WATER BUFFALO MILK MICROBIOTA RELATED TO HEALTH STATUS

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The development of culture-independent techniques by means of high-throughput DNA sequencing has just begun to unravel the impact of the microbiota – the collection of microbial organisms inhabiting a specific environment – on animal health, suggesting the possibility to correlate a determined microbiota to a health status (1). A new concept of pathobiome, which includes pathogenic agents in the microbiota environment, is taking shape (2) and the role of micro-organisms in establishing and modulating diseases is under investigation. The aim of the present study is to provide insights into the microbiota of dairy water buffalo milk related to health status. High-throughput DNA sequencing of the 16S rRNA V1-V2 regions was carried out to determine the bacterial content of milk samples from a total of 137 quarters, divided in three groups: i) healthy quarters (nr 27) ii) quarter with clinical mastitis (nr 27) iii) quarters with sub-clinical mastitis (nr 83). The microbiota diversity of healthy samples was richer as compared to samples with sub-clinical mastitis, whose microbiota diversity were in turn richer as compared to those from clinical mastitis. The core microbiota of water buffalo milk, defined as the asset of micro-organisms shared by all healthy milk samples, includes 15 genera, namely Micrococcus, Propionibacterium, 5-7N15, Solibacillus, Staphylococcus, Aerococcus, Facklamia, Trichococcus, Turicibacter, 02d06, SMB53, Clostridium, Acinetobacter, Psychrobacter and Pseudomonas. Only two genera (Acinetobacter and Pseudomonas) were present in all the samples from sub-clinical mastitis, and no genus was shared across all in clinical mastitis milk samples, where the major genus prevalence was represented by Bacteroides and Pseudomonas, followed by Porphyromonas and Fusobacterium. Discriminant analysis shows the evidence that the microbial community of healthy and clinical mastitis could be discriminated on the background of their microbiota profiles. In conclusion, the present study, through a culture-independent metagenome approach, investigated the water buffalo milk microbiota from healthy, clinical and sub-clinical mastitic samples, demonstrating that it is possible to correlate the microbiota to a specific patho-physiological animal status.