

March 7, 2016

## **Take-Home Summary: Discussion of research from the CSU Microbial Ecology Group**

*By Dr. Paul Morley*

**Title:** Resistome diversity in cattle and the environment decreases during beef production. eLife 2016 [Accepted 18-11-2015-RA-eLife-13195].  
**Authors:** Noyes N, Yang X, Linke L, Magnuson R, Dettenwanger A, Cook S, Geornaras I, Woerner D, Gow S, McAllister T, Yang H, Ruiz J, Jones K, Boucher C, Morley PS, Belk KE.  
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### **Principal investigators are:**

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### **This represents the largest study published to date examining the ecology of antimicrobial resistance (AMR) in the beef production system using shotgun metagenomics.**

- This is important because modern genomics approaches provide a more complete view into the ecology of AMR than can be obtained with more traditional investigations, which rely upon the culture of individual bacterial isolates of species, such as generic *E. coli*. These are not true pathogens and represent a small minority of all bacteria found in the gut or in agricultural environments.
- This project is one in a series of research investigations that the Microbial Ecology Group is pursuing. We are evaluating the ecology of microbial communities using state-of-the-art genomic tools to evaluate samples collected at the animal-human, and animal-environment interface ecologies.
- **We screened genetic sequences against a custom database comprised of all published sequences for AMR genes (>3,000 total genes in the reference database).**
  - Ninety-five percent of sequenced genetic material aligned with resistance genes in the tetracycline and macrolide classes (from total of >200,000 generated sequences related to AMR genes). We are concerned about all types of resistance that can affect human and animal health. Many of the highest concerning resistances (genes for “drugs of last resort”) do not belong to these classes of drugs.
  - A few generated sequences aligned to genes of greater concern, but these were very, very rare.

- **The study is also unique because it follows the same groups of cattle from feedlot entry through the harvest process to market-ready beef products.** This type of longitudinal research is important as it helps to control for biases in research findings that might be caused by studying different cattle at different points in the production process. Longitudinal sampling through the harvest process is only possible because of the partnership between researchers and the commercial production entities.
  - Longitudinally following cattle, and the beef products produced, allows us to examine changes in the profile of common resistance genes to understand how our management protocols might be systematically affecting the entire bacterial repertoire of resistance genes.
  - Our research suggests that there is a “contraction” in the types of resistance genes as cattle progress through the food production process.
  - Notably, the resistance profile becomes more similar in cattle feces and in their pens, comparing when the cattle enter the feedlots to when they exit the feedlot and enter the harvest process.
    - This narrowing of the resistance profiles possibly occurs when cattle that are housed together develop a common microbial community, just as has been shown in people sharing a household.
    - **This is an important finding, as it suggests that our typical large-scale beef production practices could help us to “prune” the types of resistance genes that might be present in beef products or the environment through non-pharmaceutical interventions.**
    - It also provides reason to consider that if there were systematic selection of more concerning resistance genes, say perhaps through antimicrobial drug exposures, that this type of systematic narrowing of the resistance gene repertoire could potentially amplify these effects.
  - As expected, our results indicated there were small numbers of bacteria found on market-ready beef products, which is consistent with research that has previously and consistently demonstrated the efficacy of the interventions that are routinely used to promote microbial food safety.
    - While this could be predicted, the accompanying absence of detected AMR genes was striking.
    - **This is good news for producers and consumers who are concerned that beef products might be a source of exposure to AMR bacteria.**
    - While these results need to be expanded upon and confirmed using more refined methods, this state-of-the-art genomic investigation is reassuring.

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**Ongoing research by the CSU Microbial Ecology Group is described here:**

- <http://meg.colostate.edu>
- <http://source.colostate.edu/csu-researchers-trace-superbug-genes-better-understand-antibiotic-resistant-germs>