

The and other spore - mold or thermoduric



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The present work was carried out at the KAU Faculty of Sciences (Biological science Department). The aim of this study was to detect microbial contamination in camel's udder using microbial and molecular studies such as 16S rRNA gene and sequencing. The samples were taken from five breeds of camels three of them are local and the other two from Sudan and Ethiopia. Each kind obtained 20 swaps. Three types of cultures were prepared (Blood - chocolate - MacConkey agar) one was Aerobic and another Anaerobic analysis during the year 2017. Because udder microbiota and mastitis are very important to make sure camels raw milk (CRM) is free from any microbial contamination.

Camel milk is one of the main foods consumed in the many countries. People in rural areas have long considered that raw camel milk is safe and even have curative health welfare compared to another animal's milk.

(Benkerroum, et al.

, 2003). In addition, camel milk could be a source of dairy farm lactic acid bacteria (LAB) species. The micro-organism is accessible in uncooked milk, including milk from bovines, sheep, goats, and humans.

Deplete, in the lighting of its high dietary substance, can accompany a rich microbiota. This microorganism enters deplete from a shade of germ and, once in deplete, can play out different parts, for illustration, helping dairy developments (e. g.

Lactococcus, Lactobacillus, Streptococcus, Propionibacterium and parasitic masses), causing crumbling (e. g. Pseudomonas, Clostridium, B and other spore -mold or thermotolerant microorganisms), upgrading prosperity (e. g.

lactobacilli and bifidobacteria) or impelling disease (e. g. Listeria , Salmonella, Escherichia coli, Campylobacter and mycotoxin-conveying parasites) (Quigley et al.

, 2013). For instance, a sight on wellness and lifestyle recorded that one in every six UAE nationals in urban domain frequently boozing camel's milk and this rate increased significantly in the outside realm and rural areas (Kazmi 2002). The significance of the findings of production system, hygiene, and public health view, Abdurahman, (2006).

The aims of this study to detect and identify microbes in camel udder microbiota using microbial and molecular identification as modern techniques using 16S rRNA gene sequencing.