Microbial Biosystems 3(1): 12–24 (2018)
http://fungiofegypt.com/Journal/index.html

ISSN 2357-0334
Microbial Biosystems
Online Edition
ARTICLE

Physicochemical profile and Lactic Acid Bacteria genera inhabit Egyptian raw camel, sheep, goat, buffalo and cow milks

Darwish AMG[1,2]*, Allam MG[2] and Ayad EHE[2]

[1]*Departmet of Food Technology, Arid Lands Cultivation Research Institute (ALCRI), City of Scientific Research and Technological Applications (SRTA-City), Alexandria, Egypt*
[2]*Departmet of Food Science, Faculty of Agriculture, Saba Basha, Alexandria University, Egypt*

Darwish AMG, Allam MG, Ayad EHE 2018 – Physicochemical profile and Lactic Acid Bacteria genera inhabit Egyptian raw camel, sheep, goat, buffalo and cow milks. Microbial Biosystems 3(1), 12–24.

Abstract

Indigenous dairy products made of different milk sources are traditionally produced and consumed in a majority of African and Arabian countries. The aim of present study was to assess and compare physicochemical profile of camel, sheep, goat, buffalo and cow's native milks in addition to isolation, identification and technological evaluation of their content of Lactic Acid Bacteria (LAB) genera to introduce a wider image that facilitate applications of these pasteurized milks along with isolated LAB strains in dairy industry development. Milks were examined chemically and via Fourier Transform Infrared (FTIR) spectroscopy. Sixty strains out of two hundred sixty-eight of LAB were selected based on assessment of their technological properties. Chemically, sheep and buffalo milks showed the highest content of protein, fat and ash. Goat and sheep milks possessed high content of lactose, which encouraged the inhabitance of *Leuconostoc* sp. to represented 48% and 18% respectively of their total LAB isolates. Some strains showed exceptional autolytic, photolytic and antimicrobial features (10, 15 and 12 strains respectively). Obtained findings when correctly applied would lead to develop an innovative dairy processing in Egypt.

Key words– FTIR, Functional properties, LAB Isolation, Native row milks, Phenotypic identification; Proximate analysis.

Introduction

Milk as nature's most complete food, considered daily source of nutrients in most countries. Studies on milk composition of dairy animals mainly concerned cow milk (85% of consumed milk), a lesser extent on goat and sheep milk, and rather rare studies on buffalo and camel in spite of their nutritional importance (Konuspayeva *et al.* 2009). Cow milk is the most universal raw material of manufactured dairy products (Dandare *et al.* 2014). Buffalo's milk is ranked second in the world after cow's milk (Ahmad *et al.* 2008). Camel milks play a major role and they are either home-consumed or sold (Yam *et al.* 2015). Sheep milk contains higher levels of total solids and major nutrient than other milks that affect coagulation time and rate, curd firmness, and amount of rennet used (Park *et al.* 2007).

In recent years, with the huge issue in relation to green analytical technique, some scientist try to used environmentally friendly techniques. The FTIR technique has been gaining

Submitted 2 July 2018, Accepted 10 July 2018, Published online 10 July 2018

Corresponding Author: Darwish AMG – e-mail – amiragdarwish@yahoo.com

interest for raw milk quality control, because of its high level of analytical capacity, low sample manipulation and use of fewer reagents, resulting in less time and lower costs (Fadzlillah *et al.* 2013; Coitinho *et al.* 2017).

Unfortunately, traditional cheese makers value the flavor that obtained by the use of raw milk, where the microbiota contributing to the ripening has a great influence on its specifications. Lactic acid bacteria (LAB) as starter and adjunct starter cultures, by producing acids and several lipolytic, proteolytic enzymes and antimicrobial agents, play an important role in preserving and producing flavor in cheese products that could encourage cheese makers to use pasteurized milk for lower incidence of food-borne diseases (Navidghasemizad *et al.* 2009).

The aim of this study was to provide a contribution concerning physicochemical profile of camel, sheep, goat, buffalo and cow Egyptian milks in addition to isolation, identification and technological evaluation of Lactic Acid Bacteria (LAB) genera inhabit these raw milks to introduce a wider image that facilitate applications of these pasteurized milks and isolated LAB strains in dairy industry development.

Materials and Methods

Sampling

Twenty five raw milk samples (5 samples per animal) were collected from different districts in Egypt, transferred under cooling conditions and kept refrigerated at 4^{o}C for analysis.

Physicochemical and nutritional characterization

All proximate analysis determined using the Official Methods of Analysis (AOAC International 2016). Moisture, ash, protein, fat and lactose contents were determined by oven drying, furnace, Kjeldah, Gerber and titrimetric methods respectively. pH value was determined using pH meter (AD1030 ADWA, Romania). Titratable acidity of the samples was expressed as the percentage equivalent lactic acid according to (Ling 1945). Energy was calculated (Calories/ 100mL) according to the following equation:

(Protein*4+ Carbs (Lactose)*4+ Fat*9) (WHO/FAO 2002).

Specific gravity was determined according to Ling (1945) using Lactometer (Quevenne laktodensimeter, W-Germany), where Lactometer Reading (LR) = 1000* (Specific Gravity^{-1}). Its value is connected to total solids (TS) and solid no fat (SNF) values according to Rechmond Formula (Ling 1945);

$$TS = \frac{LR\ at\ 60oF}{4} + \frac{6xF}{5} + 0.14$$

$$SNF = \frac{LR\ at\ 60oF}{4} + \frac{F}{5} + 0.14$$

Where: TS: % Total Solids, LR: Lactometer Reading at 60^{o}F, F: %Fat and SNF: %Solid No Fat.

Fourier transform infrared (FTIR) spectroscopy

For wider image of milks' characteristics, FTIR spectra of examined milks were studied to mark functional groups using Fourier transform infrared spectrophotometer (Shimadzu FTIR-8400 S, Japan) equipped with (ATR 8000A). The range of spectrophotometer was from 4000–400 cm^{-1} (Cerqueira *et al.* 2011).

