Survey of Campylobacter jejuni and Campylobacter coli in different taxa and ecological guilds of migratory birds

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ABSTRACT

A total of 169 faecal samples were collected from migrating birds, belonging to the Order of Passeriformes, in Campania region in order to isolate Campylobacter spp. Campylobacter spp. were isolated from 39 of the 169 birds examined (23.1%). Among these 36 were identified as C. jejuni and the remaining strains were identified as Campylobacter coli. Given the high isolation rates wild birds could be considered natural reservoir of infection.

Key Words: Campylobacter jejuni, Campylobacter coli, Migratory birds, Taxa, Ecological guilds.

Introduction

Campylobacter jejuni is regarded as the most common cause of foodborne bacterial enteritis in humans and have been isolated from a variety of ecological sources, including wild and domestic animals, foods, and the environment.

The main sources of infection of human campylobacteriosis are considered to be the consumption of undercooked poultry meat, eggs, etc. (Chuma et al., 2000). C. jejuni contamination of poultry meat during processing has been well documented. It is also well known that broilers on growing farms are often infected with C. jejuni or C. coli (Chuma et al., 2000). However, the epidemiology of these infections to broilers is little known.

Gregory et al. (1997) reported that no specific contamination source could be identified but it
seemed to be found among any potential elements outside of broiler houses like rodents and wild birds. For decades wild birds have been considered natural vertebrate reservoirs of Campylobacter spp. (Waldeström et al., 2002) and are frequently mentioned as possible vectors for transmission to poultry and humans. Due to their great mobility, wild-living birds may function as effective spreaders of disease through fecal contamination of pastures, forage, and surface waters (Kapperud and Rosef, 1983).

The aim of present study is to carry out a monitoring on the presence of thermotolerant Campylobacter in resident and migratory wild birds of Campania region and obtain more information about the role played by wild birds in spreading and maintaining of these agents in nature.

**Material and methods**

This study was carried out from February 2005 to April 2005 attending to a monitoring and ringing program of migratory birds at Migration Study Stations located in "Parco Regionale del Matese" in Campania region.

A total of 169 faecal samples were collected from birds belonging to the Order of Passeriformes. Passerines were trapped with mist-nets. With reference to the size of the birds, faecal samples or cloacal swabs were collected and placed in Amies Transport Medium (Oxoid Ltd., Basingstoke, Hampshire, UK).

Isolation and identification of Campylobacter was carry out according to Chuma et al. (2000) procedure.

A multiplex PCR assay was carried out to all isolates in accordance with the Cloak and Fratamico procedure (2002). The primers employed in this assay are shown in table 1.

**Results and discussion**

Campylobacter spp. were isolated from 39 of the 169 birds examined. The mean prevalence of Campylobacter was 23.1% for all tested birds but varied from 0 to 46.3% between species. Among these isolates, 36 were identified as C. jejuni and the remaining strains were identified as Campylobacter coli.

The prevalence of Campylobacter spp. is heterogeneous also in different ecological guilds. No Campylobacter spp. was isolated in granivores or aerial insectivores. In contrast, most guilds that forage at ground level (E. rubecula, T. merula, L. megarhynchos), and arboreal and herbaceous insectivores (S. atricapilla, S. melanocephala, S. rubetra, C. cetti) showed high prevalence rates of Campylobacter spp (Table 2).

We compared prevalence rates to distance of migration for all species with the birds divided into two groups. The first group was made up of long-distance migrants (birds migrating to Africa, the Middle East, or Asia), while the second group was made up of short-distance migrants (birds migrating to different parts of Europe). Among long distance migrants 17 out of 99 birds (17.2%), representing 4 species (Sylvia atricapilla, Sylvia
### Table 2. Bird tested and prevalence of *Campylobacter* spp.

