

INTRODUCTIONS

To our knowledge no prevalence’s of a milk pathogens wide range, using multiplex qPCR technique from pastures of San Miguel Island (Azores, Portugal) were described before. The aim of the present study was to determine the apparent prevalence of a large wide of milk pathogens from BTM of Azorean dairy herds using a multiplex PCR method.

METHOD AND MATERIAL

From all regions of San Miguel- Azores, 92 dairy herds considering a total of 5520 adult cows were used. These herds represented 5.0% (1833) of total dairy farms according data officially reported (2014) in San Miguel Island (Figure 1).



Figure 1. Mobile milking machine.

A BTM sample from each selected herds was collected using the (Startcheck®) sampling kit (HIPRA, Spain), according the manufacturer instructions, in order to determine the presence of *coagulase-negative staphylococci* (CNS), *Escherichia coli*, *Staphylococcus aureus*, *Corynebacterium bovis*, *Enterococcus spp.*, *Streptococcus dysgalactiae*, *Streptococcus uberis*, *Actinomyces pyogenes/Peptostreptococcus indolicus*, *Klebsiella spp.*, *Streptococcus agalactiae* and *Serratia marcescens*.

RESULTS

In overall, all the 11 species/groups were detected by the qPCR assay. The mean number of bacteria species or groups for BTM was 5.6 (confidence interval 95% between 5.2 and 5.9). The group of CNS were detected in all (100%) BTM samples. *E. coli* (75.0%), *S. aureus* (62.0%), *Corynebacterium bovis* (57.6%), *Enterococcus spp.* (55.4%), more than 50% of the herds. The remaining milk pathogens, *Streptococcus uberis*, *Actinomyces pyogenes/Peptostreptococcus indolicus*, *Klebsiella spp.*, *Streptococcus agalactiae* and *Serratia marcescens* were present in 41.3%, 41.3%, 37.0%, 32.6% and 3.3% of the BTM samples, respectively (Table 1).

Bacteria	Bulk tank milk
Coagulase-negative staphylococci	100.0%; n=92
<i>Escherichia coli</i>	75.0% (65.3 to 82.7); n=69
<i>Staphylococcus aureus</i>	62.0% (51.8 to 71.2); n=57
<i>Corynebacterium bovis</i>	57.6% (47.4 to 67.2); n=53
<i>Enterococcus spp.</i>	55.4% (45.3 to 65.2); n=51
<i>Streptococcus dysgalactiae</i>	51.1% (41.0 to 61.1); n=47
<i>Streptococcus uberis</i>	41.3% (31.8 to 51.5); n=38
<i>Actinomyces pyogenes</i> / <i>Peptostreptococcus indolicus</i>	41.3% (31.8 to 51.5); n=38
<i>Klebsiella spp.</i>	37.0% (27.8 to 47.2); n=34
<i>Streptococcus agalactiae</i>	32.6% (23.9 to 42.7); n=30
<i>Serratia marcescens</i>	3.3% (1.1 to 9.6); n=3

Table 1. Apparent prevalence of bacterial pathogens from 92 BTM samples.

CONCLUSIONS

We have presented baseline figures for 11 mastitis pathogens/groups in BTM samples from Azorean dairy herds. Both environmental or contagious bacteria, CNS, *E. coli* and *S. aureus* are the pathogens more commonly found. These results emphasize once again the importance of implementing mastitis control plans for the control of milk quality and suggest that vaccination for the prevention of mastitis by these pathogens can be a real asset as an additional tool in a mastitis control plan in the Azorean dairy herds.

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