Phenotypic and genotypic comparison of salmonellae from diarrhoeic and healthy humans and cattle, Nigeria - DTU Orbit (23/12/2018)

Phenotypic and genotypic comparison of salmonellae from diarrhoeic and healthy humans and cattle, Nigeria

The sources and modes of transmission of non-typhoidal Salmonella particularly zoonotic transmission are poorly understood in Africa. This study compared phenotypic and genotypic characteristics of Salmonellae isolated from cattle and humans. Faecal samples of diarrhoeic patients (n = 234), and a healthy population (n = 160), beef cattle at slaughter (n = 250), farms (n = 72) and market (n = 100) were cultured for salmonellae and serotyping and antimicrobial susceptibility were determined. Whole-genome sequence typing (WGST) of selected isolates and bioinformatic analysis were used to identify the multilocus sequence type (MLST), plasmid replicons, antimicrobial resistance genes and genetic relatedness by single nucleotide polymorphism (SNP) analysis. The Salmonella isolates, diarrhoeic patients (n = 17), healthy population (n = 13), cattle (abattoir, n = 67; farms, n = 10; market n = 5), revealed 49 serovars; some serovars were common to humans and cattle. Rare serovars were prevalent: Colindale (cattle and humans); Rubislaw and Bredeney (humans); and Dublin, Give, Eastbourne, Hadar, Marseille, Sundsvall, Bergen, Ekedo, Carno and Ealing (cattle). The sequence types (ST) include ST 584, ST 198, ST 560 and ST 512 for S. Colindale, S. Kentucky S. Rubislaw and S. Urbana, respectively. Clonal cluster shared by cattle and human WGST isolates was not found. Antimicrobial resistance rates were generally low and towards only chloramphenicol, ampicillin, gentamicin, ciprofloxacin, tetracycline and streptomycin, range 2.7% (chloramphenicol) to 8.9% (streptomycin). Multiply resistant isolates included serovars Kentucky, 4,5,12:i:- and Typhimurium. The study presents a baseline description of the prevalence, serotypes, antimicrobial resistance phenotypes and genetic relatedness of Salmonella isolated from healthy and diarrhoeic humans, and cattle at harvest, on farm and at market. Cattle are a reservoir of diverse salmonellae with shared serovars with humans, but WGST does not support zoonotic transmission. Further study with larger samples is recommended to determine whether epidemiological link exists between cattle and humans.

General information
State: Published
Organisations: National Food Institute, Research group for Genomic Epidemiology, University of Ibadan
Contributors: Fashae, K., Leekitcharoenphon, P., Hendriksen, R. S.
Pages: e185-e195
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Zoonoses and Public Health
Volume: 65
Issue number: 1
ISSN (Print): 1863-1959
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.59 SJR 1.248 SNIP 1.074
Web of Science (2017): Impact factor 2.688
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.3 SJR 1.119 SNIP 0.988
Web of Science (2016): Impact factor 2.323
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.27 SJR 1.263 SNIP 1.095
Web of Science (2015): Impact factor 2.574
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 1.97 SJR 1.036 SNIP 0.955
Web of Science (2014): Impact factor 2.369
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.24 SJR 0.948 SNIP 1.041
Web of Science (2013): Impact factor 2.065
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2

Phenotypic and genotypic comparison of salmonellae from diarrhoeic and healthy humans and cattle, Nigeria