126. In silico analysis of virulence and antimicrobial resistance associated genes in genomes of non-typhoidal salmonella isolates from Kenya

Martin Njau[1*], Samantha Siebel[2], Erika Ganda[2], Frank Onyambu[1]
[3]School of Health Sciences, Meru University of Science and Technology, Meru, Kenya
[2]The Pennsylvania State University
*Corresponding author email: martinkamau796@gmail.com

Subtheme: Health Sciences - Climate Change and Public Health; Response and Impact of environmental changes on Health.

Abstract

Non-typhoidal Salmonella (NTS) poses a significant global health burden, causing millions of infections and substantial mortality each year, particularly in Africa. In Kenya, the problem is worsened by the high incidence of NTS and increasing antimicrobial resistance (AMR) . To address this challenge, we propose an in silico analysis of Kenyan NTS genomes to identify virulence factors and AMR-associated genes.This study involves a secondary data analysis using publicly available whole genome sequencing data. We will conduct bacterial genomic analysis that will include quality control, assembly, annotation, pan-genome, and phylogenetic analyses. Abricate software will be used to scan the following databases for antimicrobial resistance genes: CARD, ARGannot, ResFinder, and MegaRes. It will also be utilized to scan the VFDB database for virulence factors. These analyses will result in detailed phylogenetic trees, identification of virulence factors and AMR genes. The Phylogenetic trees will help us understand transmission dynamics and relationships among NTS isolates, while the identification of virulence factors and AMR genes will highlight strains linked to severe illness. This project aims to strengthen Kenya's genomic analysis capacity. We will adopt a One Health approach where we integrate data from clinical, environmental and animal sources to explain the complex interactions that lead to the spread of non-typhoidal salmonella. This research will also foster local bioinformatics expertise

Keywords: *Antimicrobial resistance, Non-typhoidal Salmonella*