# Project Summary Beef Safety

**Project Title:** Antibiotic Resistant Bacteria Carried by Flies in Cattle Farms versus Nonfarm Environments

**Principle Investigator(s):** J. Chen, Y. Cui and N. Hinkle

**Institution(s):** Department of Food Science and Technology, University of Georgia

**Completion Date:** June 2015

## Background

Multidrug antimicrobial resistance in bacteria has become a public health concern due to a gradual decline in the number of antibiotics that are effective for treatment of both human and animal infections. A connection between antibiotic use in food animals and antibiotic resistance of clinical bacterial isolates has been speculated. However, until the ecology of antibiotic resistant bacteria and mobile DNA elements carrying antibiotic resistance genes in animal production environment is well understood, this will remain a controversial issue.

The objectives of this study were to determine the incidence of antibiotic resistant bacteria in various flies and to compare the incidences of antibiotic resistant bacteria in flies from cattle versus non-cattle environments.

## Methodology

Flies were captured from cattle and non-cattle environments in Central Georgia from September, 2014 to April, 2015 using sweep nets. Captured flies were classified according to their morphologies before being processed for isolation of selected bacterial pathogens including *Salmonella* and *Staphylococcus*. Presumptive *Salmonella* colonies were inoculated on MacConkey agar. Colorless colonies were confirmed by growth in Triple Sugar Iron Agar and Lysine Iron Agar as well as slide agglutination using *Salmonella* poly AI & Vi antiserum. Confirmed *Salmonella* colonies were characterized further by screening for antibiotic resistance against 16 antibiotics on Mueller-Hinton agar using the disk diffusion method.

## Findings

The type of flies collected included common house fly (*Muscidae* including *Musca* and *Hydrotaea*), lesser house fly or little house fly (*Fannia canicularis*), blow fly (*Calliphondae*), horn fly (*Haematobia*), face fly (*Liohippelates*), stable fly (*Stomoxys*) and flesh fly (*Sarcophaga*). *Salmonella* was isolated from blow flies (n = 4), common house flies (n = 24), and little house flies (n = 2). Twenty-six out of the 224 flies from cattle sources (11.16%) and 4 out of the 125 flies from non-cattle environments tested positive for *Salmonella*.

None of the 16 antibiotics could inhibit the growth of all the 128 *Salmonella* colonies tested in the study. All of the *Salmonella* isolates resisted sulfosoxazole except for Isolate 066. Isolates of cattle origin demonstrated common resistance to cephazolin, sulfosoxazole, cephalothin, ampicillin and amoxicillin whereas non-cattle *Salmonella* isolates resisted tetracycline, sulfosoxazole and deoxycycline. All *Salmonella* isolates of cattle origin resisted at least 3

Funded by the Beef Checkoff

antibiotics. Among the 108 *Salmonella* isolates obtained from cattle origin, 4 developed resistance to 3 antibiotics, 1 to 4 antibiotics, 83 to 5 antibiotics, 17 to 6 antibiotics and 5 to 7 antibiotics. One of the isolates resisted 8 antibiotics and intermediately resisted another. Among the 20 *Salmonella* isolates obtained from non-cattle origin, 18 developed resistance to 3 antibiotics, and 2 to 4 antibiotics, and the latter two isolates also demonstrated intermediate resistant to 2 additional antibiotics.

An estimated 250 presumptive *Staphylococcus* colonies have been collected. The identities of these colonies are being confirmed. Antibiotic susceptibility tests will be conducted once the confirmation process is completed.

## Implications

Flies have a close and frequent contact with cattle, it is important to understand whether they carry antibiotic resistant bacteria and whether they can serve as a vehicle for dissemination of antibiotic resistant bacteria, particularly pathogens among different animals and from farms to areas where food is produced and processed. This understanding will not only benefit beef and milk consumers from a food safety standpoint, it will also benefit beef producers. Antibiotic resistance genes in bacteria carried by flies can be horizontally transferred to antibiotic susceptible bacteria, causing the development of new antibiotic resistant pathogens in cattle production environments. The emergence of these pathogens will further reduce the therapeutic value of current available antibiotics for the treatment of human and animal infections. The consequence of the situation to beef producers could be devastating in terms of both animal health and cattle production yield. Therefore, it is important to understand the ecology of antibi- otic resistant bacteria and mobile DNA elements carrying antibiotic resistance genes in insects that have a close contact with cattle. With this information, effective interventions can be developed.

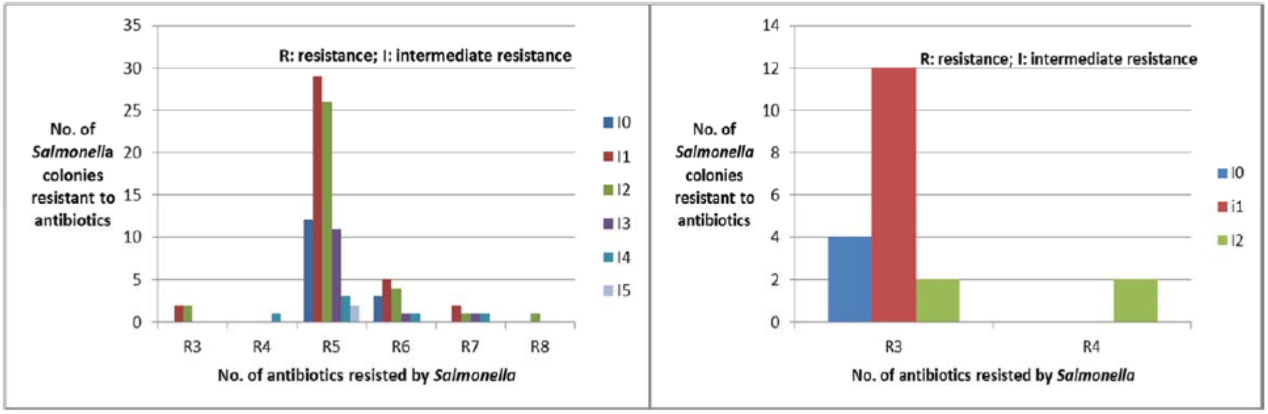

Figure 1. Number of antibiotics resisted and intermediately resisted by *Salmonella* and cattle (A) *vs*. non-cattle (B) origin. R3-R8: resistance to 3 to 8 antibiotics; Io-I5: intermediate resistance to 0-5 antibiotics.

Figure 2. Research materials of the project.

Funded by
the Beef Checkoff