003)
	Wheat and rye sourdoughs	11, 12, 17, 18, 26, 27, 34, 35, 36, 38, 39, 43, 44, 45, 55, 58, 62, 68, 69	PCR-DGGE, AFLP	Scheirlinck et al. (2008)

(continued)

Table 2.17 (continued)

Country	Product	Species of LAB present	Methods for isolation and identification	Reference
Italy	Panettone, Brioche	11, 38	Phenotypic	Galli and Ottogalli (1973)
	Panettone, Brioche	24, 38, 45, 55	Phenotypic	Galli et al. (1988)
	Umbrian wheat sourdoughs	38, 45	Phenotypic	Gobbetti et al. (1994)
	Pizza (Naples)	38, 44, 55	Phenotypic	Coppola et al. (1996)
	Verona sourdoughs	45	RAPD-PCR	Zapparoli et al. (1996)
	Apulian wheat sourdoughs	9, 10, 11, 20, 24, 38, 45, 51, 53, 69	16S rDNA sequencing and 16S/23S rRNA spacer region PCR	Corsetti et al. (2001)
Iran	Sangak	11, 38, 55	Phenotypic	Azar et al. (1977)
Mexico	Pozole (maize)	10, 13, 19, 38, 50	16S rDNA sequencing	Escalante et al. (2001)
Morocco	Sourdough ferments and traditional starters	11, 12, 13, 38, 55	Traditional methods	Boraam et al. (1993)
	Sponges	13, 55 and <i>Pediococcus</i> sp.	Phenotypic	Faid et al. (1994)
	Soft wheat flour	12, 13, 19, 38, 45, 55, 62	Phenotypic	Faid et al. (1994)
Portugal	Broa	1, 2, 4, 11, 18, 19, 51	Phenotypic	Rocha and Malcata (1999)
Russia	Rye sourdough	11, 25, 38	Phenotypic	Kazanskaya et al. (1983)
Spain	Wheat sourdough	11, 38	Phenotypic	Barber et al. (1983)
	Wheat sourdough	11, 38	Phenotypic	Barber et al. (1983)
Sudan	Kisa (sorghum sourdough)	10b, 24, 41	Molecular and traditional method	Hamad et al. (1997)

(continued)

Table 2.17 (continued)

Country	Product	Species of LAB present	Methods for isolation and identification	Reference
Sweden	Kisa	3, 24, 27, 50	RAPD	Spicher (1987) Lönner et al. (1986) Kline and Sugihara (1971) Zhang et al. (2011)
	Rye/Wheat	9, 11, 19, 24, 38, 42, 45, 71	Phenotypic	
	Rye sourdough	<i>Lactobacillus</i> sp., 62	Phenotypic	
USA	San Francisco sourdough	45	Phenotypic	
	French bread			
China	Traditional sourdough	2, 11, 18, 17, 24, 27, 33, 36, 38, 43, 45, 50, 53, 55, 68, 69	16S rRNA genes sequences and DGGE analysis	

Note 1. *E. casseliflavus*, 2. *E. durans*, 3. *E. faecalis*, 4. *E. faecium*, 5. *E. gallinarum*, 6. *E. italicus*, 7. *E. thailandicus*, 8. *Lb. acetotolerans*, 9. *Lb. acidophilus*, 10. *Lb. alimentarius*, 10b. *Lb. amylovorus*, 11. *Lb. brevis*, 12. *Lb. buchneri*, 13. *Lb. casei*, 14. *Lb. confusus*, 15. *Lb. coryniformis* subsp. *torquens*, 16. *Lb. crispatus*, 17. *Lb. crustorum*, 18. *Lb. curvatus*, 19. *Lb. delbrueckii* subsp. *bulgaricus*, 20. *Lb. delbrueckii* subsp. *delbrueckii*, 21. *Lb. delbrueckii* subsp. *indicus*, 22. *Lb. delbrueckii* subsp. *lactis*, 23. *Lb. diolivorans*, 24. *Lb. frumenti*, 25. *Lb. graminis*, 25b. *Lb. johnsonii*, 26. *Lb. hamsteri*, 27. *Lb. helveticus*, 28. *Lb. hilgardii*, 29. *Lb. kefiranoformis* subsp. *kefiranoformis*, 30. *Lb. kefiranoformis* subsp. *kefiranoformis*, 31. *Lb. kefiranoformis*, 32. *Lb. keffrii*, 33. *Lb. mindensis*, 34. *Lb. parabuchneri*, 35. *Lb. paracasei*, 36. *Lb. paralimentarius*, 37. *Lb. pentosus*, 38. *Lb. plantarum*, 39. *Lb. pontis*, 40. *Lb. rapi*, 41. *Lb. reuteri*, 42. *Lb. rhamnosus*, 43. *Lb. rossia*, 44. *Lb. sakei*, 44a. *Lb. salivarius*, 45. *Lb. sanfrancisco*, 46. *Lb. spicheri*, 47. *Lb. sunkii*, 48. *Lb. uvarum*, 49. *Lc. garvieae*, 50. *Lc. lactis* subsp. *cremoris*, 51. *Lc. lactis* subsp. *lactis*, 52. *Lc. raffinolactis*, 53. *Leuc. citreum*, 54. *Leuc. lactis*, 55. *Leuc. mesenteroides*, 56. *Leuc. mesenteroides* subsp. *mesenteroides*, 56b. *Leuc. mesenteroides* subsp. *dextranicum*, 57. *Leuc. pseudomesenteroides*, 58. *P. acidilactici*, 59. *P. damnosus*, 60. *P. ethanolivorans*, 61. *P. parvulus*, 62. *P. pentosaceus*, 63. *S. bovis*, 64. *S. parauberis*, 65. *S. thermophilus*, 66. *S. mutans*, 67. *S. salivarius*, 68. *W. cibaria*, 69. *W. confusa*, 70. *V. camiphilus*, 71. *W. viridescens*, *W. paramesenteroides*
A. *Corynebacteria pseudodiphtherium*, B. *Saccharomyces cerevisiae*, C. *Candida kefyr*, D. *Candida lusitanae*, E. *Candida colliculosa*, F. *Kluyveromyces maxianus*, G. *Debaryomyces hansenii*, H. *Pichia farinosa*, I. *Pichia guilliermondii*, J. *Pichia anomala*, K. *Candida humilis*, L. *Rhodotorula mucilaginosa*

Kimchi is a traditional fermented vegetable from Korea. Most kimchi is characterised by its hot taste because of the fairly high quantities of chilli pepper used. Lactic acid bacteria (LAB), including *Lb. plantarum*, *Lb. brevis*, *Lb. acidophilus*, *Lb. homohiochii*, *Leuconostoc* species and *Lc. lactis* have all been isolated from Korean kimchi (Lee et al. 1999; Park et al. 2010). The most abundant LAB is the hetero-fermentative species *Leuc. mesenteroides*, particularly at the initial to the middle stages of fermentation. However, the total number of this species decreases sharply as fermentation proceeds and the pH drops below 4.0. At the final fermentation stages the homofermentative species *Lb. plantarum* predominates (Mheen and Kwon 1984). In the last 10 years, ten further species have been recorded from kimchi: *Lb. kimchii* (Yoon et al. 2000), *Lb. xiangfangensis* (Gu et al. 2013), *Lb. futsaii* (Chao et al. 2012), *Lb. plantarum* subsp. *plantarum* (Bringel et al. 2005), *Lb. kimchicus* (Liang et al. 2011), *Lb. koreensi* (Bui et al. 2011), *Lc. kimchii* (Kim et al. 2002), *Lc. inhae* (Kim et al. 2003), *W. kimchii* (Choi et al. 2002) and *W. koreensis* (Lee et al. 2002).

Suan cai (pickled vegetable), also known as fu tsai, pao cai or suan-tsai, is a very popular food in western and northeastern China and Taiwan. There are more than 11 different types of fermented vegetables or pickled vegetables in China (Hui et al. 2012). In recent years, the diversity of LAB has been determined using the 16S rRNA genes sequence and housekeeping gene sequence (*dnaA*, *pheS* and *rpoA*) analysis (Chen et al. 2006a; Chao et al. 2009). Eighteen species of LAB from five genera have been reported from suan cai from Taiwan, including *Enterococcus* (1 species), *Lactobacillus* (11 species), *Leuconostoc* (3 species), *Pediococcus* (1 species) (Chao et al. 2009).

2.4.4.3 LAB in Traditional Sausage and Fermented Meat-Based Food

Meat plays an important role in people's diet but it requires special storage measures since it is highly sensitive to microbial spoilage. Traditional methods for preservation of meat are drying, salting and fermentation. Worldwide, there is a vast variety of fermented food based on meat and fish. For example, 330 different types of sausages are produced in Germany alone (Lerche 1975). Fermented sausages are common products throughout world, and they are made using a diversity of production methods resulting in characteristics unique to the different countries or regions of the same country from which they originate (Table 2.18). It is well known that in the traditional fermentation process bacteria, yeast and fungi work in combination and affect the final quality of the fermented sausage. LAB are regarded as having an important contribution to the ripening process (Hammes et al. 1990) and they vary in species composition between different products (Table 2.17). Their essential role in this process was recognised first in the U.S.A. where patents for the application of *Lactobacillus plantarum*, *Lb. brevis* and *Lb. fermenti*, were obtained by Jensen and Paddock (1940). A thorough investigation of LAB in both commercial products and in ripening sausages showed that the dominant LAB were psychrophilic atypical streptobacteria (Reuter 1967).

Hammes (1985) analysed 37 samples from 12 suppliers to the German market and identified LAB including *P. acidilactici*, *P. pentosaceus*, *Lb. plantarum*, *Lb. sakei* and *Lb. surfatus* (Hammes 1985). Cocolin et al. (2004) studied the ecology of fresh sausages and characterised populations of LAB using a polyphasic approach after different storage times at 4 °C. The results showed that *Brochothrix thermosphacta* and *Lb. sakei* were the most abundant species present. In particular, *B. thermosphacta* was present throughout the process, as determined by both DNA and RNA analysis. Other bacterial species, mainly *Staphylococcus xylosus*, *Leuc. mesenteroides* and *Lb. curvatus*, were detected by DGGE. Moreover, after different storage times, different LAB species were identified, including *Lc. lactis* subsp. *lactis*, *Lb. casei*, *E. casseliflavus*, *Leuc. mesenteroides* and *Lb. sakei*.

2.4.5 LAB in Other Fermented Food

There are numerous plant-based fermented food products that are not pickled leaf vegetables as described above. These products are fermented from beans and other seeds, such as rice, maize and millet or root vegetables. LAB was involved in all of these processes, influencing the characteristics of flavour and texture, and also the probiotic qualities of the final product (Table 2.18). There are many kinds of beverage produced from fermented cereals. Dolo and pito are two similar West African traditional fermented beverages produced from sorghum grains that are popular drinks. They have contributed to the diet of people in West Africa together with other fermented foods for centuries (Odunfa 1985). Pito is common in Ghana, Togo and Nigeria, whereas dolo and other similar products (e.g. tchapalo and tchoukoutou), are common in Burkina Faso, Ivory Coast, Mali and Benin (Yao et al. 1995; Konlani et al. 1996; Kayode et al. 2004). Tarhana and tarhana-like products are traditional Turkish fermented cereal-based food products, which are well known under different names in the other countries, e.g. kishk in Syria, Palestine, Jordan, Lebanon and Egypt; talkuna in Finland; kushuk in Iraq and Iran; thanu in Hungary and trahanas in Greece (Siyamoğlu 1961; İbanoğlu and İbanoğlu 1999; Blandino et al. 2003). While their preparation techniques vary depending on region they are similar; after mixing all the ingredients dough is formed that is allowed fermenting for 1–7 days at room temperatures (25–30 °C). The fermentation is followed by drying and grinding. Yeast and LAB are the predominant microorganisms but the species composition and abundance varies between products (Table 2.19).

2.4.6 Prospects and Challenges

Throughout history traditional fermented foods have been regarded as the main source of nutrition for many rural communities and nomadic people. They

Table 2.18 Species of LAB found in fermented meat and fish-based products from around the world

Country/ region	Type of fermented product	Name of product	Method for identification	Species of LAB present	References
Turkey		Sucuk	Traditional culture- dependent and culture independent (rep-PCR fingerprinting and DGGE)	<i>Lb. alimentarius</i> , <i>Lb. plantarum</i> , <i>Lb. brevis</i> , <i>Lb. farciminis</i> , <i>Lb. sakei</i> , <i>Lb. curvatus</i> , <i>Lc. piscium</i> , <i>W. halotolerans</i> , <i>Leuc. mesenteroides</i> , <i>Leuc. citreum</i> , <i>W. viridescens</i>	Adewumi et al. (2013)
Spain	Sausages	Chorizo, fuet, salchichon	RAPD-PCR	<i>Lb. sakei</i> <i>Lb. curvatus</i> <i>Leuc. mesenteroides</i>	Aymerich et al. (2006)
Italy	Fresh sausages	Sausages	Traditional culture- dependent method and DGGE	<i>Lb. sakei</i> <i>Lb. curvatus</i> <i>Lb. casei</i> <i>Lc. lactis</i> subsp. <i>lactis</i> <i>Leuc. mesenteroides</i>	Cocolin et al. (2004)
Italy	Fermented sausages	Sausages	RAPD-PCR and DGGE	<i>Lb. sakei</i> , <i>Lb. curvatus</i> , <i>Lb. brevis</i> , <i>Lb. casei</i> , <i>Lb. plantarum</i> , <i>Lb. paraplantarum</i> , <i>Lc. garvieae</i> , <i>Lc. lactis</i> , <i>Leuc. carnosum</i> , <i>Leuc. mesenteroides</i> , <i>W. hellenica</i> , <i>W. paramesenteroides</i>	Urso et al. (2006)
Côte d'Ivoire	Fermented fish	Adjuevan	Traditional culture- dependent method and DGGE	<i>Lb. fermentum</i> , <i>Lb. delbrueckii</i> subsp. <i>bulgaricus</i> , <i>Lb. helveticus</i> , <i>Lc. garvieae</i> , <i>Lc. raffinolactis</i> , <i>Leuc. lactis</i> , <i>P. pentosaceus</i>	Clementine et al. (2012)
Italy	Fish product	Seafood salad	RAPD-PCR	<i>Lb. curvatus</i> , <i>Lb. malefermentans</i> , <i>Lb. plantarum</i> , <i>Lb. sanfranciscensis</i> , <i>C. piscicola</i> , <i>E. faecalis</i> , <i>Lc. lactis</i> , <i>Leuc. mesenteroides</i> , <i>Weissella</i> sp.	Andrighetto et al. (2009)

currently play an important role in improving the economy, finance and business of local societies. However, with accelerating urbanisation and a reduction in the nomadic life style, there are fewer and fewer traditional fermented foods routinely prepared traditionally at home. In addition, in order to meet the demand for traditional products by urban populations, and to improve food quality, safety and efficiency of production, these household fermentation technologies have been advanced to an industrial scale. However, this transition from small-scale household production to industrial manufacturing has been a challenge for food microbiologists. Advances have been made in our understanding of the species richness, diversity and behaviour of the microbial species present in fermented food. However, more work should be done to identify more LAB, to increase our knowledge of the mechanisms of fermentation, to understand the roles of each LAB species and to characterise probiotic bacteria.

