Prevalence of *Salmonella*, *Listeria monocytogenes*, *Campylobacter* spp., *Yersinia enterocolitica* and *Cryptosporidium* spp. in bulk milk, cows' faeces and effluents of dairy farms in Trinidad

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Key words

Salmonella - *Listeria monocytogenes* - *Campylobacter* - *Yersinia entero-colitica* - *Cryptosporidium* - Dairy cow - Milk - Faeces - Waste water - Dairy farm - Contamination - Trinidad and Tobago.

Summary

The prevalence of *Listeria*, *Salmonella*, *Campylobacter*, *Yersinia* and *Cryptosporidium* species in bulk milk, faeces of dairy cows and effluents of milking parlours from dairy farms in Trinidad was investigated. Of the 177 bulk milk samples studied, 3 (1.7 %), 3 (1.7 %) and 2 (1.1 %) were positive for *L. monocytogenes*, *Salmonella* spp. and *Y. enterocolitica*, respectively, but were all negative for *Campylobacter* and *Cryptosporidium* species. From 333 faecal samples tested, *L. monocytogenes*, *Campylobacter* spp. and *Cryptosporidium* spp. were detected in 11 (3.3 %), 19 (5.7 %) and 7 (2.1 %), respectively, which were significantly ($P < 0.05$; χ^2) higher than the detection rate (0 %) for *Yersinia* spp. *Salmonella* spp. were isolated from 3 (0.9 %) of the faecal samples. From 168 effluent samples cultured, *Campylobacter* spp. were isolated from 7 (4.2 %) samples while *Salmonella* was recovered from only 1(0.6 %) sample with no sample positive for either *Yersinia* or *Listeria*. The difference was significant ($P < 0.05$; χ^2). A total of 19 (73.1 %) of 26 *Campylobacter* isolates exhibited resistance to one or more of the six antimicrobial agents tested. All 14 (100 %) isolates of *L. monocytogenes* were resistant to at least one agent while all *Salmonella* and *Yersinia enterocolitica* strains were susceptible to all antimicrobial agents used. It was concluded that the five enteropathogens tested were present on dairy farms in Trinidad and the potential for milk-borne diseases, due to these pathogens, exists for consumers, emphasizing the need for good sanitary practices.

■ INTRODUCTION

Milk from dairy animals, particularly cattle, has been responsible for several outbreaks of infections and intoxications in human consumers worldwide (22, 26, 39). Most of these epidemics have been associated with the consumption of raw milk although pasteurized milk has also been implicated (20, 42).

Pathogens in milk may be aetiological agents for subclinical or clinical mastitis (1, 38), part of the normal flora of the skin of dairy animals or skin and anterior nares of their human handlers (35). Dairy cows are also carriers of several enteropathogens in their gut (41).

In Trinidad and Tobago, *Campylobacter*, *Salmonella*, *Yersinia* and *Listeria* species have been isolated from livestock (5), raw meat

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(2) and ready-to-eat foods (4) while *Cryptosporidium* oocysts have been detected in diarrhoeic livestock (5). Also, verocytotoxigenic *Escherichia coli* and enterotoxigenic *Staphylococcus aureus* have been recovered from raw cows' milk sampled at the levels of the processing plant (3) and collection centres (8). To date, information is unavailable on the prevalence of enteropathogens in bulk milk and dairy cows at the farm level.

The study was conducted to determine the prevalence of *Campylobacter*, *Listeria*, *Yersinia*, *Salmonella* and *Cryptosporidium* species in bulk milk, faeces of dairy cows and effluents of milking parlours and to characterize the enteropathogens isolated.

■ MATERIALS AND METHODS

Study design

Dairy farms supplying bulk milk to the eight collection centres (IC, 5C, 5H, 2G, 2C, 2B, 6H and 3G), where the microbial quality of milk was earlier determined (8), were investigated. With the aid of a computer print out of the list of dairy farms in these milking areas, every other farm was randomly selected to be involved in the study. On every farm selected, 20 % of lactating cows was to be sampled.

