



## RESEARCH BRIEF

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### Similar Levels of Antimicrobial Resistance in U.S. Food Service Ground Beef Products with and without a “Raised without Antibiotics” Claim

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#### Abstract

U.S. ground beef with “raised without antibiotics” (RWA) label claims are perceived as harboring fewer bacteria with antimicrobial resistance (AMR) than are found in conventional (CONV) ground beef with no such label claim. A total of 370 ground beef samples from CONV (n = 191) and RWA (n = 179) production systems were collected over 13 months from three food service suppliers. The following bacteria were cultured: *Escherichia coli*, tetracycline-resistant (TETr) *E. coli*, third generation cephalosporin-resistant (3GCr) *E. coli*, *Salmonella enterica*, TETr *S. enterica*, 3GCr *S. enterica*, nalidixic acid-resistant *S. enterica*, *Enterococcus spp.*, erythromycin-resistant *Enterococcus spp.*, TETr *Enterococcus spp.*, *Staphylococcus aureus*, and methicillin-resistant *S. aureus*. TETr *E. coli* was more frequently detected in CONV ground beef (CONV, 54.2%; RWA, 35.2%; P = 0.01), but supplier (P = 0.01) and production system  $\times$  supplier interaction (P = 0.01) effects were also significant. Metagenomic DNA was isolated from each sample, and equal amounts of metagenomic DNA were pooled by supplier, month, and production system for 75 pooled samples (38 CONV, 37 RWA). The abundance of *aac(6′)-Ia*, *aadA1*, *bla<sub>CMY-2</sub>*, *bla<sub>CTX-M</sub>*, *bla<sub>KPC-2</sub>*, *erm(B)*, *mecA*, *tet(A)*, *tet(B)*, and *tet(M)* genes was assessed by quantitative PCR. The *tet(A)* (2.9-log<sub>2</sub>-fold change, P = 0.04) and *tet(B)* (5.6-log<sub>2</sub>-fold change) (P = 0.03) genes were significantly more abundant in RWA ground beef. Phylogenetic analyses revealed that ground beef microbiomes differed more by supplier than by production system. These results were consistent with prior research suggesting antimicrobial use in U.S. beef cattle has minimal impact on the AMR of bacteria found in these products. These results should spur a reevaluation of assumptions regarding the impact of antimicrobial use during U.S. beef production on the AMR of bacteria in ground beef.

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