2.5 Review of Biodiversity of Lactic Acid Bacteria in Silage

Silage is currently the most commonly preserved cattle feed in many countries (Cai 1999). Lactic acid bacteria (LAB), including rod and cocci (Fig. 2.9), play an important role in silage fermentation. LAB, which are microorganisms that naturally exist on forage crops, are responsible for silage fermentation and the occurrence of dry matter (DM) loss and proteolysis during storage. LAB commonly grow with other plant-associated microorganisms during silage fermentation, and they generally define the fermentation characteristics of silage. Moist dairy farm silage is based on natural lactic acid fermentation. The epiphytic LAB transform the water-soluble carbohydrates into organic acids during the ensiling process. As a result, the pH is reduced, and the forage is preserved. The fermentation quality may be influenced by the diversity, quantity and activity of the epiphytic LAB (Lin et al. 1992). Some research workers realised that most of the epiphytic LAB was caused by heterofermentation, which may not have positive organisms for lactic acid-dominating fermentation in the silo (Cai 1999).

As shown in Table 2.1, the natural fermentation processes in silages of corn, sorghum, forage paddy rice and alfalfa are dominated by species of *Weissella* (*W*), *Leuconostoc* (*Le.*), *Lactococcus* (*La.*) and *Lactobacillus* (*L.*). Some isolates from forage crops and grasses have been identified as species of lactobacilli, enterococci, pediococci, weissella, lactococci and leuconostocs. Cai (1999), Lin et al. (1992) and Pang et al. (2011) examined a large number of LAB isolated from forage crops and grasses (Fig. 2.10, Table 2.20) and found that the predominant LAB were lactic acid-producing cocci and that the least numerous LAB were lactobacilli (mostly homofermentative). Ennahar et al. (2003) also found that although all LAB groups were present in paddy rice silage, homofermentative lactobacilli and lactococci and heterofermentative leuconostocs were present in greater numbers.

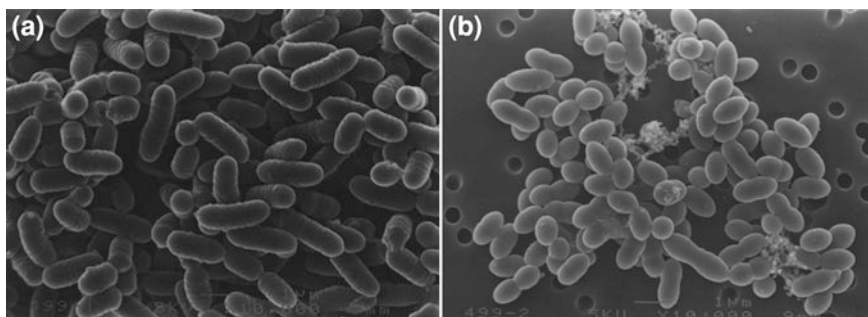


Fig. 2.9 Electronic-microscope of *Lactobacillus plantarum* (a, rod) and *Lactococcus lactis* (b, cocci) isolated from silage.

The lactobacilli play a more important role in the fermentation processes and effectively promote lactic acid fermentation for a longer period of time than lactic acid-producing cocci, e.g. enterococci, streptococci, leuconostocs, weissella and pediococci. Generally, when the lactobacilli reach a level of at least 10^5 colony forming units (cfu)/g fresh matter (FM), silage can be well preserved. *L. casei* and *L. plantarum* are usually found living in association with forage crops and silage. Many studies have been conducted on lactobacilli as the dominant microbial population on forage crops and farm silage (Cai 1999). The predominance of *L. plantarum* has been reported elsewhere (identification based on only 16S rDNA sequences and carbohydrate utilisation) (Cai 1999). Further, precise differentiation among these species was not conducted in silage samples. In addition, little is known about the prevalent subspecies of *L. plantarum*, which play a major role in silage fermentation. The most frequently presented microorganism, *L. coryniformis*, has often been found on plant material and in various silages. The presence of *L. curvatus* in sorghum silages has previously been reported, and its inoculation is highly effective in preserving silages of Italian ryegrass. The identification of *L. acidipiscis* and *L. sakei* subsp. *carneus* from forage crops was reported as useful for understanding their range of ecological niches.

The cocci, such as leuconostocs, pediococci and weissella strains, have been isolated at low frequencies in forage crops and their silages (Cai 1999; Lin et al. 1992). Certain *Weissella* (*W.*) isolates from silages have been identified as *W. paramesenteroides* (Cai 1999). The isolation of *W. hellenica* by Tohno et al. (2012) provides the first evidence that the natural habitats of this species are not only meat and meat products (Collins et al. 1993) but also vegetative forage crops with mixed pastures of timothy and orchardgrass. *W. cibaria*, was also found as epiphytic on corn stover by Pang et al. (2011, 2012). LAB strains, such as *Leuconostoc* and *Pediococcus*, have been isolated at low frequencies in forage crops and their silages (Cai 1999; Lin et al. 1992). They are also widely used as starter cultures or control barriers for food pathogens in vegetables. Pediococci are often found living in association with plant material, dairy products and foods produced by LAB (Cai

Table 2.19 LAB in other plant-based traditional fermented food from around the world

Country/ Region	Name of fermented product	Type of products	Raw material	Species of LAB	Counts of LAB as CFU/g	Reference
Zimbabwe	Chimera	Non-alcoholic and alcoholic beverages	Sorghum, bullrush millet or finger millet	ND		
Taiwan	Dochi	Seasoning for food	Black bean	4, 58, 72	4×10^1 to 1.1×10^7	Chen et al. (2006a)
Turkey	Tarhana	Cereal-based food	Wheat flour and yogurt	4, 13, 19, 24, 38, 57, 58, 65	1×10^3 to 1×10^6 varied depending on length of fermentation	Chen et al. (2006b) Sengun et al. (2009)
Mexico	Pozole	Maize dough	Maize	13, 20, 24, 38, 63	1×10^7 to 1×10^9 varied depending on length of fermentation	Omar and Ampe (2000)
Japan	Nukadoko	Fermented rice bran	Rice	8, 24, 10, 11, 19, 50, 65.		Sakamoto et al. (2011) Randazzo et al. (2002)
Africa	Gari	Fermented cassava	Cassava	11, 38, 57	1×10^6 to 1.8×10^9	Kostinek et al. (2005)
China	Sour congee	Fermented cereal gruel	Rice millet	3, 6, 11, 24, 35, 38, 51	ND	Yu et al. (2011)
China	Stinky tofu	Fermented chinese snack	Soybean	11, 12, 16, 17, 20, 24, 44, 50, 51, 53, 54, 58, 63, 65, 68, 69	1×10^5 to 1×10^7	Chaoi et al. (2008)
Ghana	Fermented cocoa beans	Raw material for chocolate	Cocoa beans	1, 4, 11, 24, 38, 50, 55, 57, 69		Camu et al. (2007)

(continued)

Table 2.19 (continued)

Country/ Region	Name of fermented product	Type of products	Raw material	Species of LAB	Counts of LAB as CFU/g	Reference
China	Vinegar	Seasoning for food	Sorghum pea, millet, wheat bran			
Africa	Dolo and Pito	Fermented beverages	Sorghum	19, 20, 24, 51, 54, 58		Sawadogo- Lingani et al. (2007)

Note 1. *E. casseliflavus*, 2. *E. durans*, 3. *E. faecalis*, 4. *E. faecium*, 5. *E. gallinarum*, 6. *E. italicus*, 7. *E. thailandicus*, 8. *Lb. acetotolerans*, 9. *Lb. acidophilus*, 10. *Lb. alimentarius*, 11. *Lb. brevis*, 12. *Lb. buchneri*, 13. *Lb. casei*, 14. *Lb. confuses*, 15. *Lb. coryniformis* subsp. *torquens*, 16. *Lb. crispatus*, 17. *Lb. crustorum*, 18. *Lb. curvatus*, 19. *Lb. delbrueckii* subsp. *bulgaricus*, 20. *Lb. delbrueckii* subsp. *delbrueckii*, 21. *Lb. delbrueckii* subsp. *indicus*, 22. *Lb. delbrueckii* subsp. *lactis*, 23. *Lb. diolivorans*, 24. *Lb. fermentum*, 25. *Lb. graminis*, 26. *Lb. hamsteri*, 27. *Lb. helveticus*, 28. *Lb. hilgardii*, 29. *Lb. kefiranoferiens* subsp. *kefiranoferiens*, 30. *Lb. kefiranoferiens* subsp. *kefirgranum*, 31. *Lb. kefirgranum*, 32. *Lb. kefiri*, 33. *Lb. mindensis*, 34. *Lb. parabuchneri*, 35. *Lb. paracasei*, 36. *Lb. paralimentarius*, 37. *Lb. pentosus*, 38. *Lb. plantarum*, 39. *Lb. pontis*, 40. *Lb. rapi*, 41. *Lb. reuteri*, 42. *Lb. rhamnosus*, 43. *Lb. rossia*, 44. *Lb. sakei*, 45. *Lb. sanfrancisco*, 46. *Lb. spicheri*, 47. *Lb. sunkii*, 48. *Lb. uvarum*, 49. *Lc. garvieae*, 50. *Lc. lactis* subsp. *cremoris*, 51. *Lc. lactis* subsp. *lactis*, 52. *Lc. raffinolactis*, 53. *Leuc. citreum*, 54. *Leuc. lactis*, 55. *Leuc. mesenteroides*, 56. *Leuc. mesenteroides* subsp. *mesenteroides*, 57. *Leuc. pseudomesenteroides*, 58. *P. acidilactici*, 59. *P. damnosus*, 60. *P. ethanolidurans*, 61. *P. parvulus*, 62. *P. pentosaceus*, 63. *S. bovis*, 64. *S. parauberis*, 65. *S. thermophilus*, 66. *S. mutans*, 67. *S. salivarius*, 68. *W. cibaria*, 69. *W. confusa*, 70. *V. carniphilus*, 71. *W. viridescens*, *W. paramesenteroides*
A. *Corynebacteria pseudodiphtherium*, B. *Saccharomyces cerevisiae*, C. *Candida kefyr*, D. *Candida lusitanae*, E. *Candida colliculosa*, F. *Kluyveromyces maxianus*, G. *Debaryomyces hansenii*

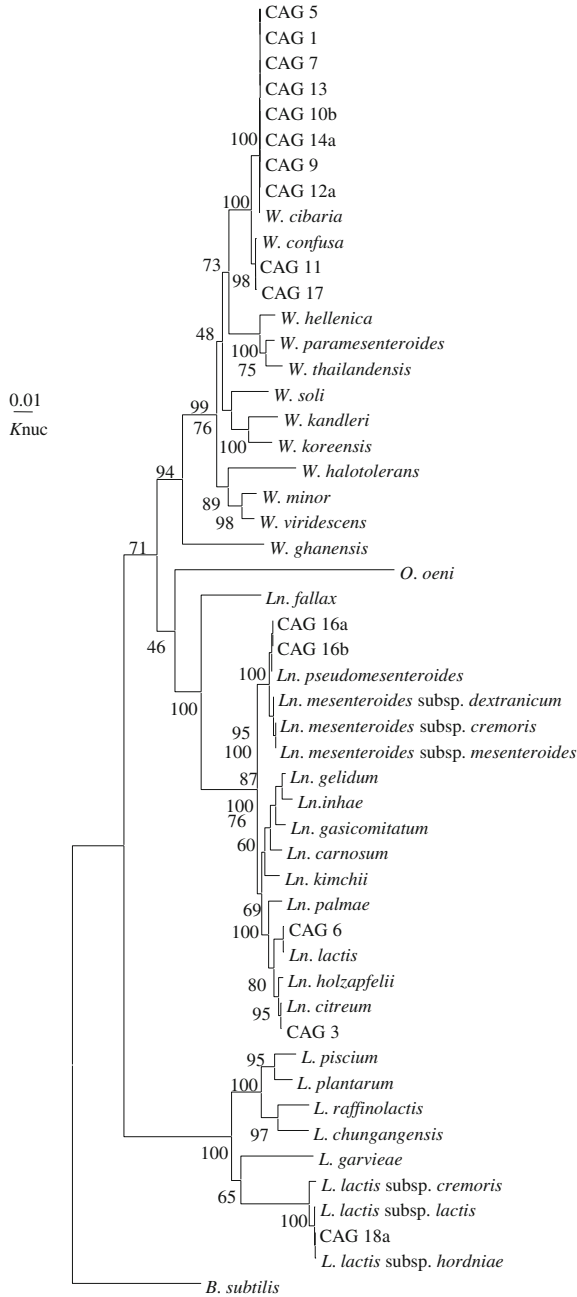


Fig. 2.10 Phylogenetic tree showing the relative positions of silage strains with *Weissella*, *Leuconostoc* and *Lactococcus* species, as inferred by the neighbour-joining method with 16S rRNA gene sequences. *B. subtilis* is used as an outgroup. Bootstrap values for a total of 1,000 replicates are shown at the nodes of the tree. The bar indicates 1 % sequence divergence. Knuc, nucleotide substitution rates. W., *Weissella*; Ln., *Leuconostoc*; L., *Lactococcus*

Table 2.20 The distribution of Lactic acid bacteria on silages (CFU/g of FM)

Silage	<i>W. cibaria</i>	<i>W. confusa</i>	<i>Le. citreum</i>	<i>Le. lactis</i>	<i>Le. pseudomesenteroides</i>	<i>Lc. Lactis</i> subsp. <i>lactis</i>	<i>Lb. paraplantarum</i>	<i>Lb. plantarum</i>
Corn (Cultivar: Zhongyuandan 32)	4.6×10^7	ND	ND	ND	ND	ND	ND	ND
Corn (Nongda 108)	3.0×10^8	ND	ND	ND	ND	ND	ND	ND
Corn (Nongda 95)	6.0×10^7	ND	ND	ND	ND	ND	ND	ND
Corn (Yousi)	4.5×10^7	4.5×10^7	ND	ND	ND	ND	ND	ND
Corn (Tiandan)	2.6×10^8	ND	ND	ND	ND	ND	ND	ND
Sorghum (Tiangaoliang M-81)	ND	ND	0.2×10^9	ND	ND	ND	ND	0.4×10^9
Forage paddy rice (Shuidao 305)	0.3×10^8	0.3×10^8	ND	0.3×10^8	ND	0.3×10^8	ND	0.9×10^8
Alfalfa (Derfy)	ND	ND	ND	ND	0.5×10^7	ND	0.3×10^7	0.2×10^7