Source, type and collection of samples

Bulk milk was pooled from the churns containing the morning's yield of each selected farm. Approximately, 100 ml of bulk milk samples were collected per dairy farm. In practice, a bulk milk sample originated from each dairy farm studied (table I). The median number of lactating dairy cows per farm in each milking centre during the visits is shown in brackets as follows: IC (9), 5C (4), 5H (2), 2G (5), 2C (2), 2B (12), 6H (2) and 3G (3). Overall, a total of 177 dairy farms across 8 milking centres were studied with a median number of lactating dairy cows per farm of 4. Faeces, or rectal swabs in cases where faeces could not be collected, were obtained from the rectum with the use of gloves and immediately put into sterile wide-mouthed plastic containers. Effluents were collected, from the most distal point of the milking parlour or shed, into wide-mouthed sterile containers. Approximately, 100 ml of effluent were collected.

Isolation and identification of microorganisms

To detect *Listeria* spp. in 1 g of faeces or 25 ml of bulk milk or effluent, the faecal and milk or effluent samples were enriched in 9 ml and 225 ml, respectively, of nutrient broth (Difco, USA) at 4°C for 6 weeks. Subcultures were made onto *Listeria* selective media with Oxford suplement (Oxoid, UK) forthnightly. Inoculated plates were incubated at 37°C in 5 % CO_2 in a CO_2 incubator (Forma Scientific, USA) for 24-48 h. Typical black colonies were Gram-stained and tested for catalase and oxidase activities. Colonies that were Gram-positive short rods were inoculated into triple sugar iron (TSI) agar slants, urea slants and motility medium. Isolates with acid/acid, reaction without gas in TSI, urease-positive and typical umbrella-shaped motility were subjected to further biochemical tests (32).

Salmonella spp. were detected in either 1 g of faeces and 25 ml each of bulk milk or effluent which were inoculated into 9 ml of selenite cystine (SC) broth and 225 ml of lactose broth (LB), respectively, and incubated overnight at 42°C. Enriched faecal samples were inoculated onto xylose lysine desoxycholate (XLD) agar and incubated at 37°C for 24 h. One millilitre each of pre-enriched bulk milk and effluent in LB was inoculated into 10 ml each of selenite cystine and tetrathionate broth and incubated overnight at 37°C. Typical pink colonies with black centres on XLD and colonies with characteristic silvery appearance on BS plates were subjected to biochemical tests using standard methods (32). Serologic identification was initially carried out using the slide agglutination test with the polyvalent antiserum A-I α Vi. Confirmation of *Salmonella* isolates and complete serological typing was kindly done at the Caribbean Epidemiology Centre (CAREC), Port of Spain, Trinidad.

For the isolation of *Campylobacter* spp., a loopful of samples (faeces, bulk milk or effluent) was inoculated directly onto

Table I

Prevalence of species of *Listeria*, *Salmonella*, *Campylobacter*, *Yersinia* and *Cryptosporidium* in bulk milk

Milking Centre	Num. of bulk milk samples tested	Number (%) of samples positive				
		Listeria spp.*	*Salmonella* spp.**	*Campylobacter* spp.	*Yersinia* spp.***	*Cryptosporidium*
IC	43	0 (0.0)	3 (7.0)	0 (0.0)	1 (2.3)	0 (0.0)
5C	35	1 (2.9)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
5H	33	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2G	16	1 (6.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2C	15	1 (6.7)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2B	14	0 (0.0)	0 (0.0)	0 (0.0)	1 (7.1)	0 (0.0)
6H	11	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
3G	10	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Total	177	3 (1.7)	3 (1.7)	0 (0.0)	2 (1.1)	0 (0.0)

* Made up of *L. monocytogenes*

** All isolates were *S. agona*

*** Both isolates were *Yersinia enterocolitica*, serotype 0:3, biotype 4

Campylobacter blood-free agar with CCDA supplement (Oxoid, UK). Inoculated plates were incubated in a CO_2 incubator (Forma Scientific Inc., USA) with 8-10 % CO_2 at 42°C for 24-48 h. Suspect colonies were Gram-stained. Gram-negative slender, sea-gull appearing microorganisms were subcultured onto blood agar and incubated at 42°C for 24 h in 8-10 % CO_2 and subsequently subjected to biochemical tests as suggested by Lior (31). Hippurate hydrolysis was used to distinguish between *C. jejuni* and *C. coli* (31).