Isolation and phenotypic identification of LAB strains

For enrichment, one mL of milk samples were incubated in 10 mL sterilized reconstituted skim milk (RSM) (12.5%), at different incubation temperatures; 30^{o}C, 42^{o}C and 37^{o}C for 24 h. Selective media M17 and MRS (Biolife, Italy), were used for the isolation of LAB aerobic strains (De Man *et al.* 1960). The isolates were purified using streak plate method. Colonies were picked up according to shape and color, Gram-positive, catalase-negative isolates were

phenotypically identified to the genus level using (CO_2 production, growth at 45^{o}C, 10^{o}C, growth in of 6.5% NaCl, in pH 9.6 and in SF medium) and biochemical characterization via carbohydrate fermentation (MacFaddin 1976). The identified isolated strains were stored at -20^{o}C in RSM (12.5%) supplemented with 15% glycerol and were registered in Faculty of Agriculture Saba Basha, Alexandria University Culture Collection (FABA).

Technological characterization of selected identified strains

Based on earlier observations, that suggested a causal relationship between microbial taxa and flavor, flavor development in milk cultures is one of the most important attributes (Walsh *et al.* 2016). Depending on a preliminary experiment of sensory evaluation of pre-grown cultures according to Ayad *et al.* (2004), sixty isolated LAB strains were selected for technological characterization; 24 isolates from camel milk, 11 from sheep milk, 6 from goat milk, 13 from buffalo milk and 6 from cow milk. The autolytic activity was determined as the percentage decreased in the absorbance (OD_{650}) at time intervals comparing the strain growth to blank M17 broth (Allam *et al.* 2017). Proteolytic activity represents the strain ability to hydrolyse milk protein as halo of proteolysis around the strain growth (Ayad 2001). Antibacterial activity was determined by agar well-diffusion assay against *E. coli* obtained from Netherlands Institute for Dairy Research (NIZO) according to Ayad *et al.* (2002). Exopolysaccharides production was determined by touching incubated strains with a sterile inoculation loop, strains were considered positively EPS producer if the length of slime exceeded 1.5 mm according to Knoshaug *et al.* (2000).

Statistical analysis

Statistical analysis was performed using Analytical Software SPSS® 13.0 (Statistical Package for the Social Sciences). Differences were considered significant at $p < 0.05$. All experiments were performed in five replicas.

Results and Discussion

Chemical and nutritional characterization of raw milks

Chemical and nutritional characteristics of the five raw milks; camel, sheep, goat, buffalo and cow are illustrated in Table (1). Specific gravity (SG) values ranged between a minimum of 1.033 (in cow milk) and a maximum of 1.036 (in sheep milk). Normal milks were reported to record specific gravity values not less than 1.030 (LR 30) to guarantee absence of adulteration by water addition. Accordingly, obtained results correlated with fat, TS and SNF of analyzed milk samples. The highest SG showed by sheep and buffalo milks (1.036 and 1.035) accompanied with their high TS, SNF and fat content (21.47% and 17.36%, 12.22% and 10.99%, 9.25% and 6.64% respectively), whilst, the lowest SG of cow milk (1.033) reflected lower content of TS, SNF and fat (13.13%, 9.92% and 3.21% respectively). On the other hand, the equal SG values of camel and goat milks (1.034) indicated the insignificant differences in their TS, SNF and fat content (14.45% and 14.80%, 10.03% and 10.55%, 4.43% and 4.25% respectively). Anyways, the fat content is used to be a measure of satisfaction indicating the overall milk quality taking in account TS content to avoid suspicion of adulteration using other fats (Kanwal *et al.* 2004).

Table (1) results reflected the energy as nutritional parameter (calories gained by 100g of milk sample), which arranged the milks as follows; sheep, buffalo, goat, camel and cow milks with energy values of 121.67, 94.24, 77.55, 70.97 and 59.39 calories respectively.

Noticing that goat milk exceeded camel milk in energy which could be attributed to its high lactose content (5.73%), the principle carbohydrate in milk, that exceeded significantly the other tested milks followed by sheep milk lactose content (5.56%), while in the three other milks lactose content was around 4%.

Table 1 Physicochemical and nutritional characteristics of 100 mL raw milks. Data were presented as the mean of five replicates followed by the standard deviation (mean ± SD).

Parameters	Unit	Camel milk	Sheep milk	Goat milk	Buffalo milk	Cow milk
Specific Gravity	-	1.034 ± 0.002^{ab}	1.036 ± 0.001^{a}	1.034 ± 0.001^{ab}	1.035 ± 0.002^{ab}	1.033 ± 0.001^{b}
pH	-	6.60 ± 0.014^{c}	6.88 ± 0.035^{a}	6.63 ± 0.007^{c}	6.72 ± 0.021^{b}	6.60 ± 0.028^{c}
TA	%	0.145 ± 0.007^{abc}	0.133 ± 0.004^{c}	0.150 ± 0.014^{ab}	0.135 ± 0.007^{bc}	0.155 ± 0.007^{a}
Fat	%	4.43 ± 0.11^{c}	9.25 ± 0.35^{a}	4.25 ± 0.35^{c}	6.64 ± 0.01^{b}	3.21 ± 0.30^{c}
Protein	%	3.68 ± 0.17^{c}	4.05 ± 0.07^{b}	4.10 ± 0.14^{b}	4.54 ± 0.08^{a}	3.61 ± 0.16^{c}
TS	%	14.45 ± 0.70^{c}	21.47 ± 0.43^{a}	14.80 ± 0.51^{c}	17.63 ± 0.38^{b}	13.13 ± 0.38^{d}
SNF	%	10.03 ± 0.81^{c}	12.22 ± 0.07^{a}	10.55 ± 0.16^{bc}	10.99 ± 0.37^{b}	9.92 ± 0.08^{c}
Lactose	%	4.11 ± 0.13^{c}	5.56 ± 0.06^{b}	5.73 ± 0.11^{a}	4.09 ± 0.06^{c}	4.02 ± 0.04^{c}
Ash	%	0.81 ± 0.04^{a}	0.77 ± 0.01^{ab}	0.59 ± 0.13^{c}	0.70 ± 0.03^{abc}	0.66 ± 0.02^{bc}
Energy	Calories	70.97 ± 2.71^{d}	121.67 ± 2.65^{a}	77.55 ± 3.32^{c}	94.24 ± 0.07^{b}	59.39 ± 3.44^{e}

$^{a,b,c,..}$ Means values in the same row marked with unlike letters are significantly different ($p<0.05$)

Ash content results reflected the valuable minerals content of camel and sheep milks (0.81% and 0.77%) followed by buffalo, cow and goat mineral content (0.70, 0.66 and 0.59% respectively).

pH values were near the neutral pH which ranged between 6.60 in camel and cow milk and 6.88 in sheep milk, and subsequently reflected on titratable acidity values which ranged between 0.133% in sheep milk to 0.155% in cow milk.

