Microbiological Quality of Raw Goat's and Ewe's Bulk-Tank Milk in Switzerland

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ABSTRACT

A total of 407 samples of bulk-tank milk (344 of goat's milk and 63 of ewe's milk) collected from 403 different farms throughout Switzerland, was examined. The number of farms investigated in this study represents 8% of the country's dairy-goat and 15% of its dairy-sheep farms. Standard plate counts and *Enterobacteriaceae* counts were performed on each sample. Furthermore, the prevalence of *Staphylococcus aureus*, *Campylobacter* spp., Shiga toxin-producing *Escherichia coli*, *Salmonella* spp., and *Mycobacterium avium* ssp. *paratuberculosis* was studied. The median standard plate count for bulk-tank milk from small ruminants was 4.70 log cfu/ml (4.69 log cfu/ml for goat's milk and 4.78 log cfu/ml for ewe's milk), with a minimum of 2.00 log cfu/ml and a maximum of 8.64 log cfu/ml. *Enterobacteriaceae* were detected in 212 (61.6%) goat's milk and 45 (71.4%) ewe's milk samples, whereas *S. aureus* was detected in 109 (31.7%) samples of goat's milk and 21 (33.3%) samples of ewe's milk.

Campylobacter spp. and *Salmonella* spp. were not isolated from any of the samples. However, 16.3% of the goat's milk and 12.7% of the ewe's milk samples were polymerase chain reaction (PCR)-positive for Shiga toxin-producing *E. coli*. Seventy-nine (23.0%) goat's tank-milk and 15 (23.8%) ewe's tank-milk samples were PCR-positive for insertion sequence 900, providing presumptive evidence for the presence of *M. avium* ssp. *paratuberculosis*. These results form the basis for determining the microbiological quality standards for goat's and ewe's milk. Moreover, the data presented form part of the risk assessment program for raw milk from small ruminants in Switzerland.

(Key words: food-borne pathogen, goat's and ewe's milk, microbiological quality, prevalence)

Abbreviation key: CI = confidence interval, IS = insertion sequence, MAP = *Mycobacterium avium* ssp. *paratuberculosis*, SPC = standard plate count, STEC = Shiga toxin-producing *Escherichia coli*, D-value = decimal reduction time.

INTRODUCTION

Public health problems associated with consumption of unpasteurized cow's milk and raw-milk products have been well documented (Barrett, 1986; Keene et al., 1997; Cody et al., 1999; De Valk et al., 2000; Kalman et al., 2000; De Buyser et al., 2001; Harrington et al., 2002). There is no evidence that the risk from unpasteurized goat's or ewe's milk is any lower (Hutchinson et al., 1985; Allerberger et al., 2001; McIntyre et al., 2002). Pathogenic microorganisms can gain access to milk either by fecal contamination or by direct excretion from the udder into the milk.

Unlike cow's milk, which is subject to stringent hygiene and quality regulations, microbiological standards for production and distribution of goat's and ewe's milk are more relaxed in Switzerland and are not subject to specific microbiological standards in a legal sense. Furthermore, the literature provides only limited data on the microbiology of goat's and ewe's milk in other countries (Roberts, 1985; Little and Louvois, 1999; Foschino et al., 2002) and none at all for Switzerland.

Nevertheless, there is growing demand for unpasteurized goat's and ewe's milk by consumers in Switzerland. This is due to the increasing number of children suffering from intolerance to cow's milk as well as to the demand for natural and unprocessed food. Furthermore, traditional Swiss goat's and sheep's cheese is typically made from raw milk with the natural microflora responsible for enhancing desirable flavor characteristics of the final product. So there is a clear need to find out more about the present situation regarding the quality of goat's and ewe's milk in Switzerland.

The objectives of this study were to 1) determine the microbiological status of goat's and ewe's milk in Swit-

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Figure 1. Sampling of small ruminant's milk throughout 25 of Switzerland's 26 cantons (goat's bulk-tank milks/ewe's bulk-tank milks).

zerland and 2) study the prevalence of food-borne pathogens, especially *Staphylococcus aureus*, *Campylobacter* spp., Shiga toxin-producing *Escherichia coli* (STEC), *Salmonella* spp. and *Mycobacterium avium* ssp. *paratuberculosis* (MAP).

