



## RESEARCH BRIEF

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### Impact of “Raised without Antibiotics” Beef Cattle Production Practices on Occurrences of Antimicrobial Resistance

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#### ABSTRACT

The specific antimicrobial resistance (AMR) decreases that can be expected from reducing antimicrobial (AM) use in U.S. beef production have not been defined. To address this data gap, feces were recovered from 36 lots of “raised without antibiotics” (RWA) and 36 lots of “conventional” (CONV) beef cattle. Samples ( $n = 719$ ) were collected during harvest and distributed over a year. AMR was assessed by (i) the culture of six AM-resistant bacteria (ARB), (ii) quantitative PCR (qPCR) for 10 AMR genes (ARGs), (iii) a qPCR array of 84 ARGs, and (iv) metagenomic sequencing. Generally, AMR levels were similar, but some were higher in CONV beef cattle. The prevalence of third-generation cephalosporin-resistant (3GC<sup>r</sup>) *Escherichia coli* was marginally different between production systems (CONV, 47.5%; RWA, 34.8%;  $P = 0.04$ ), but the seasonal effect (summer, 92.8%; winter, 48.3%;  $P < 0.01$ ) was greater. Erythromycin-resistant (ERY<sup>r</sup>) *Enterococcus sp.* concentrations significantly differed between production systems (CONV, 1.91 log<sub>10</sub> CFU/g; RWA, 0.73 log<sub>10</sub> CFU/g;  $P < 0.01$ ). Levels of *aadA1*, *ant(6)-I*, *bla<sub>ACI</sub>*, *erm(A)*, *erm(B)*, *erm(C)*, *erm(F)*, *erm(Q)*, *tet(A)*, *tet(B)*, *tet(M)*, and *tet(X)* ARGs were higher ( $P < 0.05$ ) in the CONV system. Aggregate abundances of all 43 ARGs detected by metagenomic sequencing and the aggregate abundances of ARGs in the aminoglycoside, β-lactam, macrolide-lincosamide-streptogramin B (MLS), and tetracycline AM classes did not differ (log<sub>2</sub> fold change < 1.0) between CONV and RWA systems. These results suggest that further reductions of AM use in U.S. beef cattle production may not yield significant AMR reductions beyond MLS and tetracycline resistance.

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