Results of camel milk surpassed North African camel milk values reported by Konuspayeva *et al.* (2009) except for lactose content that was 4.65%. Park *et al.* (2007) reported comparable SG and SNF results of sheep milk in present study, while differed in parameters of cow milk. Obtained analysis of goat milk agreed with Da Costa *et al.* (2014), except for protein results that scored higher content in current samples, and were near to results of Greece and Spain breads reported by Raynal-Ljutovac *et al.* (2008), which could be relied to similar weather condition in Egypt and the two countries. Buffalo characteristics matched with The Nili-Ravi Chinese buffalo breed reported by Han *et al.* (2007). However, complexity that underlies regional differences, including breeds, feeding conditions and seasonal or physiological variations, comprises a difficulty in comparing milk physical and chemical characteristics with previous results (Konuspayeva *et al.* 2009).

Fourier transform infrared (FTIR) spectroscopy

Fourier Transform Infrared (FTIR) spectroscopy is a qualitative rapid technique for the determination of the "fingerprint" of organic compounds because their functional groups exhibit characteristic vibrational absorption/ transmittance frequencies in specific infrared region (Durazzo *et al.* 2015). Figure (1) demonstrated FTIR results of the five milk types from different sources, camel, sheep, goat, buffalo and cow.

The milk protein connected bands are shown in the transmission bands observed at 3433, 3478, 3428 and 3426 cm^{-1} in camel, goat, buffalo and cow milk respectively (Nicolaou *et al.* 2010) and at 1540 to 1650 cm^{-1} which attributed to amide due to C=O and amine groups (N-H) (Durazzo *et al.* 2015). Obtained results could not reflect the minor significant differences exhibited in milks' protein content (Table 1). At the same time, the typical transmittance spectra for water located between 3650–3000 cm^{-1} represented in the hydroxyl group (O-H) (Coitinho *et al.* 2017).

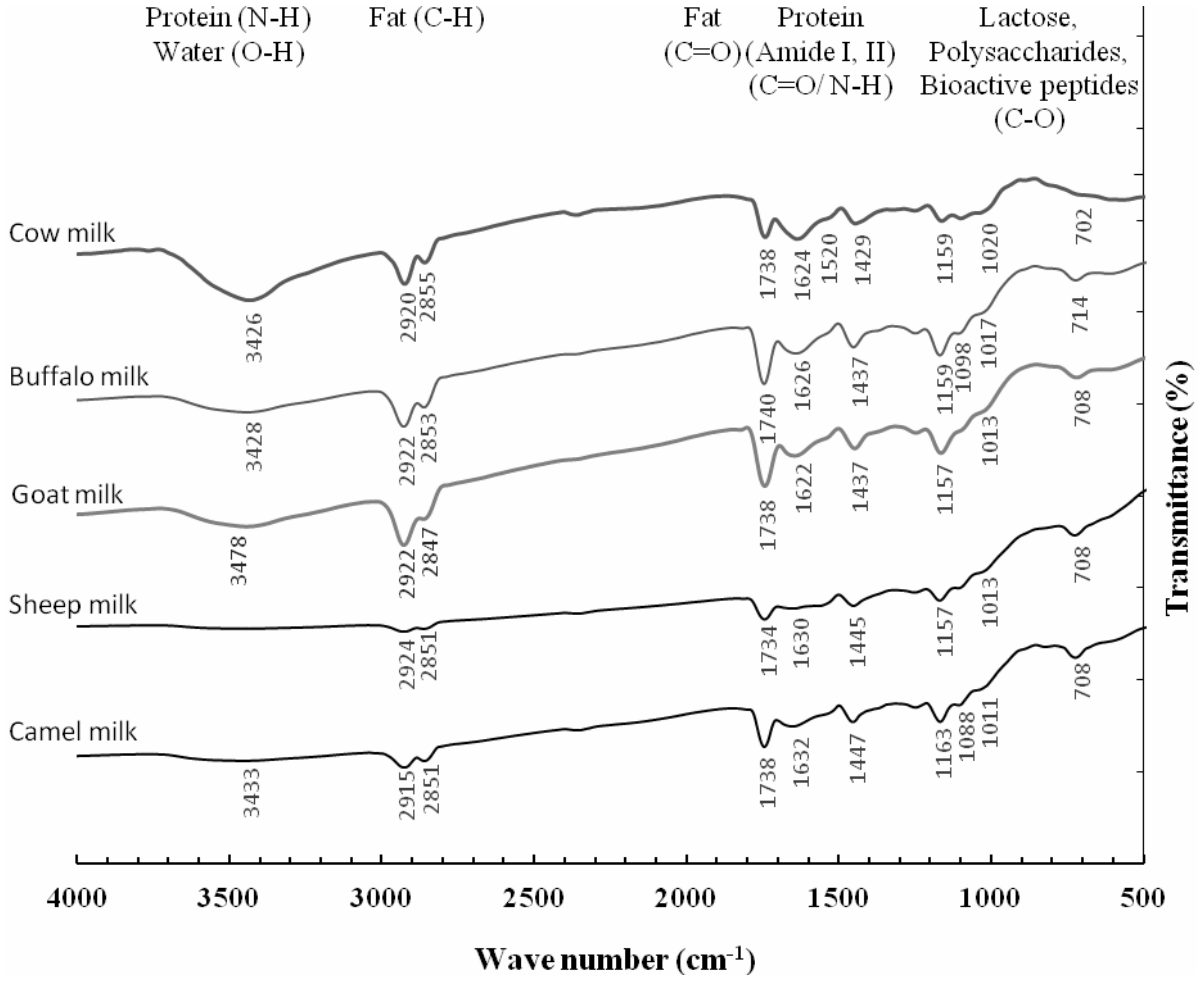

Fig. 1- Fourier transform infrared spectra (FTIR) of raw milks under investigation.