ND not detected; CFU colony forming unit; FM fresh matter
W, *Weissella*; *Le.*, *Leuconostocs*; *Lc.*, *Lactococcus*; *Lb.*, *Lactobacillus*

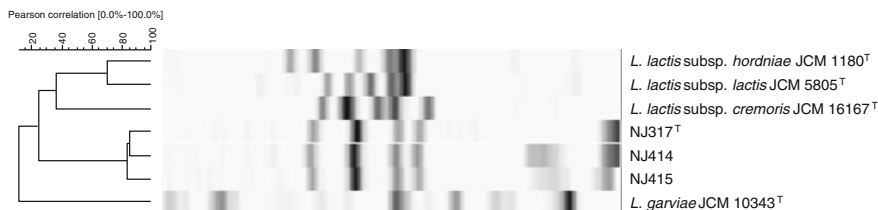


Fig. 2.11 A dendrogram illustrating the relatedness of the ribotyping patterns of NJ 317^T among closely related species of the genus *Lactococcus*. The dendrogram was analysed by Pearson similarity coefficient analysis and UPGMA algorithm

1999; Lin et al. 1992), and several papers have reported pediococci as the dominant microbial population on forage crops and silage. Some isolates from forage crops and silage have been identified as *P. acidilactici* and *P. pentosaceus* (Lin et al. 1992). The presence of *Enterococcus* (*E.*) *faecalis* suggests a faecal origin for some PRS microorganisms. The natural habitat of lactococci is milk, but *La. lactis* subsp. *lactis* has been isolated previously from plants, vegetables and cereals. Native LAB populations on plants are not the same from crop to crop. Native LAB levels are generally lower in alfalfa (*Medicago sativa* L.), perennial grasses (10^5 cfu/g FM and greater) or (10^6 cfu/g FM), corn (*Zea mays* L., 10^7 cfu/g FM) and sorghum (*Sorghum bicolor* L. Moench, 10^7 cfu/g FM) (Pahlow et al. 2003). Environmental conditions also have an effect on native LAB levels. In alfalfa, native LAB was higher in warmer temperatures, after a longer wilting time and when rainfall occurred during wilting (Muck 1989). Moreover, native LAB is low in the standing crop and increases exponentially after chopping in both corn and alfalfa (Lin et al. 1992).

The populations of epiphytic LAB in farm silage are not always large enough or do not have a composition suitable for promoting efficient homo-lactic fermentation. The effectiveness of silage inoculants depends upon the quality (growth rate and environmental adaptability) and quantity of the microorganisms used, among other things. In general, favourable improvements in the rate of pH decline and increased lactic acid levels have been noted with legumes, grasses and cereal silages. In previous investigations of Cai et al. (1999), the inoculation of various forages with homofermentative *Lactobacillus* spp. (predominantly *L. plantarum*) in combination with *Pediococcus*, *Enterococcus* or *Lactococcus* spp. had beneficial effects (Fig. 2.11).

The genetic interrelationships of the silage strains and related LAB have been studied extensively by using Ribotyping, 16S rDNA sequence analysis and DNA–DNA hybridisation experiments, and some new species, such as *Lactococcus fujiensis* from Chinese cabbage silage and *Lactobacillus nasuensis* from sudangrass silage, have been added by Cai et al. (2011, 2012). As shown in Fig. 2.3, the ribotyping patterns revealed that strains NJ 317, NJ 414 and NJ 415 were well separated from the reference *Lactococcus* species.

Table 2.21 Characteristics and diversity of lactic acid bacteria strains isolated from silage

Character	Group A CAG 1	Group B CAG 11	Group C CAG 3	Group D CAG 6	Group E CAG 16a	Group F CAG 18a	Group G CAG 20	Group H CAG 18b
Shape	Cocci	Cocci	Cocci	Cocci	Cocci	Cocci	Rod	Rod
Gram stain	+	+	+	+	+	+	+	+
Catalase	-	-	-	-	-	-	-	-
Gas from glucose	+	+	+	+	+	-	-	-
Optical form of lactate	D(-)	D(-)	D(-)	D(-)	D(-)	L(+)	DL	DL
Fermentation type	Hetero	Hetero	Hetero	Hetero	Hetero	Homo	Homo	Homo
Growth at temperature (°C):								
10	-	-	+	+	+	-	+	+
15	+	+	+	+	+	+	+	+
40	+	+	+	+	+	+	+	+
45	-	-	-	-	-	-	-	-
Growth in NaCl:								
3.0 %	+	+	+	+	+	+	+	+
6.5 %	-	-	-	-	-	-	w	-
Growth at pH:								
3.0	-	-	-	-	-	-	w	-
3.5	-	-	-	-	-	-	+	w
4.0	+	+	+	+	+	+	+	+
8.0	+	+	+	+	+	+	+	+

+, 90 % or more of the strains positive; -, 90 % or more of the strains negative; w weakly positive; *Homo* homofermentative; *Hetero* heterofermentative
^a Group F strain was able to produce γ-aminobutyric (GABA) from L-monosodium glutamate, and grow in 0.1 % bile salt

Table 2.22 DNA base composition and DNA relatedness among *Lactococcus fujiensis* and phylogenetically closely related *Lactococcus* species

Strain	G+C content (mol%)	DNA–DNA reassociation (%) with NJ 317 ^T	JCM 5805 ^T	JCM 10343 ^T
NJ 317 ^T	42.1	100.0	15.4	15.6
NJ 414	42.2	96.6	17.7	12.4
NJ 415	42.5	98.2	17.6	9.8
<i>Lactococcus lactis</i> subsp. <i>lactis</i> JCM 5805 ^T	39.4	20.2	100.0	13.2
<i>Lactococcus lactis</i> subsp. <i>hordniae</i> JCM 1180 ^T	nd	11.7	85.6	10.4
<i>Lactococcus lactis</i> subsp. <i>cremoris</i> JCM 16167 ^T	nd	9.4	80.2	17.0
<i>Lactococcus garvieae</i> JCM 10343 ^T	44.3	12.3	8.4	100.0
<i>Lactococcus piscium</i> JCM 11055 ^T	38.5	8.6	7.8	18.6
<i>Lactococcus plantarum</i> JCM 11056 ^T	nd	10.3	10.3	8.6
<i>Lactococcus raffinolactis</i> JCM 5706 ^T	41.5	11.3	12.4	10.0

JCM Japan Collection of Microorganisms. ^T type strain. *nd*, no data

These strains shared similar phenotypic characteristics and exhibited intragroup DNA homology values of over 96.6 %, which indicates that they are a single species. The G+C contents of the DNA for the strains were 42.1–42.5 mol%. DNA–DNA hybridisation indicated that these strains had low levels (<20.2 %) of DNA relatedness with *Lactococcus lactis*, *Lactococcus garvieae* and other type strains of previously described species, which shows that they were different species (Table 2. 21). Therefore, these strains, which are isolated from the silage, are placed in the genus *Lactococcus* as a new species, *Lactococcus fujiensis* (Table 2.22).

References

- Abdel Moneim ES, Abdalla AI, Ahmed AF. Chemical and microbiological quality of Garri Sudanese fermented camel's milk product. *Food Sci Technol*. 2006;42:321–328.
- Abdel Gadir WS, Ahmeda TK, Dirar HA. The traditional fermented milk products of the Sudan. *Int J Food Microbiol*. 1998;44:1–13.
- Abriouel H, Martin-Platero A, Maqueda M, Valdivia E, Martinez-Bueno M. Biodiversity of the microbial community in a Spanish farmhouse cheese as revealed by culture-dependent and culture-independent methods. *Int J Food Microbiol*. 2008;127:200–8.
- Adams MR. Safety of industrial lactic acid bacteria. *J Biotechnol*. 1999;68:171–8.
- Adewumi GA, Oguntuyinbo Folarin A, Keisam S, Romi W, Jeyaram K. Combination of culture-independent and culture-dependent molecular methods for the determination of bacterial community of iru, a fermented Parkia latilobosa seeds. *Frontiers in Microbiol*. 2013;3(2):436.

- Afzal MI, Jacquet T, Delaunay S, Borges F, Millièrè JB, Revol-Junelles AM, Cailliez-Grimal C. *Carnobacterium maltaromaticum*: identification, isolation tools, ecology and technological aspects in dairy products. *Food Microbiol.* 2010;27:573–9.
- Aguirre M, Collins MD. Phylogenetic analysis of some *Aerococcus*-like organisms from urinary tract infections: description of *Aerococcus urinae* sp. nov. *J Gen Microbiol.* 1992;138:401–5.
- Ahmed AM. The common microorganisms in the Sudanese white soft cheese. *Sud J Vet Sci Anim Husb.* 1997;36:109–12.
- Ahmed IAM, Morishima I, Babiker EE, Mori N. Characterisation of partially purified milk clotting enzyme from *Solanum dubium* Fresen seeds. *Food Chem.* 2009;116:395–400.
- Airidengcaicike, Chen X, Du XH, Wang WH, Zhang JC, Sun ZH, Liu WJ, Li L, Sun TS, Zhang HP. Isolation and identification of cultivable lactic acid bacteria in traditional fermented milk of Tibet in China. *Int J Dairy Technol.* 2010;63(3):437–44.
- Akabanda F, Owusu-Kwarteng J, Glover LKR, Tano-Debrah K. Microbiological characteristics of Ghanaian traditional fermented milk product. *Nunu. Nat Sci.* 2010;8(9):178–87.
- Alegria A, Alvarez-Martin P, Sacristan N, Fernandez E, Delgado S, Mayo B. Diversity and evolution of the microbial populations during manufacture and ripening of Casin, a traditional Spanish, starter-free cheese made from cow's milk. *Int J Food Microbiol.* 2009;136:44–51.
- Alessandria V, Dolci P, Rantsiou K, Pattono D, Dalmasso A, Civera T, Coccolin L. Microbiota of the Planalto de Bologna: an artisanal cheese produced in uncommon environmental conditions in the Cape Verde Islands. *World J Microbiol Biotechnol.* 2010;26:2211–21.
- Andrewes FW, Ilorder TJ. A study of the Streptococci pathogenic for man. *Lancet.* 1906;ii:708–13.
- Andrighetto C, Lombardi A, Ferrati M, Guidi A, Corrain C, Arcangeli G. Lactic acid bacteria biodiversity in Italian marinated seafood salad and their interactions on the growth of *Listeria monocytogenes*. *Food Control.* 2009;20:462–8.
- Antunes A, Rainey FA, Nobre MF, Schumann P, Ferreira AM, Ramos A, Santos H, Da Costa MS. *Leuconostoc ficulneum* sp. nov., a novel lactic acid bacterium isolated from a ripe fig, and reclassification of *Lactobacillus fructosus* as *Leuconostoc fructosum* comb. nov. *Int J Syst Evol Microbiol.* 2002;52:647–55.
- Aponte M, Fusco V, Andolfi R, Coppola S. Lactic acid bacteria occurring during manufacture and ripening of Provolone del Monaco cheese: detection by different analytical approaches. *Int Dairy J.* 2008;18:403–13.
- Ashmaig AA, Hasan, El-Gaali E. Identification of lactic acid bacteria isolated from traditional Sudanese fermented camel's milk (Gariss). *Afr J Microbiol Res.* 2009;3:451–457.
- Ashmaig A, Hasan A, El-Gaali E. Identification of lactic acid bacteria isolated from traditional Sudanese fermented camel's milk (Gariss). *Afr J Microbiol Res.* 2009;3:451–7.
- Aymerich T, Marti'n B, Garriga M, Vidal-Carou M.C, Bover-Cid S, Hugas M. Safety properties and molecular strain typing of lactic acid bacteria from slightly fermented sausages. *J Appl Microbiol.* 2006;100:40–49.
- Azar M, Ter-Sarkissian N, Ghavifek H, Ferguson T, Ghassemi H. Microbiological aspects of Sangak bread. *Int J Food Sci Technol.* 1977;14:251–4.
- Bao QH, Chen X, Liu HX, Zhang WY, Liu WJ, Yu J, Wang F, Zhang HP. Isolation and identification of cultivable lactic acid bacteria from traditional goat milk cake in Yunnan province of China. *Afr J Microbiol Res.* 2011;5(29):5284–91.
- Bao QH, Yu J, Liu WJ, Qing MJ, Wang WH, Xia Chen Wang F, Li MH, Wang HM Lv Q, Zhang HP. Predominant lactic acid bacteria in traditional fermented yak milk products in the Sichuan Province of China. *Dairy Sci Technol.* 2012a;92:309–319.
- Bao QH, Liu WJ, Yu J, Wang WH, Qing MJ, Chen X, Wang F, Zhang JC, Zhang WY, Qiao JM, Sun TS, Zhang HP. Isolation and identification of cultivable lactic acid bacteria in traditional yak milk products of Gansu Province in China. *J Gen Appl Microbiol.* 2012b;58:95–105.
- Barber S, Ba'guena R, Martinez-Anaya MA, Torner MJ. Microflora de la masa madre panaria. I. Identificación propiedades funcionales de microorganismos de masas madre industriales, elaboradas con harina de trigo. *Revista de Agroquímica y Tecnología de Alimentos.* 1983;23:552–562.