To detect *Yersinia* spp., 25 ml of bulk milk or effluent were added to 225 ml of 0.067 M phosphate buffered saline (PBS), pH 7.6 while 1 g of faeces was enriched in 9 ml of 0.067 M PBS. Enrichment was done at 4°C for 3 weeks. Subcultures were made after 1 week and 3 weeks onto *Yersinia* agar containing *Yersinia* selective supplement (Oxoid, UK) and incubated at room temperature for 24-48 h. Typical colonies with "bull's eye" appearance demonstrated by a red or pink centre surrounded by a clear zone were subjected to biochemical tests (32). Serological identification of the isolates was kindly done at the Ontario Ministry of Health, Laboratory Services Branch, Ontario, Canada.

Cryptosporidium oocysts were detected in faeces and bulk milk processed within 2 h of collection by the formalin-ether concentration sedimentation technique (21). Ten millilitres of bulk milk samples were centrifuged to achieve sedimentation. The sediment was then added to formalin-ether as done for faecal samples. Smears were stained by the modified Ziehl-Neelsen method (21) and subjected to microscopic examination.

Determination of antibiograms of isolates

For the 26 isolates of *Campylobacter* spp., the following antimicrobial agents and concentrations were used: ampicillin (10 mcg), neomycin (30 mcg), streptomycin (10 mcg), kanamycin (30 mcg), chloramphenicol (30 mcg) and gentamycin (10 mcg). *Salmonella* isolates were tested for their sensitivity to: ampicillin (10 mcg), chloramphenicol (30 mcg), kanamycin (30 mcg), nalidixic acid (30 mcg), neomycin (30 mcg), streptomycin (10 mcg) and sulphamethoxazole/trimethoprim (30 mcg).

The susceptibility of *Listeria* spp. to the following antimicrobial agents and concentrations was determined using: penicillin (10 units), ampicillin (10 mcg), erythromycin (15 mcg), chloramphenicol (30 mcg), streptomycin (10 mcg), gentamycin (10 mcg) and sulphamethoxazole/trimethoprim (30 mcg). The antibiograms of *Yersinia* isolates were determined for streptomycin (10 mcg), gentamycin (10 units), chloramphenicol (30 mcg), sulpha-methoxazole/trimethoprim (30 mcg), nalidixic acid (30 mcg) and kanamycin (30 mcg). The disc diffusion method (11) was used to determine the susceptibility of all the pathogens to the various antimicrobial agents.

Statistical analysis of data

The prevalences of enteropathogens in bulk milk, faeces and effluents and the antibiotic sensitivity of the isolates were compared amongst milking centres using the chi-square test for independence, with one degree of freedom.

■ RESULTS

The prevalence of selected enteropathogens in bulk milk samples is shown in table I. Of the 177 samples tested, 3 (1.7 %), 3 (1.7 %) and 2 (1.1 %) were positive for *L. monocytogenes*, *Salmonella* spp. and *Y. enterocolitica*, respectively. All the samples were negative for *Campylobacter* spp. and *Cryptosporidium* spp. Both isolates of *Y. enterocolitica* belonged to serogroup 0:3 and biotype 4. All *Salmonella* isolates belonged to serotype *agona*.

All bulk samples collected from centres 5H, 6H and 3G were free of all the enteropathogens tested. Centres IC and 5C, however, accounted for 1 of the 3 *Listeria* isolates, 3 of 3 of the *Salmonella* isolates and 50 % (1of 2) of the *Y. enterocolitica* isolates recovered.