The fat relating bands were clearly illustrated at the transmissions observed in stretching bands presented in all milk samples between 2924 and 2855 cm^{-1} corresponded to the C-H of methyl and methylene groups located between 2900 and 2800 cm^{-1} according to Koca *et al.* (2015). Free fatty acids (FFA) reported to be present in milks resulted in carbon chains, which were most obvious in the symmetric C-H stretching region. Further, the region represented in milks between 1740 to 1520 cm^{-1} is typically used to detect the presence of carboxylic acid groups. This was an indication of presence of short chain fatty acids (SCFA) such as acetic, butyric and propionic acids which reported to be present in the milk of ruminant animals (Bourassa *et al.* 2016). This observation in accordance with what was previously reported by Nicolaou *et al.* (2010).

Lactose, milk sugar is a disaccharide composed of the monosaccharides D-glucose and D-galactose, joined in a ß-1,4-glycosidic linkage. The chemical name for lactose is 4-0-ß-D-galactopyranosyl-D-glucopyranose. The bands at 1429 to 1447 cm^{-1}, represent the bending vibration of C=O and C-O-C present in the pyranose ring. The bands between 1163 and 1011 cm^{-1} is assigned to C-O-C stretching of 1→4 glycosidic bond ring vibration and C-OH bending and is recognized as the characteristic of polysaccharide compounds. Furthermore, the band at 702 to 714 cm^{-1}, represents glycosides linkages attributable to glucopyranose (Kong *et al.* 2007). Moreover, beside saccharides, the area 900 to 1680 cm^{-1} was reported to include frequencies of bioactive molecules amides (Durazzo *et al.* 2015). It is noteworthy that bioactive peptides derived from all milk types proteins are of great interest due to their diversity and health benefits

(El-Salam *et al.* 2013). In summary, the presented FTIR features of camel, sheep, goat, buffalo and cow milks made a clear demonstration of all milk types composition that confirm the earlier conclusion of Coitinho *et al.* (2017).

Isolation and phenotypic identification of LAB strains

Two hundred sixty-eight active strains were isolated and phenotypically identified from all milk sources under investigation. Biodiversity of wild LAB inhabit Egyptian raw milks distributed as percentage of phenotypic cvriteria was presented in (Figs. 2-6).

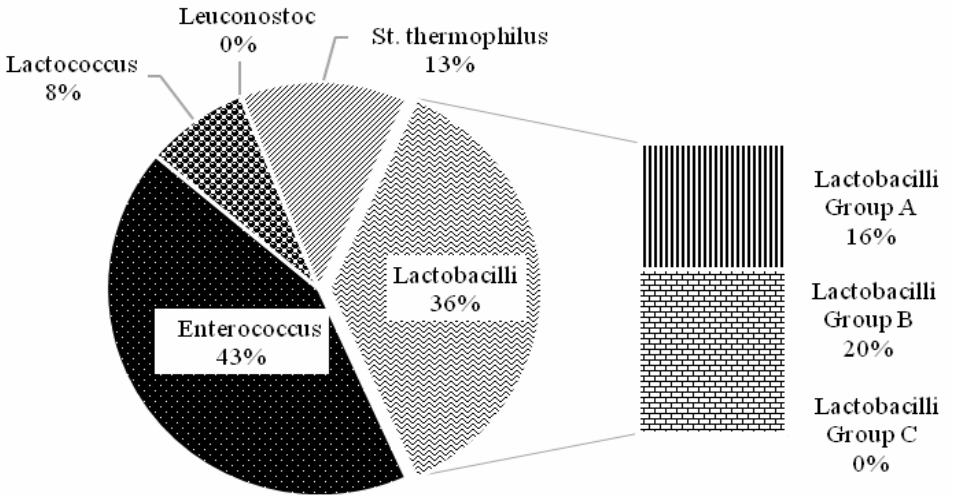

Fig. 2- Percentage distribution of 64 strains of LAB isolated from camel milk.

Above figure (Fig. 2), showed that the 64 isolates were distributed as follows; *Enterococci* (43%) and *Lactobacilli* (36%) representing the predominant genera, with low contribution of *Streptococcus thermophilus* and *Lactococcus* (13% and 8% respectively). Similar observation was recorded by Fguiri *et al.* (2015) when ten selected isolates from camel milk were identified as *Enterococcus faecium* assuring its dominance. On the other hand, Abbas *et al.* (2014) succeeded to isolate *Lactobacilli* strains from different groups from camel milk.

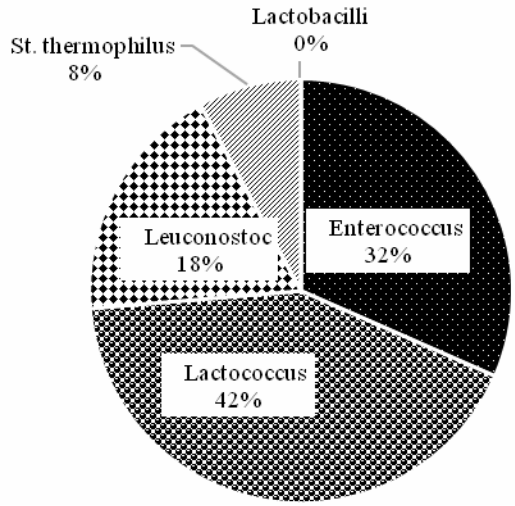

Fig. 3- Percentage distribution of 38 strains of LAB isolated from sheep milk.

Figuer (3) expressed the distribution of the 38 isolates of LAB recovered from sheep milk. *Lactococcus* sp. came first by recording 42% followed by *Enterococcus* sp. (32%) out of all recovered taxa. Other taxa namely *Leuconostoc* sp. and *St. thermophilus* recorded lower percent as 18% and 8% respectively with the complete absence of *Lactobacilli* sp. These results in contradictory with results obtained by Iranmanesh *et al.* (2012) who succeeded to isolate *Lactobacilli* strains from Iranian Ewe milk.