MATERIALS AND METHODS

Milk Samples

Between February and August 2002, a total of 407 bulk-tank milk samples (344 goat's milk and 63 ewe's milk) were collected from 403 farms with a total of approximately 11,000 animals (8000 goats and 3000 ewes). The number of farms investigated represents 8% of Switzerland's dairy-goat and 15% of its dairy-sheep farms. Goat farms ranged in size from two to 180 animals and ewe farms from 2 to 300 animals. The farms were distributed throughout 25 of Switzerland's 26 cantons (Figure 1) and were categorized in three groups (<6 animals, 6 to 25 animals, >25 animals). The numbers of farms investigated in these groups were selected according to the frequency of distribution of the various farm sizes in Switzerland.

Sampling was performed after cooling the milk aseptically either at the farm itself or from various milk-collection points. After purchase, the samples were

placed directly into cool boxes and transported to the laboratory. The samples were processed within 24 to 48 h. For the detection of MAP, 20 ml of milk was stored at -20°C before being investigated.

Standard Plate Count and *Enterobacteriaceae* Count

Standard plate count (SPC) and *Enterobacteriaceae* counts were determined by pour plate method with plate count agar (Oxoid, Basingstoke, U.K.) and violet-red bile glucose agar (BBL, Cockeysville, MD), respectively. The detection limit was at 1.0×10^0 cfu/ml.

Staphylococcus aureus

Numbers of *S. aureus* were determined by surface-plating the samples on rabbit-plasma-fibrinogen agar (Oxoid CM 275 with RPF supplement Sedia 2000-0100). The detection limit was 1.0×10^1 cfu/ml. The number of coagulase-positive staphylococci was obtained by direct enumeration of typical colonies (tellurite-positive colonies with an opaque halo).

Campylobacter spp.

Ten milliliters of milk was inoculated into 100 ml of selective enrichment broth (Brucella Bouillon [Difco

0495-17-3, Becton Dickinson, Sparks, MD] with Campylobacter growth supplement [Oxoid SR84] and Skirrow Campylobacter selective supplement [Oxoid SR69]) and incubated at 42°C for 48 h under microaerobic conditions provided by commercial gas packs (CampyGen from Oxoid). The enrichment samples were then streaked onto selective agar media (Brucella agar, [Difco 0964-17-5, Becton Dickinson] with 6% horse blood [Oxoid SR48], as well as Butzler Campylobacter selective supplement [Oxoid SR85]) and incubated at 42°C for another 48 h under microaerobic conditions. Suspicious colonies, appearing translucent white, moist, and glistening, were selected for further identification.

Shiga Toxin-Producing *E. coli*

From each sample, 25 ml was enriched in 225 ml of brilliant-green bile broth (BBL) at 37°C for 24 h. The enrichment broth was then evaluated by PCR with primers based on sequences targeting a region between *stx1* and *stx2* genes (Burnens et al., 1995). Bacterial DNA was prepared by incubating 2 µl of brilliant-green bile broth in 42 µl of double-distilled water at 100°C for 10 min. Amplifications were carried out with a total volume of 50 µl containing 200 µM of dNTP, 30 pmol of each primer, 5 µl of 10-fold concentrated polymerase synthesis buffer, and 2.5 U of Taq-DNA-polymerase (Promega, Madison, WI) in a Biometra DNA cycler. The amplified products were visualized by gel electrophoresis on 0.9% agarose gel stained with ethidium bromide.

From 40 PCR-positive samples, the enrichment broth was plated onto sheep blood agar (Trypticase-Soy-Agar, BBL with 5% sheep blood), and five single colonies were tested by the same PCR protocol to obtain STEC isolates. The strains were identified with classic biochemical tests (acid production from mannitol, *o*-nitrophenyl-β-D-galactopyranoside test, H₂S and indole production, as well as proof of urease and lysine decarboxylase). All strains were examined for sorbitol fermentation, for β-D-glucuronidase activity, and for the presence of *stx1* and *stx2* genes (Blanco et al., 2003). The PCR-RFLP was used for subtyping *stx2* variants (Piérard et al., 1998). Furthermore, PCR was employed to determine the presence of the *eae*, *hlyA*, and *astA* genes (Schmidt et al., 1994; 1995; Yamamoto and Nakazawa, 1997).

The determination of O and H antigens was carried out by the method described by Guinée et al. (1981), employing all available O (O1-O181) and H (H1-H56) antisera.

Salmonella spp.