Table II shows the prevalence of enteropathogens in the faeces of dairy cows and effluents from the milking parlour or shed. Amongst the 333 dairy cows sampled, 11 (3.3 %), 3 (0.9 %), 19 (5.7 %) and 7 (2.1 %) were shedders of *L. monocytogenes*, *Salmonella* spp., *Campylobacter* spp. and *Cryptosporidium* spp., respectively. There were statistically significant differences in the carriage of *Campylobacter* spp. ($P < 0.001$; χ^2), *L. monocytogenes* ($P < 0.05$; χ^2), compared to that for *Y. enterocolitica*. All faecal samples collected from cows in centres 3G and 6H were negative for the enteric pathogens cultured. Centres IC and 5C, however, accounted for 54.5 % (6 of 11) of the *Listeria monocytogenes* isolates, 68.4 % (13 of 19) of the *Campylobacter* isolates and 100 % (7 of 7) of the *Cryptosporidium* - positive samples. Effluents from the milking parlours were negative for *L. monocytogenes* and *Yersinia* spp., but, of the 168 samples tested, 1 (0.6 %) and 7 (4.2 %) were positive for *Salmonella* spp. and *Campylobacter* spp., respectively. *Campylobacter* spp. were isolated at a statistically significantly ($P < 0.05$; χ^2) higher rate than other pathogens. All 7 isolates of *Campylobacter* spp. originated from milking centres IC and 5C.

The sensitivity of *Campylobacter* spp. to 6 antimicrobial agents is shown in table III. Of a total of 26 strains of *Campylobacter* spp. made up of 16 (61.5 %) strains of *C. jejuni* and 10 (38.5 %) of *C. coli*, 19 (73.1 %) exhibited resistance to one or more antimicrobial agents. Resistance varied from 66.7 % (Centres IC, 2G, 2B and 3G) to 100 % (Centre 5H). Resistance was highest to ampicillin with 19 (73.1 %) strains and lowest to gentamycin with 1 (3.8 %) strain and the difference was statistically significant ($P < 0.001$; χ^2). A total of 5 (19.2 %), 4 (15.4 %), 3 (11.5 %) and 2 (7.7 %) strains were resistant to neomycin, streptomycin, kanamycin and chloramphenicol, respectively, but the differences were not statistically significant ($P > 0.05$; χ^2). Both strains of *Y. enterocolitica* were sensitive to streptomycin, gentamycin, chloramphenicol, sulphamethaxazole/trimethoprim (SXT), nalidixic acid and kanamycin. All of 7 isolates of *Salmonella* from bulk milk, cow's faeces and effluents were sensitive to the seven antimicrobial agents used, namely ampicillin, chloramphenicol, kanamycin, nalidixic acid, neomycin, streptomycin and sulphamethaxazole/trimethoprim.

For the 14 strains of *L. monocytogenes* tested, 13 (92.9 %), 13 (92.9 %), 12 (85.7 %), 4 (28.6 %) and 2 (14.3 %) exhibited resistance to ampicillin, streptomycin, sulphamethoxazole/-trimethoprim (SXT), erythromycin and penicillin, respectively. All strains were sensitive to chloramphenicol and gentamycin. Overall, 7 resistance patterns were observed amongst *L. mono-cytogenes* strains, but the prevalent patterns were ampicillin-sulphamethoxazole/trimethoprim-streptomycin, ampicillin-erythromycin-sulphamethoxazole/trimethoprim-streptomycin and ampicillin-streptomycin with 7 (50.0 %), 2 (14.3 %) and 1 (7.1 %) strains, respectively.

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Table II

Prevalence of selected pathogens in faeces of dairy cows and effluents of farms

Milking Centre	Sources of samples cultured										
	Faeces of dairy farms						Effluents* of dairy farms				
		Number (%) of faecal samples positive						Number (%) of samples positive			
	Num. of samples tested	*Listeria*	*Salmonella***	*Campylobacter*	*Yersinia*	*Cryptosporidium*	Num. of samples tested	*Listeria*	*Salmonella****	*Campylobacter*	*Yersinia*
IC	119	6 (5.0)	0 (0.0)	7 (5.9)	0 (0.0)	4 (3.4)	44	0 (0.0)	1 (2.3)	2 (4.5)	0 (0.0)
5C	56	0 (0.0)	1 (1.8)	6 (10.7)	0 (0.0)	3 (5.4)	34	0 (0.0)	0 (0.0)	5 (14.7)	0 (0.0)
5H	39	1 (2.6)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	30	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2G	27	0 (0.0)	2 (7.4)	3 (11.1)	0 (0.0)	0 (0.0)	16	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2C	19	2 (10.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	15	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2B	41	2 (4.9)	0 (0.0)	3 (7.3)	0 (0.0)	0 (0.0)	14	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
6H	11	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	5	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
3G	21	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	10	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Total	333	11 (3.3)	3 (0.9)	19 (5.7)	0 (0.0)	7 (2.1)	168	0 (0.0)	1 (0.6)	7 (4.2)	0 (0.0)