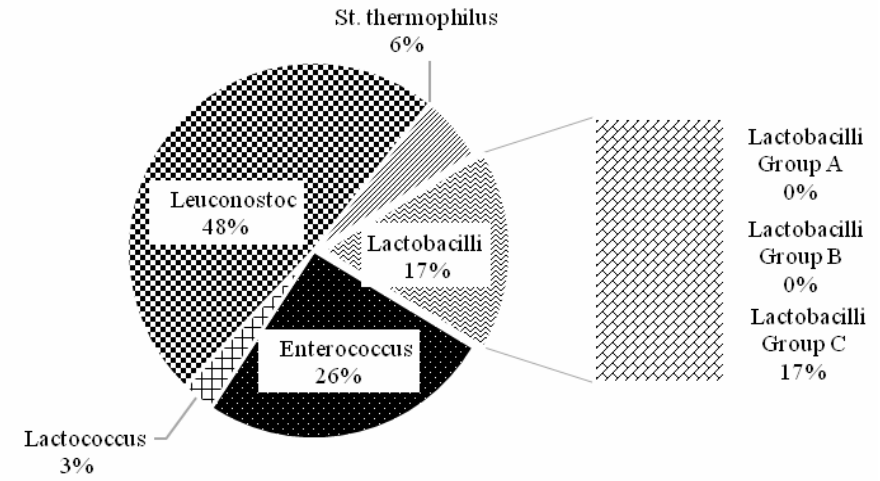

Fig. 4- Percentage distribution of 25 strains of LAB isolated from goat milk.

Five genera were recovered from goat milk samples represented by 35 isolates namely: *Enterococcus, Lactococcus, Leuconostoc, Streptococcus* and *Lactobacillus* (Fig. 4). *Leuconostoc* sp. represented almost 48% of LAB isolates assuring this genus dominance (Fig. 4). The metabolism of citrate which produces flavor compounds such as diacetyl and acetoin is an important pathway of the *Leuconostoc* species (Schmitt *et al.* 1991). Addition of lactose to *Leuconostoc* cells was reported to increase the growth rate (Huang *et al.* 1994), this observation could be connected to milk chemical composition (Table 1) where goat milk showed the highest lactose content amongst the other milks (5.73%) followed by sheep milk (5.56%) which embraced *Leuconostoc* 48% and 18% of their LAB isolates respectively.

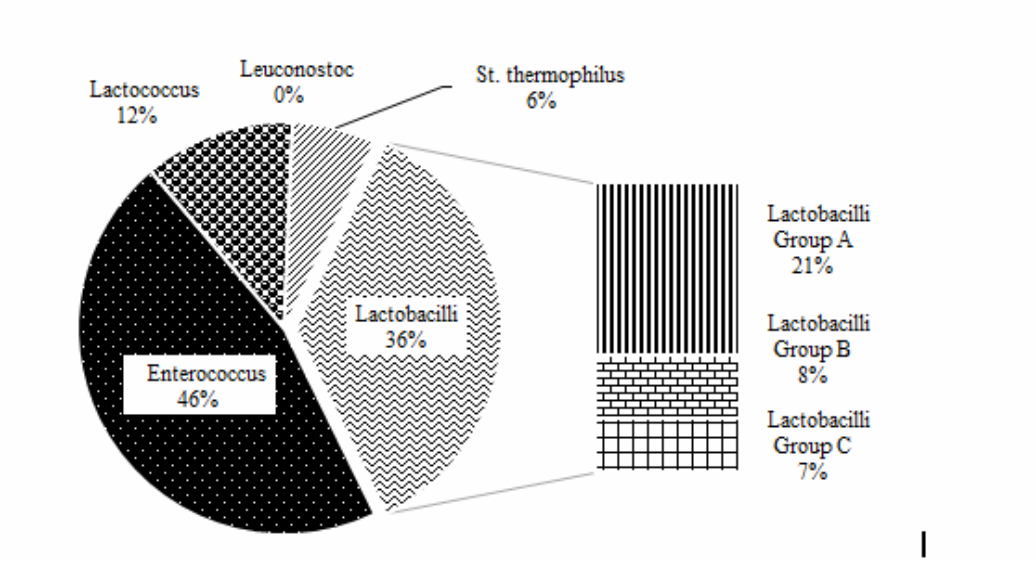

Fig. 5- Percentage distribution of 76 strains of LAB isolated from buffalo milk.

The distribution of 76 strains isolated from buffalo milk showed that *Enterococci* representing by 46% of total isolates (Fig. 5). *Lactobacilli* represented 36% of the total isolates split to majority of Group A (21%) and almost equal percentages of Group B and C (8 and 7% respectively). Relevant work of Rizqiati and hid coworkers (2016) supported our obtained results by isolating *Lactobacilli* strains as a dominant taxa from Indonesian buffalo milk.

LAB strains isolated from cow milk were 55 and their biodiversity represented in figure (6). *Lactobacilli* strains dominated the other genera with a percentage of 43% harbored a majority of Group B (27%) and low percentages of Group C and Group A (9 and 7% respectivly). *Enterococci* sp. represented 38% of isolates, while *Lactococci* showed 17% and fainted representation of *St. thermophilus* strain (2%). These results in agreement of the study carried by Abdullah *et al.* (2010).

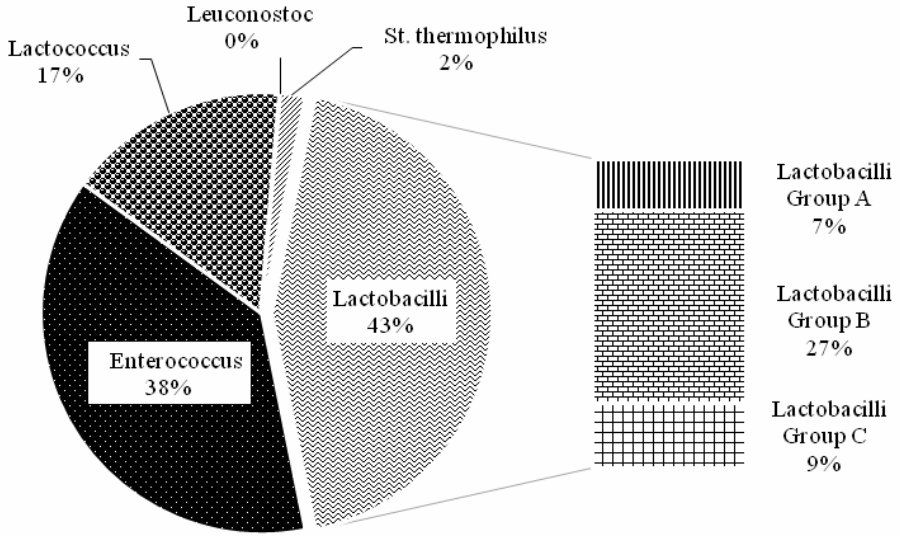

Fig. 6- Percentage distribution of 55 strains of LAB isolated from cow milk.