Salmonella spp. were detected in a two-stage enrichment procedure. Twenty-five ml of milk was pre-en-

riched in 225 ml of buffered peptone water (Oxoid CM 509) at 37°C for 24 h. Ten milliliters of the pre-enrichment sample was then incubated in 100 ml of tetrathionate (Oxoid CM 343) or 0.1 ml of the pre-enriched sample in 10 ml of Rappaport-Vassiliadis medium (Oxoid CM 669) at 37°C or 43°C for another 24 h. Enrichments were then streaked onto brilliant-green phenol red agar (Difco 0285-17-7, Becton Dickinson) and mannitol-lysine crystal-violet brilliant green agar (Brandenberger, Zurich, Switzerland). Both selective media were incubated at 37°C for 24 h.

Mycobacterium avium ssp. *paratuberculosis*

Ten milliliters of each sample was mixed with 100 µl of Triton X-100 (Calbiochem, Darmstadt, Germany) and centrifuged at 4500 rpm for 30 min. Afterwards, the pellet was transferred to a Blue Ribolysor tube (Hybaid, Ashford, U.K.), resuspended in 400 µl of mycobacterial lysis buffer (EDTA, 2mM; sodium chloride, 400 mM, TrisHCl, 10 mM (pH 8.0); 0.6% SDS; proteinase K, 33 µl/ml) and incubated overnight at 37°C. For access to target DNA, samples were centrifuged at 6.5 m/s for 45 s in a RiboLyser (Hybaid). The DNA was then extracted with 1 volume of phenol/chloroform/isoamyl-alcohol (25:24:1) and precipitated with 3 M potassium acetate for 30 min at -70°C, centrifuged (13,000 rpm, 15 min), washed in 70% ethanol, dried, and resuspended in TE-buffer (10 mM Tris, 1 mM EDTA, pH 8.0).

Five microliters of the resuspended DNA was used for an insertion sequence (IS) 900-nested PCR specific to MAP. According to Hermon-Taylor et al. (2000), the primers p90 5'-GAA GGG TGT TCG GGG CCG TCG CTT AGG-3' and p91 5'-GGC GTT GAG GTC GAT CGC CCA CGT GAC-3' were used for the first 30 amplification cycles. The PCR mix consisted of 50 µl of reaction volume containing a final concentration of 2 µM of each primer, 2.5 mM MgCl₂, 100 µM dNTP, and 2 U Taq polymerase (Promega) in 1× reaction buffer (Promega). The reactions were cycled as follows: initial denaturation at 94°C for 5 min; 30 cycles of 94°C for 1 min, 58°C for 1 min, and 72°C for 3 min; and a final extension of 72°C for 7 min.

Two microliters from the primary amplification were then used with the primers AV1 5'-ATG TGG TTG CTG TGT TGG ATG G-3' and AV2 5'-CCG CCG CAA TCA ACT CCA G-3' for the nested PCR. The PCR mix consisted of a 50-µl reaction volume containing a final concentration of 2 µM of each primer, 1.5 mM MgCl₂, 100 µM dNTP, and 2 U Taq polymerase (Promega) in 1× reaction buffer (Promega). The reactions were cycled as follows: initial denaturation at 94°C for 5 min; 40 cycles of 94°C for 1 min, 58°C for 1 min, and 72°C for 3 min; and a final extension of 72°C for 7 min. The PCR

Table 1. Selected statistical values of standard plate count (SPC) and *Enterobacteriaceae* counts (goat's milk n = 344, ewe's milk n = 63).

	SPC (log cfu/ml)		<i>Enterobacteriaceae</i> (log cfu/ml) ¹	
	Goat's milk	Ewe's milk	Goat's milk	Ewe's milk
Median	4.69	4.78	1.88	2.08
50% range	3.92–5.92	3.69–5.31	Ø–3.20	Ø–3.56
90% range	3.25–6.90	2.89–6.16	Ø–4.66	Ø–4.29
Mean	6.92	5.93	5.72	3.93
Standard deviation	7.63	6.44	6.51	4.48
Standard error	6.36	5.54	5.25	3.58
Confidence interval (95%)	6.58–7.11	5.16–6.19	5.26–5.94	2.97–4.20
Minimum	2.00	2.30	Ø	Ø
Maximum	8.64	7.26	7.64	5.34

¹Ø = below detection limit (1.0×10^0 cfu/ml).

products were visualized on 1.5% agarose gels (Eurobio, Les Ulis Cedex, France). The IS900-nested product is 298 bp in length.