* Effluent samples were not processed for *Cryptosporidium* oocysts

** Isolates from centre 5C was group D untypable, from centre 2G was *S. typhimurium* and *S. javiana*, respectively

*** *Salmonella* isolated from centre IC was *S. agona*

Table III

Resistance of *Campylobacter* strains to antibiotics tested

Milking Centre*	Num. of *Campylobacter*** strains tested	Num. (%) of strains**** resistant	Num. (%) of strains resistant to:					
			A*****	N	S	K	C	CN
IC	9	6 (66.7)	6 (66.7)	1 (11.1)	2 (22.2)	1 (11.1)	0 (0.0)	1 (11.1)
5C	7	6 (85.7)	6 (85.7)	2 (28.6)	2 (28.6)	2 (28.6)	2 (28.6)	0 (0.0)
5H	1	1 (100.0)	1 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2G	3	2 (66.7)	2 (66.7)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2B	3	2 (66.7)	2 (66.7)	2 (66.7)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
3G	3	2 (66.7)	2 (66.7)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Total	26	19 (73.1)	19 (73.1)	5 (19.2)	4 (15.4)	3 (11.5)	2 (7.7)	1 (3.8)

* No *Campylobacter* isolate was recovered from milking centres 2C and 6H

** Consisting of 16 (61.5 %) strains of *C. jejuni* and 10 (38.5 %) strains of *C. coli*

*** Resistant to one or more of the antimicrobial agents tested

**** A - Ampicillin; N - Neomycin; S - Streptomycin; K - Kanamycin; C - Chloramphenicol; CN - Gentamycin

■ DISCUSSION

It was significant that all the five enteropathogens of importance to the dairy industry studied were detected either in the bulk milk, faeces of lactating cows or the effluent of milking parlours. This is important because these agents are of zoonotic significance and, in addition, could cause economic losses to the dairy industry (24, 29).

Failure to detect a correlation between detection of enteropathogens in bulk milk, faeces of cows and effluents was not unexpected since only 20 % of lactating cows contributing milk to the bulk supply and of the effluents on each farm were sampled. It is also known that all four bacterial enteropathogens studied could cause subclinical or clinical mastitis (15, 24) and therefore be present in milking without being detected in the faeces of affected animals or the effluents.

Centres IC and 5C were observed to have comparatively high prevalences of enteropathogens from the three sources studied, suggestive of high carriage rates of these pathogens or poor sanitary practices during milking. The potential for contamination of milk during the milking process on dairy farms visited was high since 95 % of these farms (Adesiyun and others, unpublished data) practised hand-milking. The risk of faecal materials splashing into milk in milking buckets from defaecating cows was therefore high. Various practices during milking have contributed to poor microbial quality of milk on dairy farms (35).

The prevalence of *Campylobacter* species (5.7 %) in cattle's faeces is considerably lower than the rates of 12.7 % to 46.7 % reported by others (10, 23). Adesiyun *et al.* (5) had earlier reported a prevalence of 12.9 % and 16.5 % in diarrhoeic and non-diarrhoeic cattle, respectively. Although *Campylobacter* was detected in 5.7 % of cows' faeces and in 4.2 % of 168 effluent samples, none of the bulk samples was positive for the microorganism. Cerqueira *et al.* (17) also failed to isolate *Campylobacter* from raw milk, while a prevalence as high as 12.3 % was reported by Rohrbach *et al.* (37). The peroxidase system, not inactivated in the bulk milk in the present study, may have been responsible for the non-isolation of *Campylobacter* (13).

The predominance of *C. jejuni* over *C. coli* amongst *Campylobacter* spp. agrees with earlier reports of studies in Trinidad (6) and elsewhere (36). Similarly, the antibiograms of the isolates of *Campylobacter* were comparable to the findings of others (6, 36).

