

Genome analysis of *E. coli* STEC isolated from imported beef to apply the principle of one health approach

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Shiga toxin-producing *Escherichia coli* (STEC) is an enteric pathogen that causes various human diseases such as hemolytic uremic syndrome (HUS) and Urinary Tract infection (UTI), and involves in many outbreaks in food and water. STEC is responsible for around 1.3 million illnesses, 3600 HUS cases and 220 deaths annually worldwide. STEC outbreaks could come from different serotypes such as O157 and non-O157 (O26, O45, O103, O111, O121 and O145), which are known as the big six. Total of 64 imported beef samples were collected randomly from the borders of Saudi Arabia from various companies from different countries namely: India, Brazil, Sudan and Pakistan. 10 (only from Brazil) out of 64 (15.6%) samples were tested positive against the following of STEC serotypes, -O157 (n=5), -O145 (n=5) using PCR and RT-PCR methods. For a comparison reason, clinical isolates of *E. coli* non-STEC (n=3) were collected from a local hospital isolated from patients diagnosed with UTI. Then, minimum inhibitory concentration (MIC) was used to detect the antimicrobial resistance (AMR) profile of some isolates, -O157 (n=5), -O145 (n=1) and non-STEC (n=3). The result showed that three isolates of *E. coli* -O157 and -O145 were resistance to at least two antibiotics, while all clinical isolates of *E. coli* were antibiotic-susceptible. Then the next generation sequencing (NGS) was used to compare both phenotypic and genotypic AMR profiles of all MIC tested isolates. IncFIB(AP001918)_1 plasmid was dominant in almost all isolates of food and clinical. The isolates *E. coli* -O157:H7 and -O145:H28 (beef source) were possessing the same virulence genes including stx2A and stx2B. According to data extracted from Enterobase website, isolates are mainly appeared for the first time in America and European continents.

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