

# Bacteriology and Infectious Diseases

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## Changes in lipid profiles of HIV positive adults over 9 months at a Harare HIV clinic: A longitudinal study

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Human immunodeficiency virus (HIV) infection, together with antiretroviral drugs is often associated with changes in biochemical and metabolic parameters including changes in lipid profiles. The aim of the study was to compare the changes in lipid profiles among HIV positive outpatients who are on antiretroviral therapy (ART) and those who are ART-naïve over a nine months period. 171 patients were investigated, 79% were ART-experienced, while 82% of those on treatment were on NVP/EFV first line ART. More than 60% of ART-naïve and ART-experienced patients had some form of dyslipidemia either at baseline or at follow-up but the lipid median values for the two groups was within normal limits. At baseline, median levels of total cholesterol (TC) and high density lipoprotein (HDL) were slightly higher in the ART-experienced group. After nine months of antiretroviral treatment the average lipid values were still within normal limits. Interestingly, there was higher increase in HDL over time in the ART negative group compared to the ART positive group. There was a decrease in TC/HDL ratio in both groups over time. HIV positive patients frequently show various forms of dyslipidemia but there are no changes in average atherogenic lipid levels after nine months.

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## Molecular, biochemical and immunological testing on the diagnosis of potential risk of food poisoning by coagulase negative *Staphylococcus* in products from animal origin

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Food from animal origin, such as milk, dairy derivatives and meat can often be contaminated with *Staphylococci*-enterotoxigenic strains. Contamination may occur directly from infected animals, inadequate processing, like contamination of starter cultures or may result from poor hygiene during food manufacturing, retail and storage. Twenty-nine coagulase negative *Staphylococci* strains isolated from Minas frescal cheese and Italian type salami were identified by 16S rDNA sequencing: *saprophyticus*, *xylosus*, *sciuri*, *carnosus*, *succinus*, *epidermidis*, *hominis* and *piscifermentans*. A phylogenetic analysis grouped the strains into five major groups composed of 2 refined clusters containing sub clusters, where strains showed similarities over 90%. Enterotoxin encoding genes: *sea*, *seb* and *sec* showed a high prevalence in the genomes. The *sei*, *seh*, *selm* and *seln* genes were harbored by at least 33% of the strains. The *tstH1* genes were found in 7% of the salami strains. Fifteen strains were able to transcribe at least one type of mRNA enterotoxin, as evidenced by real time RT-PCR assays. *In vitro* production of the enterotoxin SEA-SEE was detected in almost all strains by ELISA assays. All strains showed multi-resistance to antimicrobials such as  $\beta$ -lactams, vancomycin and linezolid which show both human and veterinarian medicine therapeutic importance. MICs  $\leq 0.06$  mg/mL for methicillin, ampicillin and vancomycin and  $\leq 0.25$  mg/mL for linezolid were observed. High risk of food poisoning following the consumption of improperly manufactured animal origin products was emphasized, as well as the possibility of these food matrices acting as reservoirs for antibiotic resistance, spreading pathogenic strains.

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