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## Core-bacterial composition and function of ruminant animals based on integrative analysis of metagenomics data

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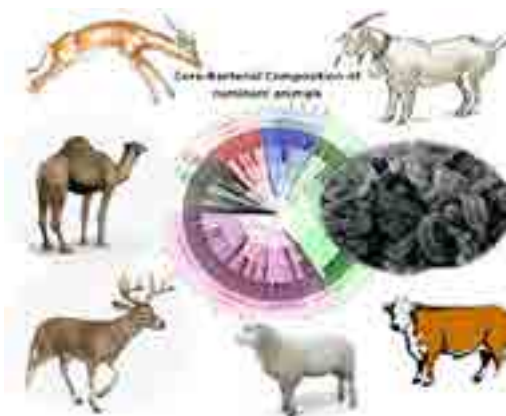
Metagenomic analysis based on high throughput sequencing is a newly developed approach, widely been applied to identify the microbial composition and diversity of ruminant animals. Despite attempts have been done to depict the microbial composition of rumen in various animals, the little attention has been devoted to finding core-bacterial composition of ruminant animals, pathogenic species. Due to integrative analysis of different datasets is expected to be more informative, in the present study, microbial composition of different animals was evaluated, using integrative analysis of metagenomic data aim to obtain holistic overview of core-bacterial population. In total, 12 datasets were analyzed using the CLC Microbial Genomics Module in CLC Genomics Workbench 9.1 (CLC Bio, Qiagen). SILVA.123 database (97%) was used for detection of operational taxonomic units (OTUs) with the similarity percentage of 97%. In total 3,471 OTUs are found based on SILVA.123 database. *Bacteroidetes* was the most abundant phylum across all samples (42.57%), followed by *Firmicutes*


(36.25%), and *Proteobacteria* (13.43%). In addition, *Prevotella1* (21.4%), *Rikenellaceae* RC9 gut group (5.9), and *Veillonellaceae* UCG-001 (4.5%) were recorded as dominant genera across all studied animals. Functional profiling of OTUs has been provided good clues about the potential role of bacterial population in ruminants. We found that high amounts of OTUs were related to human diseases such as different cancers. Taken together, our findings provided an overall insight about the core-bacterial composition and function of ruminant animals, human disease related bacteria.

### Speaker Biography

Arghavan Alisoltani has her expertise in Computational Biology and Genetic Studies of Model Plants and Animals. She has completed her PhD at the Shahrekord University, Iran. She is currently pursuing her Post-doctoral research in Department of Biotechnology, The Vaal University of Technology, South Africa. Her scientific productivity is publishing several research papers in high ranked journals.

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