- Batt CA. *Lactococcus* introduction. In: Robinson RK, Batt CA, Patel PD, editors. Encyclopedia of food microbiology. San Diego: Academic Press; 2000. P. 1164–1166.
- Boraam F, Faïd M, Larpent JP, Breton A. Lactic acid bacteria and yeasts associated with traditional sourdough Moroccan bread. *Sciences des Aliments*. 1993;13:501–9.
- Bouton Y, Guyot P, Beuvier E, Tailliez P, Grappin R. Use of PCR-based methods and PFGE for typing and monitoring homofermentative lactobacilli during Comté cheese ripening. *Int J of Food Microbiol*. 2002;76(1):27–38.
- Brinzel F, Castioni A, Olukoya DK, et al. *Lactobacillus plantarum* subsp. *argenteratensis* subsp. nov., isolated from vegetable matrices. *Int J Syst Bacteriol*. 2005;55(4):1629–34.
- Brooijmans RJW, de Vos WM, Hugenholtz J. The electron transport chains of *Lactobacillus plantarum* WCFS1. *Appl Environ Microbiol*. 2009;75:3580–5.
- Bui TPN, Kim YJ, In JG, Yang DC. *Lactobacillus koreensis* sp. nov., isolated from the traditional Korean food kimchi. *Int J Syst Evol Microbiol*. 2011;61:772–776.
- Burentegusi MT, Nakamura S, et al. Identification of lactic acid bacteria isolated from fermented mare's milk "chigee" in Inner Mongolia. *China Anim Sci Technol*. 2002;73:441–8.
- Cai Y. Identification and characterization of Enterococcus species isolated from forage crops and their influence on silage fermentation. *J Dairy Sci*. 1999;82:2466–71.
- Cai YM, Yang JS, Pang HL, Kitahara M. *Lactococcus fujiensis* sp. nov., a lactic acid bacterium isolated from vegetable matter. *Int J Syst Evol Microbiol*. 2011;61:1590–4.
- Cai YM, Pang HL, Kitahara MK, Ohkum M. *Lactobacillus nasuensis* sp. nov., a lactic acid bacterium isolated from silage, and emended description of the genus *Lactobacillus*. *Int J Syst Evol Microbiol*. 2012;62:1140–4.
- Callon C, Delbes C, Duthoit F, Montel MC. Application of SSCP-PCR fingerprinting to profile the yeast community in raw milk Salers cheeses. *Syst Appl Microbiol*. 2006;29:172–80.
- Callon C, Duthoit F, Delbes C, Ferrand M, Le Frileux Y, De Cremoux R, Montel MC. Stability of microbial communities in goat milk during a lactation year: molecular approaches. *Syst Appl Microbiol*. 2007;30:547–60.
- Camu N, De Winter T, Verbrughe K, Cleenwerck I, Vandamme P, Takrama JS, Vancanneyt M, De Vuyst L. Dynamics and biodiversity of populations of lactic acid bacteria and acetic acid bacteria involved in spontaneous heap fermentation of cocoa beans in Ghana. *Appl Environ Microbiol*. 2007;73(6):1809–24.
- Carvalho MGS, Shewmaker PL, Steigerwalt AG., Morey RE, Sampson AJ, Joyce K, Barrett TJ, Teixeira LM, Facklam RR. *Enterococcus caccae* sp. nov., isolated from human stools. *Int J Syst Evol Microbiol*. 2006;56:1505–1508.
- Chao SH, Kudo Y, Tsai YC, Watanabe K. *Lactobacillus futsaii* sp. nov., isolated from fu-tsai and suan-tsai, traditional Taiwanese fermented mustard products. *Int J Syst Evol Microbiol*. 2012;62:489–494.
- Chao SH, Wu RJ, Watanabe K, Chieh YT. Diversity of lactic acid bacteria in suan-tsai and fu-tsai, traditional fermented mustard products of Taiwan. *Int J Food Microbiol*. 2009;135:203–10.
- Chao SH, Tomii Y, Watanabe K, Tsai YC. Diversity of lactic acid bacteria in fermented brines used to make stinky tofu. *Int J Food Microbiol*. 2008;123:134–41.
- Chelule PK, Mokoena MP, Gqaleni N. Advantages of traditional lactic acid bacteria fermentation of food in Africa. In: Méndez-Vilas A, editor. Current research, technology and education topics in applied microbiology and microbial biotechnology. 2nd ed. Formatex Research Center; 2010. p. 1160–1167.
- Chen H, Wang SY, Chen MJ. Microbiological study of lactic acid bacteria in kefir grains by culture-dependent and culture-independent methods. *Food Microbiol*. 2008;(25)3:492–501.
- Chen YS, Chang CH, Pan SF, Wang LT, Chang YC. *Lactococcus taiwanensis* sp. nov., a novel lactic acid bacterium isolated from fresh cummingcordia. *IJSEM Papers in Press*. Published November 23, 2012; doi:10.1099/ij.s.0.045757-0.
- Chen XP, Liu HY, Wei XC, Ma YM, Song LJ. Study on separation and identification of lactic acid bacteria from naturally fermented sauerkraut. *Food sci China (with English abstract)*. 2006a;27(2):91–6.

- Chen YS, Yanagida F, Hsu JS. Isolation and characterization of lactic acid bacteria from suan-tsai (fermented mustard), a traditional fermented food in Taiwan. *J Appl Microbiol.* 2006;101:125–30.
- Chen YF, Sun TS, Wang JC, Airden CK, Bai M, Zhang HP. Comparison of nutrition and microbiological compositions between two types of fermented milk from Tibet in China. *Int J Food Sci Nutr.* 2009;60(S7):243–50.
- Chen YS, Lin YH, Pan SF, Ji SH, Chang YC, Yu CR, Liou MS, Wu HC, Ootoguro M, Yanagida F, Liao CC, Chiu CM, Huang BQ. *Enterococcus saccharolyticus* subsp. *taiwanensis* subsp. nov., isolated from broccoli. *Int J Syst Evol Microbiol.* 2013a;63:4691–7.
- Chen YS, Chang CH, Pan SF, Wang LT, Chang YC, Wu HC, Yanagida F. *Lactococcus taiwanensis* sp. nov., a lactic acid bacterium isolated from fresh cummingcordia. *Int J Syst Evol Microbiol.* 2013b;63:2405–9.
- Cho SL, Nam SW, Yoon JH, Lee JS, Sukhoom A, Kim W. *Lactococcus chungangensis* sp. nov., a lactic acid bacterium isolated from activated sludge foam. *Int J Syst Evol Microbiol.* 2008;58:1844–9.
- Choi HJ, Cheigh CI, Kim SB, Lee JC, Lee DW, Choi SW, Park JM, Pyun YR. *Weissella kimchii* sp. nov., a novel lactic acid bacterium from kimchi. *Int J Syst Evol Microbiol.* 2002;52:507–11.
- Clementine KA, Nguessan KF, Thomas DA, Dje MK, Montet D. Application of culture dependent methods and culture-independent methods (DGGE analysis) to study Lactic acid bacteria ecology of Ivorian fermented fish Adjuevan. *Chall Mod Technol.* 2012;3(1):51–6.
- Cocolin L, Aggio D, Manzano M, Cantoni C, Comi G. An application of PCR-DGGE analysis to profile the yeast populations in raw milk. *Int Dairy J.* 2002;12:407–11.
- Cocolin L, Rantsiou K, Iacumin L, Urso R, Cantoni C, Comi G. Study of the ecology of fresh sausages and characterization of populations of lactic acid bacteria by molecular methods. *Appl Environ Microbiol.* 2004;70(4):1883–94.
- Collins MD, Jones D, Farrow JAE, Kilpper-Balz R, Schleifer KH. *Enterococcus avium* nom. rev., comb. nov.; *E. casseliflavus* nom. rev., comb. nov.; *E. durans* nom. rev., comb. nov.; *E. gallinarum* comb. nov.; and *E. malodoratus* sp. Nov. *Int J Syst Evol Bacteriol.* 1984;34(2):220–223.
- Collins MD, Farrow JAE, Jones D. *Enterococcus mundtii* sp. nov. *Int J Syst Bacteriol.* 1986;36:8–12.
- Collins MD, Farrow JAE, Phillips BA, Ferusu S, Jones D. Classification of *Lactobacillus divergens*, *Lactobacillus piscicola*, and some catalase-negative, asporogenous, rod-shaped bacteria from poultry in a new genus, *Carnobacterium*. *Int J Syst Bacteriol.* 1987;37:310–6.
- Collins MD, Facklam RR, Farrow JAE, Williamson R. *Enterococcus raffinosus* sp. nov., *Enterococcus solitarius* sp. nov. and *Enterococcus pseudoavium* sp. nov. *FEMS Microbiol Lett.* 1989;57:283–8.
- Collins MD, Rodrigues UM, Pigott NE, Facklam RR. Validation List no. 38 *Int J Syst Bacteriol.* 1991;41:456–457.
- Collins MD, Rodrigues UM, Ash C, Aguirre M, Farrow JAE, Martinez-Murcia A, Phillips BA, Williams AM, Wallbanks S. Phylogenetic analysis of the genus *Lactobacillus* and related lactic acid bacteria as determined by reverse transcriptase sequencing of 16S rRNA. *FEMS Microbiol Lett.* 1991b;77:5–12. doi:[10.1111/j.1574-6968.1991.tb04313.x](https://doi.org/10.1111/j.1574-6968.1991.tb04313.x).
- Collins MD, Samelis J, Metaxopoulos J, Wallbanks S. Taxonomic studies on some leuconostoc-like organisms from fermented sausages: description of a new genus *Weissella* for the *Leuconostoc paramesenteroides* group of species. *J Appl Microbiol.* 1993a;75:595–603.
- Collins MD, Metaxopoulos J, Wallbanks S. Taxonomic study on some leuconostoc-like organisms from fermented sausages: Description of a new genus *Weissella* for the *Leuconostoc paramesenteroides* group of species. *J Appl Bacteriol.* 1993b;75:595–603.
- Collins MD, Jovita RM, Hutson RA, Ohlén M, Falsen E. *Aerococcus christensenii* sp. nov., from the human vagina. *Int J Syst Evol Microbiol.* 1999;49:1125–8.
- Coppola S, Pepe O, Masi P, Sepe M. Characterization of leavened doughs for pizza in Naples. *Adv Food Sci.* 1996;18:160–2.

- Coppola R, Blaiotta G, Ercolini D, Moschetti G. Molecular evaluation of microbial diversity occurring in different types of Mozzarella cheese. *J Appl Microbiol.* 2001;90:414–20.
- Corsetti A, Lavermicocca P, Morea M, Baruzzi F, Tosti N, Gobetti M. Phenotypic and molecular identification and clustering of lactic acid bacteria and yeasts from wheat (species *Triticum durum* and *Triticum aestivum*) sourdoughs of Southern Italy. *Int J Food Microbiol.* 2001;64:95–104.
- Cotta MA, Whitehead TR, Falsen E, Moore E, Lawson PA. Erratum to: Two novel species *Enterococcus lemanii* sp. nov. and *Enterococcus eurekaensis* sp. nov., isolated from a swine-manure storage pit. *Antonie Van Leeuwenhoek.* 2013;103:1409–18.
- Cousin S, Gulat-Okalla ML, Motreff L, Gouyette C, Bouchier C, Dominique Clermont, Bizet C. *Lactobacillus gigeriorum* sp. nov., isolated from chicken crop. *Int J Syst Evol Microbiol.* 2012;62:330–334.
- Cousin S, Motreff L, Gulat-Okalla ML, Gouyette C, Cathrin S, Schumann P, Begaud E, Bouchier C, Clermont D, Bizet C. *Lactobacillus pasteurii* sp. nov. and *Lactobacillus hominis* sp. nov. *Int J Syst Evol Microbiol.* 2013;63:53–9.
- David B, Dennis SN, Kim IS, Finn KV, Sawadogo-Lingania H, Derkx PMF, Jespersena L. *Lactobacillus delbrueckii* subsp. *jakobsenii* subsp. nov., isolated from dolo wort; an alcoholic fermented beverage in Burkina Faso *Int J Syst Evol Microbiol.* 2013. doi:[10.1099/ijs.0.048769-0](https://doi.org/10.1099/ijs.0.048769-0).
- De graef EM, Devriese LA, Vancanneyt M., Baele M, Collins MD, Lefebvre K, Swings J, Haesebrouck F. Description of *Enterococcus canis* sp. nov. from dogs and reclassification of *Enterococcus porcinus* (Teixeira et al. 2001 as a later synonym of *Enterococcus villorum* Vancanneyt et al. 2001). *Int J Syst Evol Microbiol.* 2003;53:1069–1074.
- De vaux A, Laguerre G., Diviès C, Prévost H. *Enterococcus asini* sp. nov. Isolated from the caecum of donkeys (*Equus asinus*). *Int J Syst Evol Bacteriol.* 1998;48:383–387.
- Delbes C, Ali-Mandjee L, Montel MC. Monitoring bacterial communities in raw milk and cheese by culture-dependent and -independent 16S rRNA gene-based analyses. *Appl Environ Microbiol.* 2007;73:1882–91.
- Dessart SR, Steenson LR. Biotechnology of dairy *Leuconostoc*. In: Hui YH, Khachatourians GG, editors. *Food biotechnology: microorganisms*. New York: Wiley-Interscience; 1995. p. 665–702.
- Devriese LA, Ceysens K, Rodrigues UM, Collins MD. *Enterococcus columbae*, a species from pigeon intestines. *FEMS Microbiol Lett.* 1990;71:247–52.
- Devriese LA, Pot B, Collins MD. Phenotypic identification of the genus *Enterococcus* and differentiation of phylogenetically distinct enterococcal species and species group. *J Appl Bacteriol.* 1993;75:399–408.
- Dewan S, Tamang JP. Dominant lactic acid bacteria and their technological properties isolated from the Himalayan ethnic fermented milk products. *Antonie van Leeuwenhoek.* 2007;92:343–352.
- Di Cagno R, Tamborrino A, Gallo G, Leone C, de Angelis M, Faccia M, Amirante P, Gobetti M. Uses of mares' milk in manufacture of fermented milks. *Int Dairy J.* 2004;14:767–75.
- Dicks LMT, Fantuzzi L, Gonzalez FC, Du toit M, Dellaglio F. *Leuconostoc argentinum* sp. nov., isolated from argentine raw milk. *Int J Syst Bacteriol.* 1993;43:347–351.
- Dicks L, Dellaglio F, Collins M. Proposal to reclassify *Leuconostoc oenos* as *Oenococcus oeni* [corrig.] gen. nov., comb. nov. *Int J Syst Evol Microbiol.* 1995;45:395–7.
- Dirar HA. The indigenous fermented foods of the sudan. A study in African food and Nutrition, CAB International, Cambridge, UK. 1993.
- Dmitriy VV, Amselle M, Beck BJ, Popham D L, Whittaker P, Wang H, Kerrigan E, Chizhikov VE. *Lactobacillus brantae* sp. nov., isolated from faeces of Canada geese (*Branta canadensis*). *J Syst Evol Microbiol.* 2012;62:2068–2076.
- Dobson A, O'sullivan O, Cotter PD, Ross P, Hill C. High-throughput sequence-based analysis of the bacterial composition of kefir and an associated kefir grain. *FEMS Microbiol Lett.* 2011;320:56–62.

