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Survey, mastitis California test implementation and microbiological composition of raw camle milk assessment in tamanrasset region (Southern Algeria)

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To facilitate the early diagnosis of subclinical mastitis in camel herds within the Tamanrasset region of Southern Algeria, we conducted a study to evaluate the effectiveness of the Camel Mastitis Test (CMT) for she-camel udder health assessment. On one hand, survey investigation was carried out by addressing tow questionnaires kinds. The first one was designed exclusively for camel breeders and focused on the breeders' level knowledge regarding subclinical mastitis in she-camels udder and raw camel milk daily quantity production. The second questionnaire specifically aimed at veterinarians to gather essential information including, the number of veterinarians currently in service, Whether veterinarians utilize the MCT test for detecting subclinical mastitis and the existence or no of a national program for the diagnosis and treatment of subclinical mastitis. On other hand, twelve raw camel milk samples were collected from peri-urban camel farms in the Tamanasset region and tested using the MCT, a chemical product similar to the well-known "California Mastitis Test" (also known as the Teepol test). Additionally, we employed culture-dependent methods to assess the Revivable Aerobic Mesophilic Microflora (RAMF) using the SP-SDS micro-titration procedure, as well as to evaluate the microbiological quality of the raw camel milk samples. Furthermore, we extracted and quantified DNA from the raw camel milk as part of the initial step of a culture-independent method. Among the twelve tested raw camel milk samples, the MCT results indicated positive reactions, with gel formation and scores of 1 observed in samples S3 and S7, while the remaining samples did not show any gel formation. In terms of physiochemical analysis, the pH of the milk samples ranged from 6.07 to 6.75, while the temperature varied between 16.6°C and 28.2°C. Microbiological analysis revealed a high bacterial count, ranging from 3.5 log9 CFU/ml to 7.4 log9 CFU/ml. Pathogenic bacteria, such as Escherichia coli, Salmonella Enteritidis, Shigella dysenteriae, and Shigella flexneri were detected on appropriate culture media. Additionally, opportunistic pathogenic bacteria, including Escherichia coli and Proteus vulgaris, which are known as commensal species in the human digestive tract, were also found. In second group raw camel milk samples (S8, S9, S10, S11, and S12), there was variability in DNA concentration, ranging from 35µg/ml to 69.5µg/ml. Notably, a significant difference in DNA concentration was observed between samples S10 and S12, which exhibited a high microbial load of over 11.48 log9 CFU/ml suggesting a significant microbial diversity among the analyzed raw camel milk samples.

Biography

Habiba DRICI -Born in 1970 in North-East of Algeria (hometown "Annaba")- PhD in Microbiology - Teacher-Researcher at University of Oran, West Algeria (2001-2011) then, at the University of Tamanghasset (CUTAM), Great South of Algeria since October 2011. Director of research laboratory of Sciences and Environment at University of Tamanghasset. Study and valorization of the South Algeria bioresources to improve food, feed and water quality. Priority of my research is dromedary field in Algeria, through safety risks assessment study by microbiological and molecular approach of raw camel milk, which is mainly consumed by nomad’s people and for whom camel milk is the survival source in the desert.