Gram-Negative, Aerobic, Enteric Pathogens Among Intestinal Microflora of Wild Turkey Vultures (Cathartes aura) in West Central Texas

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The prevalence of gram-negative bacterial species in the intestines of 20 apparently healthy turkey vultures (Cathartes aura) was determined. Edwardsiella tarda, Plesiomonas shigelloides, Salmonella, and Arizona himshawii (Salmonella arizonae) were each recovered from 15% of these birds. Turkey vultures may be important reservoirs of these bacterial pathogens.

The turkey vulture (Cathartes aura) is almost exclusively a carrion-feeding bird (7). From a bacteriological point of view, this feeding behavior is very interesting, because much of the diet of these birds must consist of animals that have died of infectious diseases.

C. aura occupies an ecological niche that may be very important in the maintenance and transmission of infectious diseases in the environment. It has been demonstrated that other carrion-feeding birds have spread bacterial pathogens in Africa (2).

Very little data exist on the intestinal microflora of carrion-feeding birds in general and C. aura in particular, even though these birds may be reservoirs of bacterial pathogens. The present study concerns the isolation and identification of the gram-negative, aerobic bacteria that exist in the small and large intestines of 20 apparently healthy specimens of C. aura.

Twenty specimens of C. aura were randomly collected in Tom Green and Irion counties of west central Texas. These birds were collected by shooting under scientific collecting permits issued to one of the authors (D.K.W.) by the Texas Parks and Wildlife Department and the U.S. Department of the Interior.

The birds were dissected aseptically under a hood within 2 h of collection. Approximately 1 g of the intestine and its contents was removed aseptically from both the small and large intestines. This material was placed in a sterile blender bowl with 5 ml of sterile physiological saline (0.85% NaCl) and finely ground.

A small portion of this intestinal suspension was streaked onto plates of MacConkey agar (Difco Laboratories) and Hektoen enteric agar (BBL Microbiology Systems). A 1-ml amount of this suspension was also inoculated into 9 ml of Selenite-F broth (BBL) for enrichment culture of Salmonella. The inoculated media were incubated at 35°C for 24 h. After incubation, the enrichment broth culture was streaked onto MacConkey and Hektoen enteric media, which were incubated at 35°C for 24 h.

After incubation, the MacConkey agar and Hektoen enteric agar plates were examined for different bacterial colony types. Isolated colonies of each type were picked and transferred to Trypticase soy agar slants (BBL). These were allowed to grow at 35°C for 24 h.

Each culture was then presumptively identified by the method of Johnson et al. (4). An oxidase test was also performed on each isolate, using 1% aqueous tetramethyl-p-phenylene diamine dihydrochloride (Marion Scientific Corp.).

The results of the preliminary identification tests of all isolates from each individual bird were compared. All isolates that were different from one another were subjected to final biochemical identification. The biochemical tests were done with the API 20E (Analytab Products, Inc.), since it is accurate in identifying gram-negative bacteria from human and animal specimens (6, 9, 10, 15). All isolates identified biochemically as species of Salmonella were confirmed serologically with Salmonella somatic polyvalent antiserum (BBL).

The results of this study are shown in Table 1. It can be seen that the most prevalent bacterial species, Escherichia coli, was isolated from 18 (90%) of the 20 birds. Proteus mirabilis, the second most prevalent species, was cultured from 50% of the specimens. Edwardsiella tarda and Plesiomonas shigelloides were found in 30% of these birds.

Salmonella was isolated from 3 (15%) of the 20 specimens cultured. Arizona himshawii (Sal-

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monella arizonae) was also recovered from 3 (15%) of the 20 birds.

This study is the first attempt to delineate the gram-negative aerobic microflora of the intestines of C. aura. The isolation of Plesiomonas shigelloides, Edwardsiella tarda, Salmonella, and A. hinshawii reflect the feeding behavior of these birds. Plesiomonas shigelloides and Edwardsiella tarda have been isolated from fish (12, 16). Edwardsiella tarda also has been cultured from other animals closely associated with aquatic environments (16) and from snakes (8). Although thought to feed on carrion exclusively, C. aura has been reported to catch live fish (3). Salmonella and A. hinshawii have been isolated in high prevalence from iguanid lizards collected in the same geographical area as these birds (5). Reptiles make up a large portion of the diet of C. aura (1).

The microflora of these birds also suggests that they are reservoirs of enteric bacterial pathogens. Salmonella and Arizona have long been recognized as enteric pathogens. Plesiomonas shigelloides and Edwardsiella tarda are recently recognized enteric pathogens (11, 12, 13, 14). The turkey vulture may be an important reservoir of these enteric pathogens in Texas. Additional studies should be done in other geographical areas to further assess the role of C. aura as a reservoir of enteric pathogens.

These data are similar to isolations of Escherichia coli, Citrobacter freundii, and Proteus vulgaris made from whiteback griffon’s vultures (Gyps africanus) in Africa by Houston and Cooper (2). These authors suggest, however, that the whiteback vultures are not important reservoirs of Salmonella because the bacteria cannot survive the acidity of the stomach. This is contrary to data from Salmonella isolations made from turkey vultures in Texas. In addition, the turkey vultures apparently harbor numerous other gram-negative, aerobic bacterial species, as compared with the whiteback vultures.

**LITERATURE CITED**


**TABLE 1. Gram-negative bacteria isolated from 20 specimens of Cathartes aura in west central Texas**

<table>
<thead>
<tr>
<th>Bacterial species</th>
<th>% of positive birds</th>
<th>No. of positive identifications</th>
</tr>
</thead>
<tbody>
<tr>
<td>Escherichia coli</td>
<td>90.0</td>
<td>18</td>
</tr>
<tr>
<td>Proteus mirabilis</td>
<td>50.0</td>
<td>10</td>
</tr>
<tr>
<td>Plesiomonas shigelloides</td>
<td>30.0</td>
<td>6</td>
</tr>
<tr>
<td>Edwardsiella tarda</td>
<td>30.0</td>
<td>6</td>
</tr>
<tr>
<td>Enterobacter cloacae</td>
<td>20.0</td>
<td>4</td>
</tr>
<tr>
<td>Salmonella sp.</td>
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<td>3</td>
</tr>
<tr>
<td>Arizona hinshawii</td>
<td>15.0</td>
<td>3</td>
</tr>
<tr>
<td>Hafnia alvei</td>
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<td>1</td>
</tr>
<tr>
<td>Enterobacter aerogenes</td>
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<td>1</td>
</tr>
<tr>
<td>Klebsiella pneumoniae</td>
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<td>1</td>
</tr>
<tr>
<td>Citrobacter freundii</td>
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<td>1</td>
</tr>
<tr>
<td>Proteus vulgaris</td>
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<td>1</td>
</tr>
<tr>
<td>Proteus retigeri</td>
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<td>1</td>
</tr>
<tr>
<td>Proteus inconstans</td>
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</table>