Statistical Analysis

The statistical significance was determined by the χ^2 -test ($P < 0.05$), the Mann-Whitney U-test ($P < 0.05$) and the Kruskal Wallis H-test ($P < 0.05$).

RESULTS

The median SPC for bulk-tank milk from small ruminants was 4.70 log cfu/ml, with a minimum of 2.00 log cfu/ml and a maximum of 8.64 log cfu/ml. Median SPC was 4.69 log cfu/ml for goat's milk and 4.78 log cfu/ml for ewe's milk. *Enterobacteriaceae* were detected in 212 (61.6%; confidence interval [CI] of 95% = 61.01 to 71.96) goat's milk and 45 (71.4%, CI 95% = 56.98 to 80.77) ewe's milk samples. The median value was 1.88 log cfu/ml for goat's milk, with a maximum of 7.64 log cfu/ml, and 2.08 log cfu/ml for ewe's milk, with a maximum of 5.34 log cfu/ml. Selected statistical values of SPC and *Enterobacteriaceae* counts are summarized in Table 1. The frequency distributions of SPC and *Enterobacteriaceae* counts for goat's and ewe's milk are shown in Figure 2.

An increase in the median SPC and *Enterobacteriaceae*, counts depending on milk delivery frequency and different farm sizes (<6 animals, 6 to 25 animals, >25 animals), is shown in Table 2. Among farms with daily milk deliveries and farms with deliveries every second or third day, significant differences in SPC results were found ($P < 0.05$). Moreover, the statistical analysis showed significant differences for SPC and *Enterobacteriaceae* counts between the described categories of farm sizes ($P < 0.05$).

Staphylococcus aureus was detected in 109 (31.7%, CI 95% = 31.22 to 42.40) goat's milk and 21 (33.3%, CI

95% = 21.95 to 46.34) ewe's milk samples. The median value for goat's and ewe's-milk samples was <1 log cfu/ml, with a maximum of 4.34 log cfu/ml for goat's and 3.56 log cfu/ml for ewe's milk.

The prevalence of *Campylobacter* spp., STEC, *Salmonella* spp., and MAP are shown in Table 3. *Campylobacter* spp. and *Salmonella* spp. were not isolated from any of the samples. However, STEC PCR was positive in 62 (15.2%) of the 407 milk samples examined. Also, 16.3% (CI 95% = 15.63 to 24.99) of goat's milk samples and 12.7% (CI 95% = 5.65 to 23.50) of ewe's milk samples were *stx* positive. Twelve STEC strains were isolated and further characterized (Table 4). All the strains belonged to the non-O157 *E. coli* group and tested positive for sorbitol and β -D-glucuronidase. One strain harbored only the *stx1* gene, one strain only the *stx2* gene, and 10 strains the *stx1* and *stx2* genes. Nine strains tested positive for EHEC-*hlyA*, one strain tested positive for the *eae* gene, and no strain harbored the *astA* gene.

Seventy-nine (23.0%, CI 95% = 21.76 to 32.06) goat's milk and 15 (23.8%, CI 95% = 13.98 to 36.21) ewe's milk samples were IS900 PCR positive. The prevalence of milk samples containing IS900 in different geographical regions of Switzerland ranged from 17 to 34%. Seventeen percent of the bulk-tank milk samples from the north-east, 26% of the samples from the center, 21% of the samples from the north-west, and 34% of the bulk-tank milk samples from the southern part of Switzerland tested IS900 PCR-positive.

DISCUSSION

No significant differences could be detected in SPC and *Enterobacteriaceae* counts as a function of the animal species (sheep/goats). Therefore, the same microbiological limit value can be used to assess the quality of both sheep's and goat's milk. According to European Council Directive 92/46/EEC, raw goat's or sheep's milk used to produce drinking milk and products from heat-

Figure 2. Frequency distributions of SPC and *Enterobacteriaceae* counts for goat's and ewe's bulk-tank milk.

Table 2. Median values (log cfu/ml) of standard plate count (SPC) and *Enterobacteriaceae* counts depending on frequency of milk delivery and farm sizes.