Technological characterization of selected strains

Technological characteristics of 60 selected strains belonging to 16 LAB genera isolated from the 5 examined native milks are summarized in Table (2). Results revealed that only 10 strains showed autolytic activity. The majority of autolytic strains belonged to camel milk (6 strains), three *E. faecium* and one strain of *E. faecalis, E. pseudoavium* and *L. lactis* subsp. *lactis.* Three strains of cow milk selected isolates showed autolytic activity, *L. lactis* subsp. *cremoris, L. lactis* subsp. *lactis* and *Lb. plantarum.* Only one strain isolated from buffalo milk belongs to *E. faecalis*. It is noticeable that more than 50% of autolytic strains belong to *Enterococci* sp., which reported to play an important role in the production of various traditional fermented food products (Allam *et al.* 2016).

Fifteen strains recorded proteolytic activity. Six strains originated from cow milk, *E. durans, L. lactis* subsp. *cremoris, L. lactis* subsp. *lactis*, *Lb. plantarum* and two strains of *Lb. paracasei* subsp. *tolerans*. Sheep milk proteolytic strains belonged to *Enterococci*, two *E. faecalis,* two *E. faecium* and one *E. durans*. Only two strains of each of camel (*L. lactis* subsp. *lactis* and *Lb. rhamnosus*) and buffalo milk (*E. faecalis* and *Lb. plantarum*) showed proteolytic activity. Despite of wild LAB stability in milk and cheese, they harbor active amino acid convertases, which is interesting for flavor formation in the manufacture of fermented dairy products (Allam *et al.* 2017).

Table 2 Technological characteristics of selected LAB strains isolated from raw milks

Strains identification	[a]Autolytic activity	Proteolytic activity	Antimicrobial potentials	EPS producing	[b]Acidification rate		
					Fast	Medium	Slow
Camel milk (24 selected strains)							
Enterococcus (19)							
E. faecalis (3)	1	0	0	0	1	0	2
E. faecium (13)	3	0	0	0	4	6	3
E. durans (1)	0	0	0	0	0	0	1
E. pseudoavium (2)	1	0	0	0	1	0	1
Lactococcus (2)							
L. lactis subsp. *lactis* (1)	1	1	0	0	0	0	1
L. garvieae (1)	0	0	0	0	0	0	1
Lactobacillus (3)							
Lb. rhamnosus (2)	0	1	0	0	2	0	0
Lb. acidophilus (1)	0	0	0	0	0	0	1
Total	6	2	0	0	8	6	10
Sheep milk (11 selected strains)							
Enterococcus (10)							
E. faecalis (7)	0	2	0	0	0	1	6
E. faecium (2)	0	2	0	0			2
E. durans (1)	0	1	0	0	0	0	1
Leuconostoc (1)							
Leu. oenos (1)	0	0	1	0	0	0	1
Total	0	5	1	0	0	1	10
Goat milk (6 selected strains)							
Enterococcus (5)							
E. faecalis (2)	0	0	1	0	0	0	2
E. durans (2)	0	0	1	0	0	0	2
E. faecium (1)	0	0	0	0	0	0	1
Streptococcus (1)							
St. thermophilus (1)	0	0	0	0	0	0	1
Total	0	0	2	0	0	0	6
Buffalo milk (13 selected strains)							
Enterococcus (8)							
E. faecalis (5)	1	1	3	0	0	2	3
E. durans (1)	0	0	1	0	0	0	1
E. faecium (1)	0	0	0	0	0	0	1
E. seriolicida (1)	0	0	1	0	0	1	0
Lactococcus (1)							
L. lactis subsp. *cremoris* (1)	0	0	0	0	0	1	0
Lactobacillus (4)							
Lb. plantarum (2)	0	1	1	0	0	0	2
Lb. casei (1)	0	0	1	0	0	1	0
Lb. paracasei subsp. *paracasei* (1)	0	0	1	0	0	1	0
Total	1	2	8	0	0	6	7
Cow milk (6 selected strains)							
Enterococcus (1)							
E. durans (1)	0	1	0	0	0	0	1
Lactococcus (2)							
L. lactis subsp. *cremoris* (1)	1	1	0	0	0	0	1
L. lactis subsp. *lactis* (1)	1	1	0	0	0	0	1
Lactobacillus (3)							
Lb. plantarum (1)	1	1	0	0	0	0	1
Lb. paracasei subsp. *tolerans* (2)	0	2	1	0	0	0	2
Total	3	6	1	0	0	0	6
Total strains	10	15	12	0	8	13	39

[a]Strains considered autolytic when score represents 30% or above.
[b]Fast, medium and slow; when a Δ pH of 0.4 unit was achieved after 3, 3-5 and >5 h respectively.

Buffalo milk selected strains showed antimicrobial potentiality surpassed other isolates when owned eight out of twelve strains with antimicrobial activity which distributed as follows, three *E. faecalis* strains, one strain belong to *E. durans, E. seriolicida* and three *Lactobacilli* strains, *Lb. plantarum, Lb. casei* and *Lb. paracasei* subsp. *paracasei.* The other four strains were *Leu. oenos* from sheep milk, *E. faecalis* and *E. durans* from goat milk and *Lb. paracasei* subsp. *tolerans* from cow milk. These results can support De Martinis *et al.* (2016) who suggested potential applications of buffalo milk LAB isolates with proved proteolytic activity and production of antimicrobials in dairy production.

Most selected strains (65%) showed slow acidification rate, while medium and fast acidifiers represented 21.7% and 13.3% respectively. All eight fast acidification strains belonged to *Enterococci* sp. and *Lactobacilli* sp. isolated from camel milk. On contrary, all goat and cow LAB isolates showed slow acidification rate. Allam *et al.* (2017) reported that slow acid producing strains could be applied to soft cheese and other dairy preparation that fast acidity is not considered a cornerstone in their manufacture. None of selected strains found to produce EPS.

