



Microbial Diversity of Bovine and Caprine Amasi, Traditionally Produced Using Metagenomic Sequencing Technique (16S rRNA)

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Abstract

The quest for health-enhancing functional foods and products has gained consumers' attention in recent times. One of the reasons for this could be the preference advocacy for natural health-benefiting food products over refined foods and this has been driving consumers towards the traditional methods of preparation. Traditionally produced products are gaining popularity and consumers are getting comfortable preparing their foods to avoid preservatives and chemicals which can be detrimental to health. This study investigated the microbial diversity of traditionally fermented Amasi (produced from cow and goat milk) to understand the microbial diversity and ecology using the 16S rRNA metagenomics approach. The Illumina Miseq platform was used to sequence the V4 region (primer 515 to 806) and sequences were assembled and categorized into operational taxonomic units (OTUs) and the core microbiome was subsequently visualized. The effective QIIME2 (Quantitative Insights into Microbial Ecology2) was used for the downstream analysis and data were presented using RStudio. The α and β diversity analysis identified 2777 sequences across all samples. The fermented milk samples had the highest number and diversity of unique species (from 130 to 1329 OTUs); cow milk Amasi (from 112 to 205 OTUs), goat milk Amasi (from 67 to 151 OTUs) had similar diversity. Collectively, *Proteobacteria* was the most abundant phyla (from 42 to 95%), followed by *Firmicutes* (1–47%), *Actinobacteria* (< 1 to 23%), and *Bacteroidetes* (< 1 to 4.8%). The most abundant genera were *Acinetobacter* (20–58%), *Pseudomonas* (14.5%), *Enterobacter* (13%), and *Lactobacillus* (6.3%). Genera with potential to be pathogenic included *Bacillus* (4%), *Salmonella* (0.85%), *Escherichia-Shigella* (0.38%), *Staphylococcus* (0.32%), *Listeria* (0.29%), *Clostridium* (0.28%), and *Cronobacter* (0.27%), which were found at lower frequencies. There are relative similarities in the microbiota of cow milk Amasi and goat milk Amasi and there is a possibility of pathogens when they are produced domestically. This study will help to improve processing and new culture development with strain-specific microbes and beneficial properties for traditional fermented milk products.

Biography: Betty Ajibade

Betty's research objectives are in food safety and quality control. As much as I will like abundant food to be available for the world teeming population as much as the food produced must be safe and healthy. Betty's research focused on the microbiology of fermented food products (indigenous functional foods) and exploring the microbial diversity of natural fermentation for the identification and characterization of microbes that are of technological importance. As it is commonly said that "the solution to the problem

of nature is in nature”, beneficial microbes from fermented foods can be applied in many areas to solve many existing problems. Presently, Betty is into microbial metagenomics data analysis and interpretation. She hopes to pursue this skill in solving the problem of food safety in Africa.