Molecular surveillance of pathogens carried by filth flies (Diptera: Muscidae) associated with poultry facilities

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Abstract

Filth flies (Diptera: Muscidae), have been documented as vectors of pathogenic bacteria, including E. coli O157:H7, which causes hemorrhagic colitis in humans, and Campylobacter jejuni, which is the principal cause of foodborne disease in humans. Recently, a molecular diagnostic technique has been developed to identify filth flies that have been exposed to bacterial pathogens using PCR of insect DNA. We used this molecular diagnostic technique to conduct a molecular diagnostic technique has been developed to identify filth flies that have been exposed to bacterial pathogens using PCR of insect DNA. We used this molecular diagnostic technique to conduct a survey of over 5,000 adult flies for Campylobacter spp. and E. coli O157:H7 from two Arkansas turkey facilities during 2002 and 2003. An average of 20% of house flies, Musca domestica L., and 27% of black garbage flies, Hydrotoma aeneascens (Weidemann), carried Campylobacter spp. Occurrence of E. coli O157:H7 was not significantly different between farms or location of black garbage fly samples. Flies were found carrying Campylobacter spp. during all 9 mo of the surveillance, with the highest proportion carrying Campylobacter spp. and E. coli O157:H7 during the summer months. We recommend that fly control be targeted towards flies found within poultry facilities and towards female flies, which carry a greater proportion of bacterial pathogens than male flies.

Introduction

Campylobacter spp. are important agents in acute gastroenteritis in humans (Tauxe 1992). E. coli O157:H7 has emerged as the leading cause of enterohaemorrhagic colitis and is becoming one of the most important food-born pathogens of animal origin (Altekruse et al. 1997). In poultry production facilities, the occurrence of Campylobacter spp. and E. coli O157:H7 has been documented as vectors of pathogenic bacteria, including E. coli O157:H7, which causes hemorrhagic colitis in humans, and Campylobacter jejuni, which is the principal cause of foodborne disease in humans. Recently, a molecular diagnostic technique has been developed to identify filth flies that have been exposed to bacterial pathogens using PCR of insect DNA. We used this molecular diagnostic technique to conduct a survey of over 5,000 adult flies for Campylobacter spp. and E. coli O157:H7 from two Arkansas turkey facilities during 2002 and 2003. An average of 20% of house flies, Musca domestica L., and 27% of black garbage flies, Hydrotoma aeneascens (Weidemann), carried Campylobacter spp. Occurrence of E. coli O157:H7 was not significantly different between farms or location of black garbage fly samples. Flies were found carrying Campylobacter spp. during all 9 mo of the surveillance, with the highest proportion carrying Campylobacter spp. and E. coli O157:H7 during the summer months. We recommend that fly control be targeted towards flies found within poultry facilities and towards female flies, which carry a greater proportion of bacterial pathogens than male flies.

Materials and Methods

DNA Extraction: House flies and black garbage flies were collected inside and outside of two turkey facilities during 2002 and 2003. An average of 20% of house flies, Musca domestica L., and 27% of black garbage flies, Hydrotoma aeneascens (Weidemann), carried Campylobacter spp. Occurrence of E. coli O157:H7 was not significantly different between farms or location of black garbage fly samples. Flies were found carrying Campylobacter spp. during all 9 mo of the surveillance, with the highest proportion carrying Campylobacter spp. and E. coli O157:H7 during the summer months. We recommend that fly control be targeted towards flies found within poultry facilities and towards female flies, which carry a greater proportion of bacterial pathogens than male flies.

Table 1: Percentages of male and female house flies and E. coli O157:H7 at each facility during 2002 and 2003

<table>
<thead>
<tr>
<th>Facility</th>
<th>Year</th>
<th>Male</th>
<th>Female</th>
<th>E. coli O157:H7</th>
</tr>
</thead>
<tbody>
<tr>
<td>In</td>
<td>2002</td>
<td>28.6%</td>
<td>23.9%</td>
<td>33.6%</td>
</tr>
<tr>
<td>Out</td>
<td>2002</td>
<td>28.5%</td>
<td>23.3%</td>
<td>34.7%</td>
</tr>
</tbody>
</table>

Table 2: Percentages of house flies and black garbage flies carrying Campylobacter spp. and E. coli O157:H7 inside and outside each turkey facility during 2002 and 2003

<table>
<thead>
<tr>
<th>Facility</th>
<th>Year</th>
<th>House Flies (%)</th>
<th>Black Garbage Flies (%)</th>
<th>Total Filth Flies (%)</th>
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<tr>
<td>In</td>
<td>2002</td>
<td>14.4%</td>
<td>27.1%</td>
<td>15.9%</td>
</tr>
<tr>
<td>Out</td>
<td>2002</td>
<td>16.1%</td>
<td>29.3%</td>
<td>14.4%</td>
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Results and Discussion

A total of 5,517 filth flies were subjected to DNA analysis for Campylobacter and 3,987 for E. coli O157:H7. Campylobacter spp. was found from flies from every field collection (Tables 1 and 2). The percentage of occurrence was much lower for E. coli O157:H7 than for Campylobacter spp. None of the flies collected during 2002 were positive for E. coli O157:H7. The flies positive for HT, but not for O157 were probably carrying another H7, which could be O157:H7, or O76:H7 (Hu et al. 1999).

The occurrence of Campylobacter spp. was significantly different between house flies and black garbage flies (x2=34.96; df=1; P<0.0001). There were significant differences between 2002 and 2003 for the percentage of flies positive for Campylobacter spp. (x2=67.89; df=1; P<0.0001). The prevalence of flies positive for Campylobacter spp. in 2002 was significantly greater for flies caught in the poultry facilities relative to flies caught outside the facilities (Table 2). This difference was statistically significant for house flies (x2=447.71; df=1; P<0.0001), but not for black garbage flies (x2=1.26; df=1; P=0.285). Also, the occurrence of Campylobacter spp. was greater for female flies (Table 1).

Flies positive for E. coli O157:H7 were significantly greater for house flies compared to black garbage flies (x2=23477; df=1; P<0.0001), and was significantly greater for black garbage flies caught in the poultry facilities (x2=1256.80; df=1; P<0.0001) (Table 2).

Based on our study, that house flies and black garbage flies are carriers of E. coli O157:H7 and Campylobacter spp. within turkey houses. Also, control of filth flies using insecticides, waste management, or biological methods should target female filth flies and flies located within poultry facilities. Filth flies may have a potential to distribute bacterial pathogens to the human population living in close proximity to animal production facilities.

Future studies should be implemented to determine the dispersal of filth flies among the animal production and human components of the agro-ecosystem.

Literature Cited


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Acknowledgements

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