Conclusion

Present work emphasized the differences in compositions of camel, sheep, goat, buffalo and cow Egyptian milks that could be a guide for dairy manufacturers. Sheep and buffalo milks showed the highest concentrations of protein, fat and ash in comparison with other studied milks, which should be taken into account affecting curd firmness, coagulation time and rate and amount of rennet used. FTIR results supported chemical analysis performing protein, fat, lactose and bioactive peptides. High lactose content revealed by goat and sheep milks suggested to be reflected on their LAB biota, which encouraged the inhabitance of *Leuconostoc* sp. to represented 48% and 18% respectively of their total LAB isolates. Furthermore, some isolated strains showed exceptional features such as, *Lb. plantarum* from buffalo milk and *Lb. paracasei* subsp. *tolerans* from cow milk that brought together photolytic and antimicrobial potentials, while *L. lactis* subsp. *lactis* from camel milk, *L. lactis* subsp. *cremoris, L. lactis* subsp. *lactis* and *Lb. paracasei* subsp. *tolerans* from cow milk that assembled autolytic and photolytic activities. These findings and LAB strains when correctly employed in dairy processing as starter or adjunct cultures, this would lead to developed innovative dairy products.

Conflict of Interest

The authors do not have any conflicts of interest.

Acknowledgements

Present work was a product of cooperation between the project MILAB funded by Alexandria Research Enhancement Program (ALXREP), Alexandria University and Arid Lands Cultivation Research Institute (ALCRI) and Advanced Technology and New Materials Research Institute (ATNMRI), City of Scientific Research and Technological Applications (SRTA-City).

References

Abbas M. M., and Mahasneh A. M. 2014. Isolation of Lactobacillus strains with probiotic potential from camels milk. African Journal of Microbiology Research, 8(15): 1645–1655. Available at: http://academicjournals.org/journal/AJMR/article-abstract/A82EDBC43860.

Abdullah S. A. and Osman M. M. 2010. Isolation and Identification of Lactic Acid Bacteria from Raw Cow Milk, White Cheese and Rob in Sudan. Pakistan Journal of Nutrition, 9(12): p.1203–1206.

Ahmad S., Gaucher I., Rousseau F., Beaucher E., Piot M., Grongnet J. F. and Gaucheron F. 2008. Effects of acidification on physico-chemical characteristics of buffalo milk: A

comparison with cow's milk. Food Chemistry, 106(1):11–17.
Allam M. G., Darwish A. M. G. and Ayad E. H. E. 2017. Improve hygienic quality of Egyptian Karish cheese employing isolated antagonistic lactobacilli strains. Annual Research and Review in Biology, 19(2): 1–13.
Allam M. G. M., Darwish A. M. G., Ayad E. H. E., Shokery E. S., Mashaly R.E. and Darwish S. M. 2016. In vivo evaluation of safety and probiotic traits of isolated Enterococcus feacium strain KT712. Research Journal of Microbiology, 11(6): 169–177.
Allam M. G. M., Darwish A. M. G., Ayad E. H. E., Shokery E. S. and Darwish S. M. 2017. *Lactococcus* species for conventional Karish cheese conservation. LWT - Food Science and Technology, 79: 625–631.
AOAC International. 2016. Official methods of analysis 20th ed. G. W. Latimer (ed). AOAC International, Rockville, Maryland 20850–3250, USA.
Ayad E. H., Nashat S., El-Sadek N., Metwaly H. and El-Soda M. 2004. Selection of wild lactic acid bacteria isolated from traditional Egyptian dairy products according to production and technological criteria. Food Microbiology, 21(6):715–725. Available at: http://www.sciencedirect.com/science/article/pii/S0740002004000450 [Accessed January 9, 2016].
Ayad E. H., Verheul A., Wouters J. T. and Smit G. 2002. Antimicrobial-producing wild lactococci isolated from artisanal and non-dairy origins. International Dairy Journal, 12(2–3): 145–150. Available at: http://www.sciencedirect.com/science/article/pii/S0958694601001339 [Accessed January 9, 2016].
Ayad E. H. E. 2001. Characterisation of lactococci isolated from natural niches and their role in flavour formation of cheese. PhD Thesis, Wageningen Agricultural University, Wageningen, The Netherlands, ISBN: 90-5808-403-5.
Bourassa M. W., Alim I., Bultman S. J., and Ratan R. R. 2016. Butyrate, neuroepigenetics and the gut microbiome: Can a high fiber diet improve brain health? Neuroscience Letters, 625: 56-63. Available at: http://dx.doi.org/10.1016/j.neulet.2016.02.009.
Cerqueira M. A., Souzaa B. W. S., Simõesb J., Teixeiraa J. A., Dominguesb M. R. M., Coimbrab M. A. and Vicente A. A. 2011. Structural and thermal characterization of galactomannans from non-conventional sources. Carbohydrate Polymers, 83(1):179–185. Available at: http://dx.doi.org/10.1016/j.carbpol.2010.07.036.
Coitinho T. B., Cassoli L. D., Cerqueira P. H. R., da Silva H. K., Coitinho J. B. and Machado P. F. 2017. Adulteration identification in raw milk using Fourier transform infrared spectroscopy. Journal of Food Science and Technology, 54(8): 2394–2402.
Da Costa W. K. A., de Souza E. L., Beltrao-Filho E. M., Vasconcelos G. K.V., Santi-Gadelha, T., Gadelha C. A., Franco O. L., et al. 2014. Comparative protein composition analysis of goat milk produced by the alpine and saanen breeds in Northeastern Brazil and related antibacterial activities. PLoS ONE, 9(3): e93361.
Dandare S. U., Ezeonwumelu I. J. and Abubakar M. G. 2014. Comparative analysis of nutrient composition of milk from different breeds of cows. European Journal of Applied Engineering and Scientific Research, 3(2): 33–36.
De Man J. C., Rogosa M. and Sharpe, M.E. 1960. A readily prepared medium for the cultivation of the lactobacilli. Journal of bacteriology, 23: 130–135.
Durazzo A., Gabrielli P. and Manzi P. 2015. Qualitative Study of Functional Groups and Antioxidant Properties of Soy-Based Beverages Compared to Cow Milk. Antioxidants 4(3): 523–532. Available at: http://www.mdpi.com/2076-3921/4/3/523/.
El-Salam M. H. A. and El-Shibiny S. 2013. Bioactive Peptides of Buffalo, Camel, Goat, Sheep, Mare, and Yak Milks and Milk Products. Food Reviews International, 29(1): p.1–23.
Fadzlillah N. A., Rohman A., Ismail A., Mustafa S. and Khatib A. 2013. Application of FTIR-