- Doi K, Nishizaki Y, Fujino Y, Ohshima T, Ohmomo S, Ogata S. *Pediococcus lolii* sp. nov., isolated from ryegrass silage. *Int J Syst Evol Microbiol*. 2009;59:1007–1010.
- Dolci P, Alessandria V, Rantsiou K, Rolle L, Zeppa G, Cocolin L. Microbial dynamics of Castelmagno PDO, a traditional Italian cheese, with a focus on lactic acid bacteria ecology. *Int J Food Microbiol*. 2008;122:302–11.
- Dolci P, Alessandria V, Rantsiou K, Bertolino M, Cocolin L. Microbial diversity, dynamics and activity throughout manufacturing and ripening of Castelmagno PDO cheese. *Int J Food Microbiol*. 2010;143:71–5.
- Duan Y, Tan Z, Wang Y, Li Z, Li Z, Qin G, Huo Y, Cai Y. Identification and characterization of lactic acid bacteria isolated from Tibetan Qula cheese. *J Gen Appl Microbiol*. 2008;54:51–60.
- Duthoit F, Godon JJ, Montel M. Bacterial community dynamics during production of registered designation of origin Salers cheese as evaluated by 16S rRNA gene single-strand conformation polymorphism analysis. *Appl Environ Microbiol*. 2003;69:3840–8.
- El Mardi MM. A study on fermented milk 'roub'. M.Sc. thesis, University of Khartoum, Sudan. 1988.
- El-Baradei G, Delacroix-Buchet A, Jean-Claude O. Biodiversity of bacterial ecosystems in traditional Egyptian Domiati Cheese. *Appl Environ Microbiol*. 2007;73(4):1248–1255.
- El-Owni AOO, Hamid OIA. Effect of storage period on weight loss, chemical composition, microbiological and sensory characteristics of Sudanese white cheese (Gibna Bayda). *Pak J Nutr*. 2008;7:75–80.
- EI-Sheikh NAA. Production of Mudaffara cheese from cows and goats milk. M.Sc. Thesis, University of Khartoum, Sudan. 1997.
- Elisa S, Sandra T, Felis GE. The Genus *Lactobacillus*: a taxonomic update. *Probiotics Antimicro Prot*. 2012;4:217–226.
- Elmagli AAO, El-Zubeir IEM. Study on the compositional quality of pasteurized milk in Khartoum state (Sudan). *Int J Dairy Sci*. 2006;1:12–20.
- Endo A, Irisawa T, Futagawa-Endo Y, Takano K, MT, Okada S, Dicks L M. T. Characterization and emended description of *Lactobacillus kunkeei* as a fructophilic lactic acid bacterium. *Int J Syst Evol Microbiol*. 2012;62:500–504.
- Endo A, Okada S. Reclassification of the genus *Leuconostoc* and proposals of *Fructobacillus fructosus* gen. nov., comb. nov., *Fructobacillus durionis* comb. nov., *Fructobacillus ficulneus* comb. nov. and *Fructobacillus pseudoficulneus* comb. nov. *Int J Syst Evol Microbiol*. 2008;58:2195–205.
- Endo A, Futagawa-Endo Y, Schumann P, Pukall R, Dicks LMT. *Bifidobacterium reuteri* sp. nov., *Bifidobacterium callitrichos* sp. nov., *Bifidobacterium saguini* sp. nov., *Bifidobacterium stellenboschense* sp. nov. and *Bifidobacterium biavatii* sp. nov. isolated from faeces of common marmoset (*Callithrix jacchus*) and red-handed tamarin (*Saguinus midas*). *Syst Appl Microbiol*. 2012;35:92–7.
- Engelen B, Meinken K, von Wintzingerode F, Heuer H, Malkomes HP, Backhaus H. Monitoring impact of a pesticide treatment on bacterial soil communities by metabolic and genetic fingerprinting in addition to conventional testing procedures. *Appl Environ Microbiol*. 1998;64:2814–21.
- Ercolini D, Mauriello G, Blaiotta G, Moschetti G, Coppola S. PCR-DGGE fingerprints of microbial succession during a manufacture of traditional water buffalo mozzarella cheese. *J Appl Microbiol*. 2004;96:263–70.
- Escalante A, Wachter C, Farres A. Lactic acid bacterial diversity in the traditional Mexican fermented dough pozol as determined by 16S rDNA sequence analysis. *Int J Food Microbiol*. 2001;64:21–31.
- Euzeby JP. List of prokaryotic names with standing in nomenclature—genus leuconostoc. <http://www.bacterio.cict.fr/leuconostoc.html> (2009). Accessed 02/05 2010.
- Facklam RR, Elliot JA. Identification, classification, and clinical relevance of catalase-negative, gram-positive cocci, excluding the streptococci and enterococci. *Clin Microbiol Rev*. 1995;8:470–95.

- Faid M, Boraam F, Zyani I, Larpent JP. Characterization of sourdough bread ferments made in the laboratory by traditional methods. *Zeitschrift für Lebensmittel Untersuchung und Forschung*. 1994;198:287–91.
- Farah Z, Mollet M, Younan M, Dahir R. Camel dairy in Somalia: limiting factors and development potential. *Livest Sci*. 2007;110:187–91.
- Farrow JAE, Collins MD. *Enterococcus hirae*, a new species that includes amino acid assay strain NCDO 1258 and strains causing growth depression in young chickens. *Int J Syst Bacteriol*. 1985;35:73–5.
- Farrow JAE, Facklam RR, Collins MD. Nucleic acid homologies of some vancomycin-resistant leuconostocs and description of *Leuconostoc citreum* sp. nov. and *Leuconostoc pseudomesenteroides* sp. nov. *Int J Syst Bacteriol*. 1989;39:279–83.
- Felis GE, Dellaglio F. Taxonomy of lactobacilli and bifidobacteria. *Curr Issues Intest Microbiol*. 2007;8:44–61.
- Felis GE, Torriani S, Dellaglio F. Reclassification of *Pediococcus urinaeequi* (ex Mees 1934) Garvie 1988 as *Aerococcus urinaeequi* comb. nov. *Int J Syst Evol Bacteriol*. 2005;55:1325–1327.
- Fennema OF, Hui YH, Karel M, Walstra P, Whitaker JR. Lactic acid bacteria (Microbiological and Functional Aspects) In: Salminen S, von Wright A, editors. Food science and technology a series of monographs, textbooks, and reference books. 3rd ed. New York: Marcel Dekker, Inc.; 2004. P. 19–30.
- Feresu SB, Muzondo MI. Identification of some lactic acid bacteria from two Zimbabwean fermented milk products. *World J Microbiol Biotechnol*. 1990;6:178–86.
- Feurer C, Irlinger F, Spinnler HE, Glaser P, Vallaes T. Assessment of the rind microbial diversity in a farmhouse-produced vs a pasteurized industrially produced soft red-smear cheese using both cultivation and rDNA-based methods. *J Appl Microbiol*. 2004;97:546–56.
- Forsum U, Holst E, Larsson PG, Vasquez A, Jakobsson T, Mattsby-Baltzer I. Bacterial vaginosis—a microbiological and immunological enigma. *Minirev APMIS*. 2005;113:81–90.
- Fortina MG, Ricci G, Mora D, Manachini PL. Molecular analysis of artisanal Italian cheeses reveals *Enterococcus italicus* sp. nov. *Int J Syst Evol Bacteriol*. 2004;54:1717–1721.
- Frolková P, Pavel Švec, Sedláček I, Mašláňová I, Černohlavková J, Ghosh A, Zurek L, Radimsky T and Literák I. *Enterococcus alcedinis* sp. nov., isolated from common kingfisher (*Alcedo atthis*). *Int J Syst Evol Microbiol*. 2013;63:3069–3074.
- Gadaga TH, Mutukumira AN, Narvhus JA. Growth characteristics of *Candida kefir* and two strains of *Lactococcus lactis* subsp. *lactis* isolated from Zimbabwean naturally fermented milk. *Int J Food Microbiol*. 2001;70(1–2):11–9.
- Gagnaire V, Thierry A, L'eonil J. Propionibacteria and facultatively heterofermentative lactobacilli weakly contribute to secondary proteolysis of Emmental cheese. *Lait*. 2001;81:339–353.
- Gala E, Landi S, Solieri L, Nocetti M, Pulvirenti A, Giudici P. Diversity of lactic acid bacteria population in ripened Parmigiano Reggiano cheese. *Int J Food Microbiol*. 2008;125:347–51.
- Galli A, Franzetti L, Fortina MG. Isolation and identification of sour dough microflora. *Microbiologie–Aliments–Nutrition*. 1988;6:345–351.
- Galli A, Ottogalli G. Aspetti della microflora degli impasti panettone. *Annali di Microbiologia e Enzimologia*. 1973;23:39–49.
- Garrity GM, Bell JA, Lilburn TG. Taxonomic outline of the procaryotes. *Bergey's manual of systematic bacteriology*, 2nd ed, Release 5.0. New York: Springer. 2004; doi:<http://dx.doi.org/10.1007/bergeysoutline200405>.
- Garvie EI. Hybridization between deoxyribonucleic acids of some strains of heterofermentative lactic acid bacteria. *Int J Syst Bacteriol*. 1976;26:116–22.
- Garvie EI. *Pediococcus urinaeequi* nom. rev. In validation of the publication of new names and combinations previously effectively published outside the IJSB, List no. 25. *Int J Syst Bacteriol*. 1988;38:220–2.

- Garvie, E. Genus *Leuconostoc*. In: Sneath PHA, Mair NS, Sharpe ME, Holt JG, editors. Bergey's manual of systematic bacteriology. Vol 2. Baltimore: The Williams & Wilkins Co.; 1986. p. 1071.
- Gobbetti M, Corsetti A, Rossi J. The sourdough microflora. Interactions between lactic acid bacteria and yeasts: metabolism of amino acids. *World J Microbiol Biotechnol*. 1994;10:275–9.
- González-Arenzana L, López R, Santamaría P, López-Alfaro I. Dynamics of lactic acid bacteria populations in Rioja wines by PCR-DGGE, comparison with culture-dependent methods. *Appl Microbiol Biotechnol*. 2013;97(15):6931–41.
- Goodfellow M. Phylum XXVI. Actinobacteria phyl. nov. In: Goodfellow M, Kämpfer P, Busse HJ, Trujillo M, Suzuki KI, Ludwig W et al., editors. Bergey's manual of systematic bacteriology. New York: Springer; 2012. p. 171–188.
- Gu CT, Li CY, Yang LJ, Huo GC. *Lactobacillus heilongjiangensis* sp. nov., isolated from Chinese pickle. *Int J Syst Evol Microbiol*. 2013;63:4094–4099.
- Gu CT, Wang F, Li CY, Liu F, Cheng HG. *Lactobacillus xiangfangensis* sp. nov., isolated from Chinese pickle. *Int J Syst Evol Microbiol*; 2012;62:860–863.
- Hamad SH, Dieng MC, Ehrmann MA, Vogel RF. Characterization of the bacterial flora of Sudanese sorghum flour and sorghum sourdough. *J Appl Microbiol*. 1997;83:764–70.
- Hamid IA, AO El Owni. Microbiological properties and sensory characteristics of white cheese (Gibna bayda) collected in Zalengei area West Darfur. *Res J Anim Vet Sci* 2007;2:61–5.
- Hammes WP. Starterkulturpräparate in der Fleishwirtschaft. *Cherm Mikrobiol. Technol Lebensmittel*. 1985;9:131–43.
- Hammes WP, Hertel C. Genus I. *Lactobacillus* Beijerinck 1901 In: De Vos P, Garrity GM, Jones D, Krieg NR, Ludwig W, Rainey FA, Schleifer KH, Whitman WB, editors. Bergey's manual of systematic bacteriology, vol. 3, 2nd ed. Berlin: Springer; 2009. p. 465–510.
- Hammes WP. Annegret Banfleon and Seunghwa Min. Lactic acid bacteria in meat fermentation. *FEMS Microbiol Rev*. 1990;87:165–174.
- Hammes WP, Hertel C. The Genera *Lactobacillus* and *Carnobacterium*. In: Dwork M, editor. *The Prokaryotes Release 3.15*. 2003. p. 320–440.
- Hammes WP, Vogel RF. The genus *Lactobacillus*. In: Wood BJB, Holzapfel WH, editors. *The genera of lactic acid bacteria*. London: Blackie Academic & Professional; 1995. p. 19–54.
- Hamza AA, El Gaali IE, Mahdi AA. Use of the RAPD-PCR fingerprinting and API system for clustering lactic acid bacteria isolated from traditional Sudanese sour milk (Roab). *Afr J Biotechnol*. 2009;8:3399–404.
- Hassan AR, El-Zubeir MEI, Babiker AS. Chemical and microbial measurements of fermented camel milk Garris from transhumant and nomadic herds in Sudan. *J Basic Appl Sci*. 2008;2:166–171.
- Henri-Dubernet S, Desmasures N, Gueguen M. Diversity and dynamics of *lactobacilli* populations during ripening of RDO Camembert cheese. *Canad J Microbiol*. 2008;54:218–28.
- Hill GB, Eschenbach DA, Holmes KK. Bacteriology of the vagina. *Scand J Urol Nephrol*. 1984;86:23–39.
- Hiu SF. *Lactobacillus piscicola*, a new species from salmonid fish. *Int J Syst Evol Bacteriol*. 1984;34:393–400.
- Holzapfel WH, Gerber ES. *Lactobacillus divergens*. sp. nov. a new heterofermentative *Lactobacillus* species producing L(+)-lactate. *Syst Appl Microbiol*. 1983;4:522–534.
- Horvath P, Coûté-Monvoisin AC, Romero DA, Boyaval P, Fremaux C, Barrangou R. Comparative analysis of CRISPR loci in lactic acid bacteria genomes. *Int J Food Microbiol*. 2009;131:62–70.
- Hugenholtz P, Pitulle C, Hershberger KL, Pace NR. Novel division level bacterial diversity in a Yellowstone hot spring. *J Bacteriol*. 1998;180:366–76.
- Hui YH, Evarnuz Ó, Noé Arroyo-López F. Handbook of plant-based fermented food and beverage technology. Boca Raton: CRC Press; 2012. p. 58–61.