L. monocytogenes has been reported to cause milk-borne listeriosis following comsumption of raw or pasteurized milk and milk products (14, 20). The finding that 2 % of raw bulk milk in the present study contained *L. monocytogenes* is therefore of public health significance since over 30 % of dairy farmers and their families in Trinidad consume raw cows' milk (Adesiyun and others, unpublished data). The low rate of detection of *L. monocytogenes* in bulk milk (2 %) and faeces (3 %) of dairy cows agrees with published studies (25, 34).

Y. enterocolitica appeared to pose the least risk to consumption of milk from Trinidadian dairy farms with a failure to isolate the organism from faecal and effluent samples and only 1 % of bulk milk samples positive. *Y. enterocolitica* is known to be mostly harboured by pigs and the microorganism has been found on pork products (9) although other animals have been found to be carriers (5, 40). The isolation rate of *Y. enterocolitica* in bulk milk (1 %) is slightly lower than the 2.7 % reported by Davidson *et al.* (18).

Of epidemiological relevance was the finding that both *Y. enterocolitica* strains belonged to serotype 0:3 and biotype 4. All but one of the strains of *Y. enterocolitica* isolated from livestock (5) and slaughter pigs (7) in Trinidad were the same serotype 0:3 and biotype 4. *Y. enterocolitica* serotype 0:3 and biotype 4 may therefore be important as a cause of human yersiniosis in Trinidad, a prevalence presently unknown. Cryptosporidiosis, a disease not known to be associated with consumption of milk, has been associated with waterborne outbreaks (16, 33). The detection of *Cryptosporidium* oocysts in the faeces of cattle in milking parlours is therefore important from the viewpoint of environmental contamination. The faecal prevalence (2 %) of *Cryptosporidium* oocysts is however much lower than the 9.4 % and 7.6 % reported for diarrhoeic and non-diarrhoeic calves, respectively, in Trinidad (5). In addition to

Cryptosporidium being able to cause diarrhoea in dairy calves (12), parasitized dairy cows have been demonstrated to experience reduced milk yield, as much as 3.2 kg per day (19). The zoonotic significance of cryptosporidiosis was emphasized by reports that dairy farmers had significantly higher risk of contracting cryptosporidiosis compared to non-farmers (30).

The 1.7 % prevalence of *Salmonella* in bulk milk compares favourably with prevalences of 2 % for milk filters (27) and 0.25 % for milk of dairy cows with subclinical mastitis (28). Rohrbach *et al.* (37) reported a much higher prevalence of 8.9 % for *Salmonella* in bulk milk. Adesiyun *et al.* (5) reported finding 6.0 % and 2.5 % of diarrhoeic and non-diarrhoeic calves, respectively, positive for *Salmonella*.

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Résumé

Adesiyun A.A., Webb L.A., Romain H., Kaminjolo J.S. Prévalence de *Salmonella*, *Listeria monocytogenes*, *Campylobacter* spp., *Yersinia enterocolitica* et *Cryptosporidium* spp. dans du lait en vrac, des matières fécales de vaches et des effluents de fermes laitières à Trinidad

La prévalence de *Listeria*, *Salmonella*, *Campylobacter*, *Yersinia* et *Cryptosporidium* dans du lait en vrac, les matières fécales des vaches laitières et des effluents à lait des fermes laitières de l'île de la Trinité, a été evaluée. Des 177 échantillons de lait en vrac testés, 3 (1,7 p. 100), 3 (1,7 p. 100) et 2 (1,2 p. 100) étaient positifs respectivement pour *Listeria monocytogenes*, *Salmonella* spp. et *Yersinia enterocolitica* mais négatifs pour *Campylobacter* spp. et *Cryptosporidium* spp. Des 333 échantillons fécaux testés, *L. monocytogenes*, *Campylobacter* spp. et *Cryptosporidium* spp. étaient présents dans respectivement 11 (3,3 p. 100), 19 (5,7 p. 100) et 7 (2,1 p. 100) des cas. Ces taux étaient signifi-cativement ($P < 0,05$; χ^2) plus élevés, que le taux de détection (0 p. 100) pour *Yersinia* spp. *Salmonella* spp. a été detectée dans 3 (0,9 p. 100) échantillons fécaux. Des 168 échantillons prélevés des effluents à lait, *Campylobacter* spp. était présent dans 7 (4,2 p. 100) échantillons alors que *Salmonella* spp. l'était dans seulement 1 (0,6 p. 100) échantillon. Aucun échantillon n'était positif pour *Yersinia* spp. et *Listeria* spp. (différence significative, $P \leq 0,05$; χ^2). Sur 26 isolats de *Campylobacter* spp., 19 (73,1 p. 100) étaient résistants à au moins un des six agents antimicrobiens testés. Les 14 isolats (100 p. 100) de *L. monocytogenes* étaient résistants à au moins un agent antimicrobien alors que les souches de *Salmonella* spp. et *Y. enterocolitica* étaient sensibles à tous les agents utilisés. En conclusion, les cinq espèces entero-pathogènes testées étaient présentes dans les fermes laitières de l'île de la Trinité. Les risques de maladie, dus à la présence de ces agents pathogènes dans le lait, existent pour le consommateur, renforçant ainsi la nécessité d'améliorer les pratiques sanitaires.