| Family and species | Guild* | N. of birds tested | N. of positive C. jejuni | C. coli | % of positivity per bird species |
|--------------------|--------|-------------------|-------------------------|---------|---------------------------------|
| **Sylviidae**      |        |                   |                         |         |                                 |
| Sylvia atricapilla | AI     | 24                | 9/24                    | 1/24    | 41.6                            |
| Sylvia cantillans  | EI     | 11                | -                       | -       | -                               |
| Sylvia melanocephala | EI | 8                 | 3/8                     | -       | 37.5                            |
| Sylvia communis    | EI     | 7                 | -                       | -       | -                               |
| Sylvia borin       | AI     | 2                 | -                       | -       | -                               |
| Phylloscopus sibilatrix | AI | 2                 | -                       | -       | -                               |
| Philloscopus trochius | AI | 2                 | -                       | -       | -                               |
| Hippolais icterina | AI     | 1                 | -                       | -       | -                               |
| Philloscopus collybita | AI | 1                 | -                       | -       | -                               |
| **Muscipulidae**   |        |                   |                         |         |                                 |
| Erithacus rubecula | GFI    | 41                | 17/41                   | 2/41    | 46.3                            |
| Luscinia megarhynchos | GFI | 10               | 3/10                    | -       | 30                              |
| Turdus merula      | GFI    | 10                | 2/10                    | -       | 20                              |
| Ficedula hypoleuca | I      | 9                 | -                       | -       | -                               |
| Saxicola rubetra   | EI     | 8                 | 1/8                     | -       | 12.5                            |
| Cettia cetti       | EI     | 4                 | 1/4                     | -       | 25                              |
| Turdus philomelos  | GFI    | 3                 | -                       | -       | -                               |
| Muscicapa striata  | I      | 2                 | -                       | -       | -                               |
| Phoenicurus phoenicurus | AI | 1                 | -                       | -       | -                               |
| Oenanthe oenanthe  | GFI    | 1                 | -                       | -       | -                               |
| Ficedula albicollis | I    | 1                 | -                       | -       | -                               |
| Fringillidae       |        |                   |                         |         |                                 |
| Serinus serinus    | GFG    | 1                 | -                       | -       | -                               |
| Carduelis chloris  | GFG    | 1                 | -                       | -       | -                               |
| **Passeridae**     |        |                   |                         |         |                                 |
| Prunella modularis | GFG    | 2                 | -                       | -       | -                               |
| Passer hispaniolensis | GFG | 2                | -                       | -       | -                               |
| **Paridae**        |        |                   |                         |         |                                 |
| Parus major        | AI     | 6                 | -                       | -       | -                               |
| Parus caeruleus    | AI     | 1                 | -                       | -       | -                               |
| **Hirundinidae**   |        |                   |                         |         |                                 |
| Hirundo rustica    | I      | 8                 | -                       | -       | -                               |

* Guild: AI: arboreal insectivores; EI: herbaceous insectivores; GFI: ground-foraging invertebrate feeders; I: aerial insectivores; GFG: ground-foraging granivores.
melanocephala, Luscinia megarhynchos, Saxicola rubetra), tested positive for Campylobacter spp. In contrast, out of 70 tested birds, 22 (31.5%) of the short-distance migrants, representing 3 species (Erithacus rubecula, Turdus merula, Cettia cetti), were positive.

Conclusions

In accordance with literature (Waldeström et al., 2002), we found a high prevalence of Campylobacter spp. in migrating birds (23.1%). However, the distribution of Campylobacter among bird taxa and guilds was very heterogeneous. Certain bird taxa, representing 2 families (Sylviidae and Muscicapidae), showed high prevalences, e.g., S. atricapilla (41.6%), E. rubecula (46.3%), S. melanocephala (37.5%), C. cetti (25%), T. merula (20%), while others did not. The prevalence of Campylobacter spp. was highly influenced by feeding habits. In some ecological guilds, e.g., most types of aerial insectivores and granivores, Campylobacter spp. were never isolated. In contrast, in other guilds, such as ground-foraging invertebrate feeders and arboreal and herbaceous insectivores guilds, prevalence was found to be high.

Furthermore, in this study and in several others, high prevalences of Campylobacter were found in apparently healthy birds (Kapperud and Rosef, 1983). High isolation rates could be interpreted as evidence for a coexistence between Campylobacter species and their bird hosts, which could be considered natural reservoir of infection. In addition, migration is a great stress for birds and resistance to infection, typical of wild avian species, might be decreased and the level of bacteremia might increase. Consequently, the shedding rate of pathogens increase, resulting in contamination of water and soil with faeces and in dissemination and survival of the agent in a new environment.

We do not know if the Campylobacter isolates found in this study are transmissible to humans or domesticated animals, but there might nevertheless be some epidemiological considerations. Given the occurrence of C. jejuni and C. coli in bird species capable of long-distance migration, many bird species could potentially act as vectors in long-distance transmission of these pathogens to domesticated animals or humans. Finally, given the diversity of habitats occupied by different bird species and the resulting possibility of different species being exposed to Campylobacter spp. from different sources, we believe that this question deserves further investigation.

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