- Humblot C, Guyot JP. Pyrosequencing of tagged 16S rRNA gene amplicons for rapid deciphering of the microbiomes of fermented foods such as pearl millet slurries. *Appl Environ Microbiol.* 2009;75:4354–61.
- Infantes M, Tourneur C. Etude de la flore lactique de levains naturels de panification provenant de différentes régions françaises. *Sciences des Aliments.* 1991;11:527–45.
- Jay JM. *Modern food microbiology* 5th edition. New York: Chapman & Hall, 1996; p. 137–41, 328–42, 347–52.
- Jiri MT, Cui P, Ding F, Geng J, Gao H, Zhang H, Yu J, Hu S, Meng H. Monophyletic origin of domestic bactrian camel (*Camelus bactrianus*) and its evolutionary relationship with the extant wild camel (*Camelus bactrianus ferus*). *Anim Genet.* 2009;40:377–82.
- Jones D. Composition and differentiation of the genus *Streptococcus*. In *Streptococci.* 1978; p. 1–49.
- Jung JY, Lee SH, Kim JM, Park MS, Bae JW, Hahn Y, Madsen EL, Jeon CO. Metagenomic analysis of kimchi, a traditional Korean fermented food. *Appl Environ Microbiol.* 2011;77:2264–74.
- Kandler O. Carbohydrate metabolism in lactic acid bacteria. *Antonie Van Leeuwenhoek.* 1983;49:209–24.
- Kandler O, Weiss N. The genus *Lactobacillus*. In: Sneath PHA, Mair NS, Sharpe ME, Holt JG, editors. *Bergey's manual of systematic bacteriology.* Vol 2. Baltimore: Williams & Wilkins; 1986. P. 1209–1235, 1208–1234.
- Kazanskaya LN, Afanasyeva OV, Patt VA. Microflora of rye sours and some specific features of its accumulation in bread baking plants of the USSR. In Holas J, Kratochvil F editors. *Developments in food science. Progress in cereal chemistry and technology.* Vol 5B. London: Elsevier; 1983. p. 759–763.
- Kebede A, Viljoen BC, Gadaga H, Narvhus JA, Analie LH. The effect of incubation temperature on the survival and growth of yeasts in Sethemi, South African naturally fermented milk. *Food Technol Biotechnol.* 2007;45(1):21–6.
- Keller JJ, Jordan I. Fermented milks for the South African market. *Afric J Dairy Sci.* 1990;22:47–9.
- Kesmena Z, Yetimana AE, Gulluce A, Kacmazc N, Sagdic O, Cetine B, Adiguzelf A, Sahing F, Yetima H. Combination of culture-dependent and culture-independent molecular methods for the determination of lactic microbiota in sucuk. *Int J Food Microbiol.* 2012;53(3):428–435.
- Killer J, Kopečný J, Mrázek J, Koppová I, Havlík J, Benada O, Kott T. *Bifidobacterium actinocoloniforme* sp. nov. and *Bifidobacterium bohemicum* sp. nov., from the bumblebee digestive tract. *Int J Syst Evol Microbiol.* 2011;61:1315–1321.
- Kim M-S, Seong WR, Nam YD, Yoon JH, Bae JW. *Carnobacterium jeotgali* sp. nov., isolated from a Korean traditional fermented food. *Int J Syst Evol Bacteriol.* 2009;59:3168–3171.
- Kim TW, Lee JY, Jung SH, Kim YM, Jo JS, Chung DH, Lee HJ, Kim HY. Identification and distribution of predominant lactic acid bacteria in kimchi; a Korean traditional fermented food. *J Microbiol Biotechnol.* 2002;12:635–42.
- Kim B, Lee J, Jang J, Kim J, Han H. *Leuconostoc inhae* sp. nov., a lactic acid bacterium isolated from kimchi. *Int J Syst Evol Microbiol.* 2003;53:1123–6.
- Kim J, Kim JY, Kim MS, Roh SW, Bae JW. *Lactobacillus kimchiensis* sp. nov., isolated from a fermented food. *Int J Syst Evol Microbiol.* 2013;63:1355–9.
- Klaenhammer TR, Altermann E, Arigoni F, Bolotin A, Breidt F, Broadbent J, Cano R, Chaillou S, Deutscher J, Gasson M, van de Guchte M, Guzzo J, Hartke A, Hawkins T, Hols P, Hutkins R, Kleerebezem M, Kok J, Kuipers O, Lubbers M, Maguin E, McKay L, Mills D, Nauta A, Overbeek R, Pel H, Pridmore D, Saier M, van Sinderen D, Sorokin A, Steele J, O'Sullivan D, de Vos W, Weimer B, Zagorec M, Siezen R. Discovering lactic acid bacteria by genomics. *Antonie Van Leeuwenhoek.* 2002;82:29–58.
- Klaenhammer TR, Barrangou R, Buck BL, Azcarate-Peril MA, Altermann E. Genomic features of lactic acid bacteria effecting bioprocessing and health. *FEMS Microbiol Rev.* 2005;29:393–409.

- Kleerebezem M, Hugenholtz J. Metabolic pathway engineering in lactic acid bacteria. *Curr Opin Biotechnol.* 2003;14:232–7.
- Klein G, Alexander P, Christine B, Gerhard R. Taxonomy and physiology of probiotic lactic acid bacteria. *Int J Food Microbiol.* 1998;41:103–25.
- Kline L, Sugihara TF. Microorganisms of the San Francisco sour dough bread process. II. Isolation and characterization of undescribed bacterial species responsible for the souring activity. *Appl Microbiol.* 1971;21:459–65.
- Konigs WN, Kok J, Kuipers OP, Poolman B. Lactic acid bacteria: the bug of the new millennium. *Curr Opin Microbiol.* 2000;3:276–82.
- Koort J, Coenye T, Vandamme P, Sukura A, Björkroth J. *Enterococcus hermanniense* sp. nov., from modified-atmosphere-packaged broiler meat and canine tonsils. *Int J Syst Evol Microbiol.* 2004;54:1823–7.
- Kostinek M, Specht I, Edward VA, Schillinger U, Hertel C, Holzapfel WH, Franz CMAP. Diversity and technological properties of predominant lactic acid bacteria from fermented cassava used for the preparation of Gari, a traditional African food. *Syst Appl Microbiol.* 2005;28:527–40.
- Kudo Y, Oki K, Watanabe K. *Lactobacillus delbrueckii* subsp. *sunkii* subsp. nov. isolated from sunki, a traditional Japanese pickle. *Int J Syst Evol Microbiol.* 2012;62:2643–9.
- Kurmann JA, Rasic JLJ, Kroger M. Encyclopedia of fermented. Fresh milk products. New York: Van Nostrand Reinhold; 1992.
- Kusuda R, Kawai K, Salati F, Banner CR, Fryer JL. *Enterococcus seriolicida* sp. nov., a fish pathogen. *Int J Syst Bacteriol.* 1991;41:406–9.
- Lafarge V, Ogier JC, Girard V, Maladen V, Leveau JY, Gruss A, Delacroix-Buchet A. Raw cow milk bacterial population shifts attributable to refrigeration. *Appl Environ Microbiol.* 2004;70:5644–5650.
- Lahtinen S, Salminen S, Ouwehand A, Wright AV. Lactic acid bacteria, Microbiological and functional aspects. 4th ed. Boca Raton: CRC Press; 2011.
- Lancefield RC. A serological differentiation of human and other groups of hemolytic streptococci. *J Exp Med.* 1933;57(4):571–95. doi:10.1084/jem.57.4.571. PMC 2132252. PMID 19870148.
- Lattanzi A, Minervini F, Di Cagno R, Diviccaro A, Antonielli L, Cardinali G, Cappelle S, De Angelis M, Gobbetti M. The lactic acid bacteria and yeast microbiota of eighteen sourdoughs used for the manufacture of traditional Italian sweet leavened baked goods. *Int J Food Microbiol.* 2013;163:71–9.
- Law-Brown J, Meyers PR. *Enterococcus phoeniculicola* sp. nov., a novel member of the enterococci isolated from the uropygial gland of the Red-billed Woodhoopoe, *Phoeniculus purpureus*. *Int J Syst Evol Microbiol.* 2003;53:683–5.
- Lawson PA, Falsen E, Ohlén M, Collins MD. *Aerococcus urinaehominis* sp. nov., isolated from human urine. *Int J Syst Evol Bacteriol.* 2001a;51:683–686.
- Lawson PA, Falsen E, Truberg-Jensen K, Collins MD. *Aerococcus sanguicola* sp. nov., isolated from a human clinical source. *Int J Syst Evol Bacteriol.* 2001b;51:475–479.
- Lee HJ, Park CH, Joo YJ, Kim SH, Yoon JH, Park YH, Hwang IK, Ahn JS, Mheen TI. Identification and characterization of bacteriocin-producing lactic acid bacteria isolated from kimchi. *J Microbiol Biotechnol.* 1999;9:282–91.
- Lee JS, Lee KC, Ahn JS, Mheen TI, Pyun YR, Park YH. *Weissella koreensis* sp. nov., isolated from kimchi. *Int J Syst Evol Microbiol.* 2002;52:1257–61.
- Lei Xiao, Sun Guipeng, Xie Jingli, Wei Dongzhi. *Lactobacillus curieae* sp. nov., isolated from stinky tofu brine. *Int J Syst Evol Microbiol.* 2013;63:2501–5.
- Leisner JJ, Vancanneyt M, Van Der Meulen R, Lefebvre K, Engelbeen K, Hoste B, Laursen BG, Bay L, Rusul G, De Vuyst L, Swings J. *Leuconostoc durionis* sp. nov., a heterofermenter with no detectable gas production from glucose. *Int J Syst Evol Microbiol.* 2005;55:1267–70.
- Leisner JJ, Laursen BG, Prevost H, Drider D, Dalgaard P. Carnobacterium: positive and negative effects in the environment and in foods. *FEMS Microbiol Rev.* 2007;31:592–613.

- Lerche M. Die deutschen Wurslerzeufluue. Eine Systematik der Wurstarten Wursterzeugnisse in der Bundesrepublik und in Westberlin. Arbeium der DLG. Band 134 DLG-Verlag Frankfurt a. M; 1975.
- Li W, Shang H, Li J, Xu Z, Qin L. The content of Microorganism of yak's milk of Tianjin regions. *Chin J Anim Quarant.* 2002;19:36.
- Liang ZQ, Sathiyaraj Srinivasan et al. *Lactobacillus kimchicus* sp. nov., a β -glucosidase-producing bacterium isolated from kimchi. *Int J Syst Bacteriol.* 2011;61:894–897.
- Lin C, Bolsen KK, Brent BE, Fung DYC. Epiphytic lactic acid bacteria succession during the pre-ensiling and ensiling periods of alfalfa and maize. *J Appl Bacteriol.* 1992;73:375–87.
- Liu WJ, Sun ZH, Zhang JC, Gao W, Wang WH, Wu L, Sun TS, Chen W, Liu XM, Zhang HP. Analysis of microbial composition in acid whey for dairy fan making in Yunnan by conventional method and 16S rRNA sequencing. *Curr Microbiol.* 2009;59:199–205.
- Lönnér C, Welander T, Molin N, Dosta'lek M, Blickstad E. The microflora in a sour dough started spontaneously on typical Swedish rye meal. *Food Microbiol.* 1986;3:3–12.
- Luo Z, Li SYY, Han B. Research on the microflora and physicochemical index of the kurut in Tibet. *China Brewing (in Chinese).* 2005;10:40–1.
- Mann EJ. Kefi r and koumiss. *Dairy Ind Int.* 1989;54(9):9–10.
- Martinez-Murcia AJ, Collins MD. A phylogenetic analysis of the genus *Leuconostoc* based on reverse transcriptase sequencing of 16S rRNA. *FEMS Microbiol Lett.* 1990;70:73–83.
- Martinez-Murcia AJ, Collins MD. A phylogenetic analysis of an atypical leuconostoc: description of *Leuconostoc fallax* sp. nov. *FEMS Microbiol Lett.* 1991a;82:55–60.
- Martinez-Murcia AJ, Collins MD. *Enterococcus sulfureus*, a new yellow-pigmented *Enterococcus* species. *FEMS Microbiol Lett.* 1991b;80:69–74.
- Martinez-Murcia AJ, Harland NM, Collins MD. Phylogenetic analysis of some *leuconostocs* and related organisms as determined from large-subunit rRNA gene sequences: assessment of congruence of small and large-subunit rRNA derived trees. *J Appl Microbiol.* 1993;74:532–41.
- Mathara JM, Schillinger U, Kutima PM, Mbugua SK, Holzapfel WH. Isolation, identification and characterisation of the dominant microorganisms of kule naoto: the Maasai traditional fermented milk in Kenya. *Int J Food Microbiol.* 2004;94:269–78.
- Mathara JM, Schillinger U, Guigas C, Franz C, Kutima PM, Mbugua SK, Shin HK, Holzapfel WH. Functional characteristics of *Lactobacillus* spp. from traditional Maasai fermented milk products in Kenya. *Int J Food Microbiol.* 2008;126(1–2):57–64.
- Menghebilige, Wu RN, Wang LP, Yang XJ, Xu J, Dong Y, Sun ZH, Zhang HP. Isolation and identification of *Lactobacillus* from koumiss collected in Inner Mongolia and people's Republic of Mongolia (Chinese with English abstract). *China Dairy Ind.* 2004;32(11):6–11.
- Merk K, Borelli C, Korting HC. *Lactobacilli*—bacteria host interactions with special regard to the urogenital tract. *Int J Med Microbiol.* 2005;295:9–18.
- Meroth CB, Walter J, Hertel C, Brandt M, Hammes WP. Monitoring the bacterial population dynamics in sourdough fermentation processes by using PCR-denaturing gradient gel electrophoresis. *Appl Environ Microbiol.* 2003;69:475–82.
- Mheen TI, Kwon TW. Effect of temperature and salt concentration on kimchi fermentation. *Korean J Food Sci Technol.* 1984;16:443–50.
- Rosenbach FJ. Mikro-Organismen bei den Wund-bfektions-Krankheiten des Menschen JF Bergman, Wiesbaden; 1884.
- Miller A III, Morgan ME, Libbey LM. *Lactobacillus malraromicus*, a new species producing a malty aroma. *Int J Syst Bacteriol.* 1974;24:346–54.
- Minervini F, Di Cagno R, Lattanzi A, De Angelis M, Antonielli L, Cardinali G, Cappelle S, Gobbetti M. Lactic acid bacterium and yeast microbiotas of 19 sourdoughs used for traditional/typical Italian breads: interactions between ingredients and microbial species diversity. *Appl Environ Microbiol.* 2012;78:1251–64.
- Miyazaki K, Matsuzaki T. Health Properties of Milk Fermented with *Lactobacillus casei* strain Shirota (LcS). In: Farnworth ER, editor. *Handbook of fermented functional foods*. 2nd ed. New York: CRC Press, Taylor & Francis Group; 2008. p. 165–208.