Mots-clés : *Salmonella* - *Listeria monocytogenes* - *Campylobacter* - *Yersinia enterocolitica* - *Cryptosporidium* - Vache laitière - Lait - Fèces - Eau usée - Exploitation laitière - Contamination - Trinité et Tobago.

Resumen

Adesiyun A.A., Webb L.A., Romain H., Kaminjolo J.S. Prevalencia de *Salmonella*, *Listeria monocytogenes*, *Campylobacter* spp., *Yersinia enterocolitica* y *Cryptosporidium*, en leche de tanque (no embalada), en heces de vacas lecheras y en efluentes de lecherías en Trinidad

Se investiga la prevalencia de *Listeria*, *Salmonella*, *Campylobacter*, *Yersinia* y *Cryptosporidium* spp. en leche de tanque (no embalada), en heces de vacas lecheras y en efluentes de lecherías en Trinidad. De las 177 muestras de tanque obtenidas, 3 (1,7 p. 100), 3 (1,7 p. 100) y 2 (1,2 p. 100) fueron positivas para *L. monocytogenes*, *Salmonella* spp. y *Y. enterocolitica*, respectivamente, pero todas fueron negativas para *Campylobacter* y *Cryptosporidium* spp. De las 333 muestras fecales, *L. monocytogenes*, *Campylobacter* spp. y *Cryptosporidium* spp. se detectaron en 11 (3,3 p. 100), 19 (5,7 p. 100) y 7 (2,1 p. 100), respectivamente, resultados significativamente ($P < 0,05$; χ^2) mas elevados que la tasa de deteccion (0 p. 100) para *Yersinia* spp. *Salmonella* spp. se detectó en 3 (0,9 p. 100) de las muestras fecales. De las 168 muestras obtenidas de efluentes y sometidas a cultivos bacterianos, *Campylobacter* spp. se aisló en 7 (4,2 p. 100), mientras que *Salmonella* se encontro unicamente en 1 (0,6 p. 100) muestra, ninguna muestra fue positiva para *Yersinia* o *Listeria*, La diferencia fue estadísticamente significativa ($P < 0,05$; χ^2). Un total de 19 (73,1 p. 100) de los 26 aislamientos de *Campylobacter* presentaron resistencia a uno o más de los seis agentes antimicrobianos examinados. Los quatorce (100 p. 100) aislamientos de *L. monocytogenes* fueron resistentes al menos a un agente, mientras que todas las cepas de *Salmonella* y *Yersinia* fueron susceptibles a todos los agentes antimicrobianos utilizados. Se concluye que los cinco enteropatógenos examinados estaban presentes en las lecherías en Trinidad y que el posibilidad de enfermedades relacionadas con la leche, debido a estos patógenos, existe para los consumidores, haciendo enfasis en la necesidad de buenas practicas sanitarias.

Palabras clave: *Salmonella* - *Listeria monocytogenes* - *Campylobacter* - *Yersinia enterocolitica* - *Cryptosporidium* - Vaca lechera - Leche - Heces - Agua residual - Granja lechera - Contaminación - Trinidad y Tobago.