Salmonella enterica isolates from Western Australian rangeland goats remain susceptible to critically important antimicrobials

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The aim of this study was to investigate the occurrence and antimicrobial resistance of Salmonella enterica recovered from faecal samples of slaughtered rangeland goats in I, Western Australia. Faecal samples (n=400) were collected at slaughter from four consignments of goats from Carnarvon, Shark Bay, Yalgoo and Wooramel. From the 400 faecal samples, 106 Salmonella isolates (26.5%; 95% CI: 22.4–31.0%) were recovered. Prevalence observed ranged from (30%; 95% CI: 21.7–39.5%) to (23%; 95% CI: 15.6–31.9%) in the goats from the Shark Bay and Yalgoo respectively. PCR assay targeting STM2755 and STM4497 genes revealed 84.9% of the isolates were of serovar Typhimurium. S. chester (11/106, 10.4%) and S. saintpaul (5/106, 4.7%) were characterized at invA and ompF genes. Antimicrobial susceptibility testing demonstrated that 84.0% of the isolates were susceptible to all tested (n=13) antimicrobials. None of the isolates were classified as multi-drug resistant or resistant to critically important antimicrobial such as fluoroquinolones and extended spectrum cephalosporins. However, 13.1% of the isolates were resistant to two or more antimicrobials. Commonly identified antimicrobial resistance were azithromycin (14.2%), tetracycline (10.4%), amoxicillin–clavulanate and cefoxitin (3.8%), trimethoprim/sulfamethoxazole (1.9%), gentamicin and streptomycin (0.9%). No data was presented for nalidixic acid due to lack of breakpoints. This study for the first time investigates the prevalence of Salmonella carriage and antimicrobial resistance among Salmonella isolates from rangeland goats in Australia. The low antimicrobial resistance rates among the Salmonella isolates from goats are encouraging. However, the high carriage of Salmonella among rangeland goats may indicate downstream carcass contamination and food safety concerns. This warrants further investigation.

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