- Montanari G, Grazia L. Galactose-fermenting yeasts as fermentation microorganisms in traditional koumiss. *Food Technol Biotech.* 1997;35:305–8.
- Montanari G, Zambonelli C, Grazia L, Kamesheva GK, Shigaeva MK. *Saccharomyces unisporus* as the principal alcoholic fermentation microorganism of traditional koumiss. *J Dairy Res.* 1996;63:327–31.
- Morandi S, Cremonesi P, Povolo M, Brasca M. *Enterococcus lactis* sp. nov., from Italian raw milk cheeses. *Int J Syst Evol Bacteriol.* 2012;62:1992–1996.
- Morea M, Baruzzi F, Cocconcelli PS. Molecular and physiological characterization of dominant bacterial populations in traditional Mozzarella cheese processing. *J Appl Microbiol.* 1999;87:574–582.
- Morita H, Nakano A, Onoda H, Toh H, Oshima K, Takami H, Murakami M, Fukuda S, Takizawa T, Kuwahara T, Ohno H, Tanabe S, Hattori M. *Bifidobacterium kashiwanohense* sp. nov., isolated from healthy infant faeces. *Int J Syst Evol Microbiol.* 2011;61:2610–5.
- Müller, M. R. A., Wolfrum, G., Stolz, P., Ehrmann, M. A., & Vogel, R. F. Monitoring the growth of *Lactobacillus* species during arye flour fermentation. *Food Microbiol.* 2001;18:217–227.
- Muck RE. Effects of inoculation level on alfalfa silage quality. *Trans ASAE.* 1989;32:1153–8.
- Mundt JO. Lactic acid bacteria associated with raw plant food material. *J Milk Food Technol.* 1970;33:550–3.
- Naser SM, Vancanneyt M, De graef E, Devriese LA, Snauwaert C, Lefebvre K, Hoste B, Švec P, Decostere A, Haesebrouck F, Swings J. *Enterococcus canintestini* sp. nov., from faecal samples of healthy dogs. *Int J Syst Evol Microbiol.* 2005;55:2177–2182.
- Nguyen DTL, Cnockaert M, Hoorde KV, Brandt ED, Snauwaert I, Snauwaert C, Vuyst LD, Le BT, Vandamme P. *Lactobacillus porcinae* sp. nov., isolated from traditional Vietnamese nem chua. *Int J Syst Evol Microbiol.* 2013;63:1754–9.
- Niemi RM, Ollinkangas T, Paulin L, Švec P, Vandamme P, Karkman Antti, Kosina Marcel, Lindström K. *Enterococcus rivorum* sp. nov., from water of pristine brooks. *Int J Syst Evol Microbiol.* 2012;62:2169–2173.
- Nikolic M, Terzic-Vidojevic A, Jovicic B, Begovic J, Golcic N, Topisirovic L. Characterization of lactic acid bacteria isolated from Bukuljac, a homemade goat's milk cheese. *Int J Food Microbiol.* 2008;122:162–70.
- Odufa SA. African fermented Food. In: Wood BJB, editor. *Microbiology of fermented food.* Vol 2. Essex, England: Elsevier Applied Science Publishers Ltd. 1985;155–191.
- Ogier JC, Son O, Gruss A, Tailliez P, Delacroix-Buchet A. Identification of the bacterial microflora in dairy products by temporal temperature gradient gel electrophoresis. *Appl Environ Microbiol.* 2002;68:3691–701.
- Oki K, Kudo Y, Watanabe K. *Lactobacillus saniviri* sp. nov. and *Lactobacillus senioris* sp. nov., isolated from human faeces. *Int J Syst Evol Microbiol.* 2012;62:601–7.
- Omar NB, Ampe F. Microbial community dynamics during production of the Mexican fermented maize dough pozol. *Appl Environ Microbiol.* 2000;66(9):3664–73.
- Orla-Jensen S. The lactic acid bacteria Fred Host and Son. Copenhagen; 1919.
- Ottogalli G, Galli A, Foschino R. Italian bakery products obtained with sour dough: characterization of the typical microflora. *Adv Food Sci.* 1996;18:131–44.
- Ouadghiri M, Amar M, Vancanneyt M, Swings J. Biodiversity of lactic acid bacteria in Moroccan soft white cheese (Jben). *FEMS Microbiol Lett.* 2005;251:267–71.
- Pahlow G, Muck RE, Driehuis F. Microbiology of ensiling. In: *Silage science and technology.* Madison. Proceedings... Madison: ASCSSA-SSSA, Agronomy. 2003;42:31–93.
- Palomba S, Blaiotta G, Ventorino V, Saccone A, Pepe O. Microbial characterization of sourdough for sweet baked products in the Campania region (southern Italy) by a polyphasic approach. *Ann Microbiol.* 2011;61:307–14.
- Pang H, Qin G, Tan Z, Li Z, Wang Y, Cai Y. Natural populations of lactic acid bacteria associated with silage fermentation as determined by phenotype, 16S ribosomal RNA and recA gene analysis. *Syst Appl Microbiol.* 2011;34:235–41.
- Park W, Zhang H, Zhang B, Zhang L. Mare milk. In: Park YW, George FW, editors. *Handbook of milk of non-bovine mammals.* 1st ed. Haenlein: Blackwell Publishing; 2006. P. 275–296.

- Park JM, Shin JH, Lee DW, Song JC, Suh HJ, Chang UJ, Kim JM. Food Sci Biotechnol. 2010;19(2):541–6.
- Pederson CS. Microbiology of food fermentations. Westport: AVI; 1971.
- Pikuta EV, Marsic D, Bej A, Tang J, Krader P, Hoover RB. *Carnobacterium pleistocenium* sp. nov., a novel psychrotolerant, facultative anaerobe isolated from permafrost of the Fox Tunnel in Alaska. Int J Syst Evol Bacteriol. 2005;55:473–478.
- Prescott SC, Dunn CG. (1957) Industrial microbiology. New York: McGraw-Hill; 1957.
- Psoni L, Tzanetakis N, Litopoulou-Tzanetaki E. Microbiological characteristics of Batzos, a traditional Greek cheeses from raw goat's milk. Food Microbiol. 2003;20:575–82.
- Quigley L, O'Sullivan O, Beresford TP, Paul Ross R, Fitzgerald GF, Cotter PD. Molecular approaches to analysing the microbial composition of raw milk and raw milk cheese. Int J Food Microbiol. 2011;15081–5094.
- Rahkila R, Johansson P, S  de E, Bj  rkroth J. Identification of enterococci from broiler products and a broiler processing plant and description of *Enterococcus viikkiensis* sp. nov. Appl Environ Microbiol. 2011;77:1196–203.
- Rahman AIE, Dirar HA, Osman MA. Microbiological and chemical changes and sensory evaluation of camel milk fermented by selected bacterial starter cultures. Afr J Food Sci. 2009;3:398–405.
- Randazzo CL, Torriani S, Akkermans AD, de Vos WM, Vaughan EE. Diversity, dynamics, and activity of bacterial communities during production of an artisanal Sicilian cheese as evaluated by 16S rRNA analysis. Appl Environ Microbiol. 2002;68(4):1882–92.
- Randazzo CL, Caggia C, Neviani E. Application of molecular approaches to study lactic acid bacteria in artisanal cheeses. J Microbiol Methods. 2009;78:1–9.
- Rantsiou K, Urso R, Dolci P, Comi G, Cocolin L. Microflora of Feta cheese from four Greek manufacturers. Int J Food Microbiol. 2008;126:36–42.
- Reuter G. Atypische Streptobakterien als dominierende flora in reifender und gelagerter Rohwurst. Fleischwirtschaft. 1967;47:397–402.
- Ring E, Gatesoupe FJ. Lactic acid bacteria in fish: a review. Aquaculture. 1998;160:177–203.
- Rocha JM, Malcata FX. On the microbiological profile of traditional Portuguese sourdough. J Food Prot. 1999;62:1416–29.
- Roh SW, Kim KH, Nam YD, Chang HW, Park EJ, Bae JW. Investigation of archaeal and bacterial diversity in fermented seafood using barcoded pyrosequencing. Int J Syst Evol Microbiol. 2010;4:1–16.
- Rosenquist H, Hansen A. The microbial stability of two bakery sourdoughs made from conventionally and organically grown rye. Food Microbiol. 2000;17:241–50.
-   vec P, Vandamme P, Bryndova' H, Holochova'P, Kosina M, Ma  la  nov  I, Sedl  cek I. *Enterococcus plantarum* sp. nov., isolated from plants. Int J Syst Evol Microbiol. 2012;62:1499–1505.
- Saeed ZK. Some technological aspects of indigenous Sudanese soups (molahs). Ph.D. thesis, University of Reading, UK. 1981.
- Sakamoto N, Tanaka S, Sonomoto K, Nakayama J. 16S rRNA pyrosequencing-based investigation of the bacterial community in nukadoko, a pickling bed of fermented rice bran. Int J Food Microbiol. 2011;144:352–9.
- Salih AMM, El Sanousi SM, El Zubeir EM. A review on the Sudanese traditional dairy products and technology. Int J Dairy Sci. 2011;6(4):227–45.
- Salovaara H, Katunp    H. An approach to the classification of Lactobacilli isolated from Finnish sour rye dough ferments. Acta Alimentaria Polonica. 1984;10:231–9.
- Sawadogo-Lingani H, Diawara VLB, Nielsen DS, M  ller PL, Traore AS, Jakobsen M. The biodiversity of predominant lactic acid bacteria in dolo and pito wort for the production of sorghum beer. J Appl Microbiol. 2007;103:765–777.
- Scheirlinck I, Van der Meulen R, Van Schoor A, Vancanneyt M, Vuyst LD, Vandamme P, Huys G. Influence of geographical origin and flour type on diversity of lactic acid bacteria in traditional Belgian sourdoughs. Appl Environ Microbiol. 2007;73(19):6262–9.

- Scheirlinck I, Van der Meulen R, Schoor AV, Vancanneyt M, Vuyst LD, Vandamme P, Huys G. Taxonomic structure and stability of the bacterial community in Belgian sourdough ecosystems as assessed by culture and population fingerprinting. *Appl Environ Microbiol.* 2008;74(8):2414–23.
- Scheirlinck I, Van der Meulen R, De Vuyst L, Vandamme P, Huys G. Molecular source tracking of predominant lactic acid bacteria in traditional Belgian sourdoughs and their production environments. *J Appl Microbiol.* 2009;106:1081–92.
- Schleifer KH, Kilpper-Bälz R. Molecular and chemotaxonomic approaches to the classification of ctreplococci, enterococci and lactococci: A review. *Sys Appl Microbiol.* 1987;10:1–10.
- Schleifer KH, Kraus J, Dvorak C, Kilpper-bälz R, Collins MD, Fischer W. Transfer of *Streptococcus lactis* and related streptococci in the genus *Lactococcus* gen. nov. *Int J Syst Appl Microbiol.* 1985;6:183–195.
- Schleifer KH, Ludwig W. Phylogenetic relationship of lactic acid bacteria. In wood BJB, Holzapfel WH, editors. The genera of lactic acid bacteria. London: Blackie Academic & Professional; 1995a. P. 7–18.
- Schleifer KH, Ludwig W. Phylogeny of the genus *Lactobacillus* and related genera. *Syst Appl Microbiol.* 1995b;18:461–467.
- Schleifer KH, Kilpper-Bälz R. Transfer of *Streptococcus faecalis* and *Streptococcus faecium* to the genus *Enterococcus* nom. rev. As *Enterococcus faecalis* comb. nov. *Int J Syst Bacteriol.* 1984;34:31–4.
- Sedláček I, Holochová P, Mašláňová I, Kosina M, Spröer C, Bryndová H, Vandamme P, Rudolf I, Hubálek Z, Švec P. *Enterococcus ureilyticus* sp. nov. and *Enterococcus rotai* sp. nov., two urease-producing enterococci from the environment. *Int J Syst Evol Microbio.* 2013;63:502–510.
- Seegers JF. Lactobacilli as live vaccine delivery vectors: progress and prospects. *Trends Biotechnol.* 2002;20(12):508–15.
- Sengun IY, Nielsen DS, Karapinar M, Jakobsen M. Identification of lactic acid bacteria isolated from Tarhana, a traditional Turkish fermented food. *Int J Food Microbiol.* 2009;135:105–11.
- Serhan M, Cailliez-Grimal C, Borges F, Revol-Junelles AM, Hosri C, Fanni J. Bacterial diversity of Dairyfeh, a Lebanese artisanal raw goat's milk cheese. *Food Microbiol.* 2009;26:645–52.
- Sharpe ME, Garvie EI, Tilbury RH. Some slime-forming heterofermentative species of the genus *Lactobacillus*. *Appl Microbiol.* 1972;23:389–397.
- Shaw BC, Harding CD. A numerical taxonomic study of lactic acid bacteria from vacuum-packed beef, pork, lamb and bacon. *J Appl Bacteriol.* 1984;56:25–40.
- Shaw BG, Harding CD. A typical lactobacilli from vacuum-packaged meats: comparison by DNA hybridization cell composition and biochemical tests with a description of *Lactobacillus carnis* sp. nov. *Syst App Microbiol.* 1985;6:291–297.
- Shaw BG, Harding CD. *Leuconostoc gelidum* sp. nov. and *Leuconostoc carnosum* sp. nov. from chill-stored meats. *Int J Syst Bacteriol.* 1989;39:217–23.
- Shuangquan B, Miyamoto T. Microflora in traditional fermented camel's milk from Inner Mongolia. *China Milchwissenschaft.* 2004;59:649–652.
- Simova E, Beshkova D, Angelov A, Hristozova Ts, Frengova G, Spasov Z. Lactic acid bacteria and yeasts in kefir grains and kefir made from them. *Int J Microbiol Biotechnol.* 2002;28(1):1–6.
- Simpson PJ, Ross RP, Fitzgerald GF, Stanton C. *Bifidobacterium psychraerophilum* sp. nov. and *Aeriscardovia aeriphila* gen. nov., sp. nov., isolated from a porcine caecum. *Int J Syst Evol Microbiol.* 2004;54:401–406.
- Sistek V, Maheux AF, Boissinot M, Bernard KA, Cantin P, Cleenwerck I, De vos P, Bergeron MG. *Enterococcus ureasiticus* sp. nov. and *Enterococcus quebecensis* sp. nov., isolated from water. *Int J Syst Evol Microbiol.* 2012;62:1314–1320.
- Smit G, Smit BA, Engels JM. Flavour formation by lactic acid bacteria and biochemical flavour profiling of cheese products. *FEMS Microbiol Rev.* 2005;29:591–610.

