Data Article

Data on prevalence and distribution of antimicrobial resistance determinants of \textit{Salmonella enterica} isolates from the formal and informal meat sector

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\textbf{Abstract}

Foodborne pathogen such \textit{Salmonella enterica} is a leading cause of human gastroenteritis worldwide. The potential to cause more severe and prolonged infection increases when the bacteria harbour resistant gene. In this dataset, \textit{S. enterica} PCR confirmed isolates recovered from the formal (\(n = 33\)) and informal (\(n = 15\)) meat sector were further tested against 15 antimicrobials and 20 resistance determinants using the disc-diffusion method on Muller-Hinton agar and the genotypic antimicrobial resistance determinants by PCR. In addition, multiple antimicrobial resistance phenotype and the multiple antimicrobial resistance indexes were shown. The data suggest that meat from the formal sector harbour resistance capacity than meat from the informal sector.

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The presented data show the prevalence and antibiogram of *Salmonella enterica* in the formal and informal meat sector (Figs. 1 and 2). In addition, the data also shows the prevalence of resistance genes and patterns of resistance of the bacteria isolates (Figs. 3 and 4).

### 2. Experimental design, materials, and methods

The swabbing of the animal carcass was done using a sterile cotton throat swab (CTS). The sterile CTS was used on a 100 cm² area on each carcass surface using disposable sterile templates. After the collection of each sample, the throat swabs were placed in individual sterile containers, transported in a cooling box containing ice packs to the Department of Biochemistry and Microbiology, University of Fort Hare laboratory for microbial analysis. Swab samples were subjected to serial dilution for bacteria counting. After the counting, a single distinct colony was taken per sample and stored in glycerol for further use. The stored isolates were resuscitated and streaked on Hektoen Enteric agar. Colonies showing characteristic green or blue with a black centre growth on Hektoen Enteric agar medium were selected as *Salmonella*. 
The selected isolate was confirmed using polymerase chain reaction. Confirmed isolates were further screened for their phenotypic antibiotic susceptibility. Criteria for determining whether the isolate is resistant, intermediate or susceptible were adopted from the National Committee for Clinical Laboratory Standards [3]. Phenotypically resistant isolates were selected for genotypic antibiotics resistance testing to 20 resistance genes.

**Fig. 1.** Percentage of *Salmonella enterica* isolated from the formal (n = 152) and informal (n = 136) meat sector.

**Fig. 2.** Number and multiple antibiotic resistance (MAR) phenotype in formal and informal sector.
Fig. 3. Percentage distributions of antimicrobial resistance determinants among *Salmonella enterica* isolates.
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Transparency document

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2019.103883.

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