	SPC		<i>Enterobacteriaceae</i>	
	Goat's milk	Ewe's milk	Goat's milk	Ewe's milk
Median	4.69 (n = 344)	4.78 (n = 63)	1.88 (n = 344)	2.08 (n = 63)
Frequency of milk delivery ¹				
Daily	4.32 (n = 197)	4.61 (n = 43)	1.00 (n = 197)	2.00 (n = 43)
Every second or third day	5.68 (n = 135)	4.88 (n = 20)	2.61 (n = 135)	2.69 (n = 20)
Farm size ²				
<6 animals	4.43 (n = 58)	3.66 (n = 7)	1.30 (n = 58)	1.30 (n = 7)
6 to 25 animals	4.66 (n = 167)	4.49 (n = 17)	1.48 (n = 167)	1.70 (n = 17)
>25 animals	4.97 (n = 86)	4.75 (n = 34)	2.45 (n = 86)	2.56 (n = 34)

¹No. of evaluated farms: 395, from 12 farms, no data were available.

²No. of evaluated farms: 369, from 38 farms, no data were available.

Table 3. Prevalence of *Campylobacter* spp., *salmonella* spp., Shiga toxin-producing *Escherichia coli* (STEC) and *Mycobacterium avium* subsp. *paratuberculosis* (MAP) for 344 goat's and 63 ewe's milk samples.

Pathogen	No. (%) of positive samples	
	Goat's milk	Ewe's milk
<i>Campylobacter</i> spp.	0 (0%)	0 (0%)
<i>Salmonella</i> spp.	0 (0%)	0 (0%)
STEC	55 (16%)	8 (13%)
MAP	79 (23%)	15 (24%)

treated milk must not contain more than 6.00 log cfu/ml (SPC), and the milk used for the manufacture of raw-milk products not more than 5.70 log cfu/ml (SPC). In our study, 77% of the goat's milk and 86% of the sheep's milk or 73% of the goat's and 81% of the sheep's milk SPC results, respectively, were below the SPC limits fixed by the EU regulations. The microbiological quality standard stipulated by European Council Directive 92/46/EEC may therefore be used as a basis for developing a specific quality standard system for milk from small ruminants in Switzerland.

The delivery frequency of the milk supplied had an impact on the SPC of the milk samples. The observed significant differences in SPC between farms with daily milk deliveries and those with deliveries every second or third day suggested some difficulty in cooling the milk on farm for a longer period. The increase in microbial contamination of milk samples obtained from farms with more animals was quite unexpected. We assumed that farms with more animals would have more professional hygiene management, resulting in lower microbial counts.

The SPC median values of goat's and ewe's milk were one log unit higher than the median value of cow's tank

milk (Stephan and Bühler, 2001). In addition, striking differences were found in the prevalence of the *Enterobacteriaceae*: 7% for cow's milk samples compared with 62% for goat's milk and 70% for sheep's milk samples. These results suggest some difficulty in managing the hygiene quality of small ruminant's milk, which may be due to a series of factors including the milking system. In contrast, the prevalence of *S. aureus* in milk samples from small ruminants (32%) is only half as frequent as that found in cow's milk samples (Stephan et al., 2002).

Other surveys of pathogen prevalence in goat's and ewe's milk provided results comparable to those of our study, showing no *Salmonella* or *Campylobacter*-positive samples (Little et al., 1999; Foschino et al., 2002; Morgan et al., 2003). However, 16.3% of the goat's milk and 12.7% of the ewe's milk samples were positive for STEC. The importance of the STEC group has increased since the first description of a food-borne infection caused by *E. coli* O157:H7 (Riley et al., 1983). Human STEC infection after raw milk consumption was first mentioned by Martin et al. (1986) and has now gained greater importance, in particular due to the very low minimum infectious dose. The risk associated with consumption of unpasteurized goat's milk is documented in the literature (Bielaszewska et al., 1997; McIntyre et al., 2002). Frequently, STEC strains isolated from patients are of serotype O157 and show a typical virulence spectrum, with such strains tending to be *stx2* and *eae*-positive (Boerlin et al., 1999). The *stx2d* variant was the principal *stx2* subtype in strains isolated from small ruminants in our study, and has so far not been detected in STEC strains isolated from patients. Only one STEC strain with serotype O157:H19 harbored *stx2* and *eae* genes. Despite the low prevalence of strains with the typical virulence pattern in bulk-tank samples,

Table 4. Characterization results of 12 Shiga toxin-producing *Escherichia coli* strains isolated from raw bulk-tank milk samples from small ruminants.