- Spicher G. Weitere Untersuchungen über die Zusammensetzung und die Variabilität der Mikroflora handelsüblicher Sauerteig-Starter. Zeitschrift für Lebensmittel Untersuchung und Forschung. 1984;178:106–9.
- Spicher G. Die Mikroflora des Sauerteiges. XXII. Mitteilung: Die in Weizensauerteigen vorkommenden Lactobacillen. Zeitschrift für Lebensmittel Untersuchung und Forschung. 1987;184:300–3.
- Spicher G. Die Mikroflora des Sauerteiges. I. Mitteilung: Untersuchungen über die Art der in Sauerteigen anzutreffenden stäbchenförmigen Milchsäurebakterien (Genus *Lactobacillus* Beijerinck). Zeitblatt für Bakteriologie II Abt. 1959;113:80–106.
- Spicher G, Schröder R, Schöllhammer K. Die Mikroflora des Sauerteiges. VII. Mitteilung: Untersuchungen über die Art der in 'Reinzuchtsauern' auftretenden Hefen. Zeitschrift für Lebensmittel Untersuchung und Forschung. 1979;169:77–81.
- Stackebrandt E, Teuber M. Molecular taxonomy and phylogenetic position of lactic acid bacteria. Biochimie. 1988;70(317):324.
- Stephan H, Neumann H. Technik der Roggen-Sauerteigführung. In: Spicher G, Stephan H, editors. Handbuch Sauerteig: Biologie, Biochemie, Technologie. 5th ed. Hamburg: Behr's Verlag; 1999a. p. 161–245.
- Stephan H, Neumann H. Technik der Weizenvorteig- und Weizensauerteigführung. In: Spicher G, Stephan H, editors. Handbuch Sauerteig: Biologie, Biochemie, Technologie. 5th ed. Hamburg: Behr's Verlag; 1999b. p. 247–75.
- Stiles ME, Holzapel WH. Lactic acid bacteria of foods and their current taxonomy. Int J Food Microbiol. 1997;36:1–29.
- Sukontasing S, Tanasupawat S, Moonmangmee S, Lee JS, Suzuki K. *Enterococcus camelliae* sp. nov., isolated from fermented tea leaves in Thailand. Int J Syst. Evol Microbiol. 2007;57:2151–2154.
- Suliman AM, Ilayan AA, El faki AE. Chemical and microbiological quality of Garris, Sudanese fermented camel's milk product. Int J food Sci Technol. 2006;41(3):321–328.
- Sun ZH, Liu WJ, Gao W, Yang M, Zhang JC, Wu L, Wang JG, Menghe BG, Sun TS, Zhang HP. Identification and characterization of the dominant lactic acid bacteria from kurut: the naturally fermented yak milk in Qinghai, China. J Gen Appl Microbiol. 2010;56:1–10.
- Švec P, Devriese LA, Sedláček I, Baele M, Vancanneyt M, Haesebrouck F, Swings J, Doškař J. *Enterococcus haemoperoxidus* sp. nov. and *Enterococcus moraviensis* sp. nov., isolated from water. Int J Syst Evol Microbiol. 2001;51:1567–74.
- Švec P, Vancanneyt M, Devriese LA, Naser SM, Snauwaert C, Lefebvre K, Hoste B, Swings J. *Enterococcus aquimarinus* sp. nov., isolated from sea water. Int J Syst Evol Microbiol. 2005a;55:2183–7.
- Švec P, Vancanneyt M, Koort J, Naser SM, Hoste B, Vihavainen E, Vandamme P, Swings J, Björkroth J. *Enterococcus devriesei* sp. nov., associated with animal sources. Int J Syst Evol Microbiol. 2005b;55:2479–84.
- Švec P, Vancanneyt M, Sedláček I, Naser SM, Snauwaert C, Lefebvre K, Hoste B, Swings J. *Enterococcus silesiacus* sp. nov. and *Enterococcus termitis* sp. nov. Int J Syst Evol Microbiol. 2006;56:577–581.
- Tailliez P. Mini-revue: les bactéries lactiques, ces êtres vivants apparus il y a près de 3 milliards d'années. Lait. 2001;81:1–11.
- Tamime AY. Fermented milks: a historical food with modern applications-a review. Eur J Clin Nutr. 2002;56(Suppl)4:1–15.
- Tamime AY. Production of Kefir, Koumiss and Other related Products. In: Tamime AY, editor. Fermented Milk Blackwell Science Ltd, Oxford, UK, 2006;174–216.
- Tanasupawat S, Sukontasing S, Lee JS. *Enterococcus thailandicus* sp. nov., isolated from fermented sausage ('mum') in Thailand. Int J Syst Evol Microbiol. 2008;58:1630–4.
- Taormina PJ. Implications of salt and sodium reduction on microbial food safety. Crit Rev Food Sci Nutr. 2010;50:209–27.

- Teixeira LM, Carvalho M da GS, Espinola MMB, Steigerwalt AG, Douglas MP, Brenner DJ, Facklam RR. *Enterococcus porcinus* sp. nov. and *Enterococcus ratti* sp. nov., associated with enteric disorders in animals. *Int J Syst Evol Microbiol*. 2001;51:1737–1743.
- Teuber M. The Genus *Lactococcus*. In: Wood BJB, Holzapfel WH, editors. The genera of lactic acid bacteria. London: Blackie; 1995. P. 173–234.
- Thiercelin M. Sur un diplocoque saprofytique de l'intestin susceptible de devenir pathogène. *C. R. Sot. Rioi. (Paris)*. 1899;51:269–271.
- Thornley MJ. Observations on the microflora of minced chicken meat irradiated with 4 MeV cathode rays. *J Appl Bacteriol*. 1957;20:286–98.
- Thunell RK. Taxonomy of the leuconostocs. *J Dairy Sci*. 1995;78:2514–22.
- Tohno M, Kitahara M, Irisawa T, Masuda T, Uegaki R, Ohkuma M, Tajima K. Description of *Lactobacillus iwatenensis* sp. nov., isolated from orchardgrass (*Dactylis glomerata* L.) silage, and *Lactobacillus backii* sp. nov. *J Syst Evol Microbiol*. 2013;63:3854–3860.
- Tohno M, Kitahara M, Uegaki R, Irisawa T, Ohkuma M, Tajima K. *Lactobacillus hokkaidonensis* sp. nov., isolated from subarctic timothy grass (*Phleum pratense* L.) silage. *Int J Syst Evol Microbiol*. 2013a;63:2526–31.
- Tohno M, Kitahara M, Irisawa T, Masuda T, Uegaki R, Ohkuma M, Tajima K. Description of *Lactobacillus iwatenensis* sp. nov., isolated from orchardgrass (*Dactylis glomerata* L.) silage, and *Lactobacillus backii* sp. nov. *Int J Syst Evol Microbiol*. 2013b;63:3854–60.
- Tohno M, Kitahara M, Irisawa T, Inoue H, Uegaki R, Ohkuma M, Tajima K. *Lactobacillus oryzae* sp. nov., isolated from fermented rice grain (*Oryza sativa* L. subsp. japonica). *Int J Syst Evol Microbiol*. 2013c;63:2957–62.
- Tooner JS. Koumiss in Mongol culture: past and present. Milk and milk products from Medieval to Modern Times In: P Lysaght, editor. Canongate Press, Edinburgh 1994; p. 130–39.
- Tyrrell GJ, Turnbull L, Teixeira LM, Lefebvre J, Carvalho MGS, Facklam RR, Lovgren M. *Enterococcus gilvus* sp. nov. and *Enterococcus pallens* sp. nov. isolated from human clinical specimens. *J Clin Microbiol*. 2002;40:1140–5.
- Tzanetakis N, Litopoulou-Tzanetaki E. Biochemical activities of *Pediococcus pentosaceus* isolates of dairy origin. *J Dairy Sci*. 1989;72(4):859–63.
- Uchida K, Hirata M, Motoshima H, Urashima T, Arai I. Microbiota of 'airag', 'tarag' and other kinds of fermented dairy products from nomad in Mongolia. *Anim Sci J*. 2007;78(6):650–8.
- Urso R, Comi G, Luca C. Ecology of lactic acid bacteria in Italian fermented sausages: isolation, identification and molecular characterization. *Syst Appl Microbiol*. 2006;29:671–80.
- Van den Berg G. Semi-hard cheeses. In: Tamime, A.Y., Law, B.A. editors, Mechanisation and Automation in Dairy Technology. Academic Press, Sheffield. 2000.
- Van Hoorde K, Verstraete T, Vandamme P, Huys G. Diversity of lactic acid bacteria in two Flemish artisan raw milk Gouda-type cheeses. *Food Microbiol*. 2008;25:929–35.
- Vedamuthu ER. The dairy Leuconostoc: use in dairy products. *J Dairy Sci*. 1994;77(9):2725–2737.
- Venturi M, Guerrini S, Vincenzini M. Stable and non-competitive association of *Saccharomyces cerevisiae*, *Candida milleri* and *Lactobacillus sanfranciscensis* during manufacture of two traditional sourdough baked goods. *Food Microbiol*. 2012;31:107–15.
- Vogel RF, Knorr R, Müller MRA, Steudel U, Gänzle MG, Ehrmann MA. Non-dairy lactic acid fermentations: the cereal world. Antonie Van Leeuwenhoek. 1999;76:403–411.
- Vuyst LD, Schrijvers V, Paramithiotis S, Hoste B, Vancanneyt M, Swings J, Kalantzopoulos G, Tsakalidou E, Messens W. The biodiversity of lactic acid bacteria in Greek traditional wheat sourdoughs is reflected in both composition and metabolite formation. *Appl Environ Microbiol*. 2002;68(12):6059–69.
- Wallbanks S, Martinez-Murcia AJ, Fryer JL, Phillips BA, Collins MD. 16S rRNA sequence determination for members of the genus *Carnobacterium* and related lactic acid bacteria and description of *Vagococcus salmoninarum* sp. nov. *Int J Syst Evol Bacteriol*. 1990;40:224–230.
- Ward DM, Weller R, Bateson MM. 16S rRNA sequences reveal numerous uncultured microorganisms in a natural community. *Nature*. 1990;345:63–5.

- Walstra P, Moomen, geurts TJ. Dutch-type varieties, in Cheese: chemistry. Physic and Microbiology, Vol. 2, In: P.F. Fox, editor, Chapman & Hall, London, 1993; p. 39–82.
- Watanabe K, Fujimoto J, Sasamoto M, et al. Diversity of lactic acid bacteria and yeasts in Airag and Tarag, traditional fermented milk products of Mongolia. *World J Microbiol Biotechnol.* 2008;24:1313–25.
- Williams REO, Hirsch A, Cowan ST. *Aerococcus*, a new bacterial genus. *J Gen Microbiol.* 1953;8:475–80.
- Williams AM, Farrow JAE, Collins MD. Validation list no. 31. *Int. J. Syst. Bacteriol.* 1989;39:495–97.
- Williams AM, Fryers JL, Collins M. *Lactococcus piscium* sp. nov. a new *Lactococcus* species from salmonid fish. *FEMS Microbiol Lett.* 1990;68:109–14.
- Collins MD, Rodrigues UM, Pigott NF, Facklam RR. *Enterococcus* species from human sources. *Lett Appl Microbiol.* 1991;12:95–98.
- Yang CH, Crowley DE, Borneman J, Keen NT. Microbial phyllosphere populations are more complex than previously realized. *Proc Natl Acad Sci USA.* 2001;98:3889–94.
- Yao AK, Kadio G, Coulybaly A, Agbo GZ. Production du ‘Tchapalo’ a partir du sorgho en Côte d’Ivoire. In: Menyonga JM, Bezuneh T, Nwasike CC, Sedogo PM, Tenkouano A editors. Processing and industrial utilization of sorghum and related cereals in Africa. Proceeding of the OUA/STRCSAFGRAD regional symposium. Ouagadougou, Burkina Faso, 22–26 November 1993, 1995; pp 55–60.
- Yi EJ, Yang JE, Lee JM, Park YJ, Park SY, Shin HS, Kook MC, Yi TH. *Lactobacillus yonginensis* sp. nov., a lactic acid bacterium with ginsenoside converting activity isolated from Kimchi. *Int J Syst Evol Microbiol.* 2013. doi:10.1099/ijs.0.045799-0.
- Yoon JH, Kang SS, Mheen TI, Ahn JS, Lee HJ, Kim TK, Park CS, Kho YH, Kang KH, Park YH. *Lactobacillus kimchii* sp. nov., a new species from kimchi. *Int J Syst Evol Microbiol.* 2000;50:1789–95.
- Yu J, Du XH, Wang WH, Zhang JC, Liu WJ, Sun ZH, Sun TS, Zhang HP. Phenotypic and genotypic characteristics of lactic acid bacteria isolated from sour congee in Inner Mongolia of China. *J Gen Appl Microbiol.* 2011;57:197–206.
- Zamfir M, Vancanneyt M, Makras L, Vaningelgem F, efebvre KL, Pot B, Swings J, De Vuyst L. Biodiversity of lactic acid bacteria in Romanian dairy products. *Syst Appl Microbiol.* 2006;29:487–495.
- Zapparoli G, De Benedictis P, Salardi C, Veneri G, Torriani S, Dellaglio F. *Lactobacilli* of sourdoughs from Verona bakery: a preliminary investigation. *Adv Food Sci.* 1996;18:163–6.
- Zhang HP, Xu J, Wang JG, Menghebilige, Sun TS, Li HP, Guo MR. A survey on chemical and microbiological composition of Kurut, naturally fermented yak milk from Qinghai in China. *Food Control.* 2008;19:578–586.
- Zhang WY, Zhang HP. Fermentation and koumiss. In: Hui YH, editor. Handbook of animal-based fermented foods and beverages. 2nd ed. Boca Raton: CRC Press; 2012. p. 165–172.
- Zhang JC, Liu WJ, Sun ZH, Bao QH, Wang F, Yu J, Chen W, Zhang HP. Diversity of lactic acid bacteria and yeasts in traditional sourdoughs collected from western region in Inner Mongolia of China. *Food Control.* 2011;22:767–74.
- Zhu G, Zhang Y. Current conditions and developing approaches of yak production in China. *Chin J Anim Sci (in Chinese).* 2005;41(1):61–3.
- Zou YQ, Liu F, Fang CX, Wan DW, Yang RT, Su QQ, Yang RF, Zhao J. *Lactobacillus shenzhenensis* sp. nov., isolated from a fermented dairy beverage. *Int J Syst Evol Microbiol.* 2013;63:1817–1823.

Lactic Acid Bacteria

Fundamentals and Practice

Zhang, H.; Cai, Y. (Eds.)

2014, VIII, 535 p. 66 illus., 37 illus. in color., Hardcover

ISBN: 978-94-017-8840-3