ATR Spectroscopy Coupled with Multivariate Analysis for Rapid Estimation of Butter Adulteration. Journal of Oleo Science, 562(8): 555–562.
Fguiri I., Ziadi M., Atigui M., Arroum S. and Khorchani, T. 2015. Biochemical and molecular identification of lactic acid bacteria isolated from camel milk in Tunisia. Emirates Journal of Food and Agriculture, 27(9): p.716–720. Available at: http://www.ejmanager.com/fulltextpdf.php?mno=186094.
Han B. Z., Meng Y., Li M., Yang Y., Ren F., Zeng Q. and Nout M. J. R. 2007. A survey on the microbiological and chemical composition of buffalo milk in China. Food Control, 18(6): 742–746.
Huang D. Q., Prevost H. and Divies C. 1994. Interrelationship of Sugar Metabolism (Glucose, Galactose, Lactose) by Leuconostoc-Mesenteroides Subsp Mesenteroides. Le Lait, 74(3): 207–215.
Iranmanesh M., Ezzatpanah H., Mojgani N., Torshizi M. A. K., Aminafshar M. and Maohamadi M. 2012. Isolation of Lactic Acid Bacteria from Ewe Milk , Traditional Yoghurt and Sour Buttermilk in Iran. European Journal of Food Research & Review, 2(3): 79–92.
Kanwal R., Ahmed T., and Mirza B. 2004. Comparative analysis of quality of milk collected from buffalo, cow, goat and sheep of Rawalpindi/Islamabad region in Pakistan. Asian Journal of Plant Sciences, 3(3): 300–305.
Knoshaug E. P., Ahlgren J. A. and Trempy J. E. 2000. Growth associated exopolysaccharide expression in *Lactococcus lactis* subspecies cremoris Ropy352. Journal of dairy science, 83(4): 633–40. Available at: http://www.journalofdairyscience.org/article/S002203020074923X/fulltext [Accessed January 9, 2016].
Koca N., Harper W. J., and Alvarez V. B. 2015. Application of Fourier Transform Infrared Spectroscopy for Monitoring Short-Chain Free Fatty Acids in Swiss Cheese. Journal of dairy science, 90: 3596–3603.
Kong J. and Yu S. 2007. Fourier transform infrared spectroscopic analysis of protein secondary structures. Acta Biochimica et Biophysica Sinica, 39(8): 549–559.
Konuspayeva G., Faye B. and Loiseau G. 2009. The composition of camel milk: A meta-analysis of the literature data. Journal of Food Composition and Analysis, 22(2): 95–101.
Ling E.R. 1945. A Textbook of Dairy Chemistry 2nd ed. Chapman and Hall LTD, London.
MacFaddin J. F. 1976. Biochemical tests for identification of medical bacteria. In 643–646. Lippincott Williams and Wilkins, U.S.A. Available at: papers3://publication/uuid/9F04BE3E-1009-41D3-BFDF-0B299D24BA17.
Navidghasemizad S., Hesari J., Saris P. and Nahaei M.R. 2009. Isolation of lactic acid bacteria from Lighvan cheese, a semihard cheese made from raw sheep milk in Iran. International Journal of Dairy Technology, 62(2): 260–264.
Nicolaou N., Xu Y., and Goodacre R. 2010. Fourier transform infrared spectroscopy and multivariate analysis for the detection and quantification of different milk species. *Journal of* Dairy Science, 93(12): 5651–5660. Available at: http://linkinghub.elsevier.com/retrieve/pii/S0022030210006144.
Park Y. W., Juarez M., Ramosc M. and Haenleind G. F. W. 2007. Physico-chemical characteristics of goat and sheep milk. Small Ruminant Research, 68(1–2): 88–113.
Raynal-Ljutovac K., Lagriffoul G., Paccard P., Guillet I. and Chilliard Y. 2008. Composition of goat and sheep milk products: An update. Small Ruminant Research, 79(1): 57–72.
Rizqiati H., Nurwantoro, Mulyani S. and Febrisiantosa A. 2016. Isolation and Identification of Lactic Acid Bacteria From Pampangan Buffalo Milk of South Sumatera Indonesia. World Journal of Pharmaceutical and Life Sciences, 2(4): 1-12.
Schmitt P. and Divies C. 1991. Co-metabolism of citrate and lactose by Leuconostoc mesenteroides subsp. cremoris. Journal of Fermentation and Bioengineering, 71(1): 72–74.

Tulini F. L., Hymery N., Haertlé T., Le Blay G. and De Martinis E. C. P. 2016. Screening for antimicrobial and proteolytic activities of lactic acid bacteria isolated from cow, buffalo and goat milk and cheeses marketed in the southeast region of Brazil. Journal of Dairy Research, 83(1): 115–124.

Walsh A. M., Crispie F., Kilcawley K., O'Sullivan O., O'Sullivan M. G., Claesson M. J. and Cottera P. D. 2016. Microbial Succession and Flavor Production in the Fermented Dairy Beverage Kefir. mSystems, 1(5): e00052-16. Available at: http://msystems.asm.org/lookup/doi/10.1128/mSystems.00052-16.

WHO/FAO. 2002. Food energy – methods of analysis and conversion. In Fao Food and Nutrition Paper, 93. Available at: http://www.fao.org/docrep/006/y5022e/y5022e00.htm#Contents%5Cnftp://ftp.fao.org/docrep/fao/006/y5022e/y5022e00.pdf.

Zarei Yam B., Khomeiri M., Mahounak A. S. and Jafari S. M. 2015. Isolation and Identification of Yeasts and Lactic Acid Bacteria from Local Traditional Fermented Camel Milk, Chal. Journal of Food Processing & Technology, 6(7): 460–466. Available at: https://www.omicsonline.org/open-access/isolation-and-identification-of-yeasts-and-lactic-acid-bacteria-from-localtraditional-fermented-camel-milk-chal-2157-7110-1000460.php?aid=56398.