Origin	Serotype	Virulence factors				
		<i>stx1</i>	<i>stx2</i>	<i>EHEC-hly</i>	<i>eae</i>	<i>astA</i>
Goat milk	O5:H ⁻¹	+	<i>stx2c</i>	+	—	—
Goat milk	O5:H ⁻¹	+	<i>stx2c</i>	+	—	—
Goat milk	O76:H19 ²	+	—	+	—	—
Ewe milk	O87:H16	—	<i>stx2d</i>	—	—	—
Ewe milk	O87:H16	—	<i>stx2d</i>	—	—	—
Goat milk	O91:H ²	+	<i>stx2d</i>	+	—	—
Goat milk	O113:H4 ²	+	<i>stx2d</i>	+	—	—
Goat milk	O113:H4 ²	+	<i>stx2d</i>	+	—	—
Goat milk	O113:H4 ²	+	<i>stx2d</i>	+	—	—
Goat milk	O113:H4 ²	+	<i>stx2d</i>	+	—	—
Goat milk	O174(OX3):H8 ²	+	<i>stx2d</i>	—	—	—
Ewe milk	ONT:H19 ¹	—	<i>stx2</i>	+	+	—

¹Serotypes previously associated with human STEC strains that caused HUS.

²Serotypes previously found in human STEC strains.

infections due to consumption of raw milk can not be excluded. However, pasteurization of milk (71.7°C for 15 s, Swiss food regulation) offers sufficient protection.

MAP is a pathogen that causes chronic, granulomatous inflammation of the intestine in various animals, including cattle and small ruminants, and can also be cultured from milk of apparently healthy animals (Streeter et al., 1995). Today, it seems increasingly probable that MAP could play a role in the etiology of Crohn's disease (Hermon-Taylor et al., 2000). However, conclusive evidence for the etiological role of MAP in Crohn's disease is still lacking.

Raw milk may be a potential vehicle for transmission of MAP to humans. Therefore, MAP has acquired special relevance to food hygiene. Moreover, results of laboratory pasteurization tests of raw whole milk spiked with MAP showed that MAP was capable of surviving pasteurization (Chiodini and Hermon-Taylor, 1993; Grant et al., 1998; Keswani and Frank, 1998; Sung and Collins, 1998). Nevertheless, conflicting results can be found in the literature. Sung and Collins (1998) reported a decimal reduction time (**D-value**) for MAP in milk of 11 s at 71°C, indicating that MAP could survive HTST pasteurization if the initial numbers were >1 log cfu/ml milk. Pearce et al. (2001), however, reported a D-value of 2.03 s at 72°C, which is equivalent to a >7 log reduction at 72°C for 15 s (HTST pasteurization). Grant et al. (2002) pasteurized raw cows' milk naturally infected with MAP and found that MAP survived commercial-scale pasteurization at 73°C for 15 s and 25 s with and without prior homogenization if the bacterial cells were present in sufficient numbers before heat treatment.

The 23% prevalence in goat's and 24% in ewe's milk IS900 PCR-positive bulk-milk samples indicates a wide distribution of subclinical MAP infections in small dairy ruminants in Switzerland. Polymerase chain reaction targeting the 5' end of IS900 has been considered specific for identification of MAP and is frequently applied to confirm the presence of this organism. However, the finding of an insertion sequence very similar to IS900 in a *Mycobacterium* sp. unrelated to MAP has raised questions concerning the reliability of PCR methods for detection of MAP (Cousins et al., 1999; Englund et al., 2002).

No other comparative data on the occurrence of MAP in goat's and ewe's milk are currently available for Switzerland. Djonne et al. (2003) examined raw goat's milk in Norway. In their study, 7.1% of the samples tested positive by an immunomagnetic separation PCR method. In a survey by Grant et al. (2001) in England, one raw goat-milk sample from 104 raw sheep's and goat's milk samples tested positive for the presence of MAP by immunomagnetic separation PCR.

In a previous study, we demonstrated that 19.7% of raw bulk-tank milk samples obtained from cows in Switzerland were IS900 positive (Corti and Stephan, 2002). Compared with cow's milk, no statistically significant regional differences in MAP herd-level prevalence were found for small ruminants.

The results of this study could form the basis for determining specific microbiological quality standards for goat's and ewe's milk in Switzerland. Moreover, they constitute part of the Swiss risk assessment program for raw milk from small ruminants.

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