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KARS YÖRESİNDE FARKLI KANATLI TÜRLERİNDEN SALMONELLA İZOLASYONU

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Özet: Bu çalışmanın amacı bölgede farklı kanatlı türlerinde *Salmonella* taşıyıcılığını ve bulunan en yaygın *Salmonella* serotiplerini belirlemektir. Araştırmada 8 kanatlı türünden alınan 664 dışkı ve kloakal svab örnekleri *Salmonella* varlığı yönünden incelendi. Kaz dışındaki kanatlı türlerinden *Salmonella* izolasyonu yapılamazken, kazlardan izole edilen 6 *Salmonella* türü Kauffmann-White şemasına göre *S. enterica* subsp. *Enterica* Serovar Typhimurium (*S.* Typhimurium) olarak identifiye edildi.
Anahtar sözcükler: *Salmonella*, izolasyon, serotiplendirme, kanatlı.

Salmonella Isolations from Different Avian Species in Kars District of Turkey

Summary: The objective of the study was to detect *Salmonella* carrier in different avian species in the district and to determine the most common *Salmonella* serotypes. In the study, a total of 664 faecal and cloacal swab samples from eight avian species were examined for the presence of *Salmonella*. While no *Salmonella* was isolated from avian species except goose, six strains were isolated from geese and all strains were identified as *S. enterica* subsp. *Enterica* Serovar Typhimurium (*S.* Typhimurium) according to Kauffmann-White Scheme.
Keywords: *Salmonella*, isolation, serotyping, avian.

INTRODUCTION

The disease caused by *Salmonella* serovars can affect all species of domestic animals; the young are the most susceptible[1]. Enteric form of Salmonellosis is the most common clinical manifestation, but a wide range of clinical signs, including acute septicaemia, arthritis and respiratory diseases, may be seen. However many infected animals show no clinical signs. Such animals may be important causing of food poisoning in humans[2]. Carrier stage of *Salmonella* varies according to the species of animal; in some cases the animal becomes a life-long *Salmonella* carrier[3-5].

Over 2500 *Salmonella* serovars have been recognised in all countries, however, only few serovar have been identified as the prime etiologic agents of human salmonellosis[6,7].

The aim of this study was to determine the prevalance of *Salmonella enterica* from asymptomatic intestinal carriers among avian species and to obtain more information about the most common *Salmonella* serovars carried by avian species.

MATERIALS and METHODS

In the present study, a total of 664 faecal and cloacal swab samples collected from eight different avian species were examined for the presence of *Salmonella*. The cloacal swabs were collected from geese (385), pigeons (30), ducks (20), hens (20) and turkey (42). In addition, faecal samples were collected from gulls (60), crows (59), sparrows (27) and hens (21) (Table-1). All the faecal and cloacal swab samples were used to detect the presence of *Salmonella* using the method of Waltman et al (8). For the isolation of *Salmonella*, Tetrathionate broth (Difco, 0104-17) and Selenite broth (Difco, 0275-01-7) were used as enrichment media; MacConkey agar (Merck, 1.05465), Salmonella-Shigella agar (Merck, 7667), Brilliant Green agar (Oxoid, CM263) and Hectoen Enteric agar (Oxoid, CM419) were used as differential and selective plating media[9]. Both cloacal swabs and faecal samples were inoculated into Tetrathionate and Selenite broths as soon as the samples were transported to the laboratory. After 18-24 hours of incubation at 37°C in Selenite broth and at 43°C in Tetrathionate broth, cultures were subcultured on differential and selective plating media. A delayed secondary enrichment (DSE) procedure was used when culture result was found negative in selective enrichment media. After samples left at room temperature for 5-7 days in Tetrathionate enriched broth one ml of the culture was transferred into 10 ml of fresh Tetrathionate enrichment broth and incubated for 24 hours[10,11]. Isolated strains were identified by three-tube method of Lassen[12].

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Isolates tentatively identified as *Salmonella* A-I serogroup with Salmonella polyvalent O (Difco polyvalent A-I and Vi L-720114-1) antisera. Identified 6 *Salmonella* spp. were serogrouped and serotyped according to Kauffmann-White scheme[13] in Department of Microbiology, Faculty of Medicine, University of Ankara.

were serotyped as *S.* Typhimurium. No *Salmonella* species was isolated from laying hens, pigeons, crows, turkeys, sparrows, gulls and ducks examined. Short duration of colonization or few number of *Salmonella* in the intestinal tract may have affected detection of *Salmonella.*

Table 1. The number and the distribution of the samples obtained from various avian species.
Tablo 1. Çeşitli kanatlı türlerinden elde edilen örneklerin sayısı ve dağılımı.

Samples	Avian species								
	Goose	Hen	Turkey	Duck	Pigeon	Crow	Sparrow	Gull	Total
Cloacal swabs	385	20	42	20	30	-	-	-	497
Faecal samples	-	21	-	-	-	59	27	60	167
Total	385	41	42	20	30	59	27	60	664

RESULTS

Six *Salmonella* spp. were isolated from geese. Isolated strains were identified by biochemical tests. The isolates were then serogrouped using Polyvalent O antisera (Difco, poly A-I, L-720114-1). Identified *Salmonella* spp. (A-I group) strains were then sent to *Salmonella* reference laboratory for serogrouping and serotyping. Serogroup of the isolates were found as B serogroup using individual single factor O group antisera. Following to the serogrouping, the isolates was serotyped based on the presence of flagellar antigen. According to Kauffmann-White scheme, antigenic formula of the *Salmonella* strains were found as 1,4,5,12: i: 1,2. Therefore, serotyped *Salmonella* spp. strains were classified as *S.* Typhimurium. In the study, no *Salmonella* spp. was isolated from other animals except for geese.

DISCUSSION

The infections caused by *Salmonella* serovars are widespread and it can be isolated from various kinds of animal species[14,15]. Several studies revealed that different *Salmonella* serotypes such as *S.* Typhimurium, *S.* Enteritidis and *S.* Essen were isolated from laying hens[4,16,17] and *S.* Gallinarum, *S.* Pullorum, *S.* Typhimurium and *S.* Infantis from broilers[15,17]. Different Salmonella serovars were also isolated from pigeons[5,18,19], gulls[20] and geese[21].

In this study, a total of 664 faecal and cloacal swab samples collected from 8 different avian species was examined for the presence of *Salmonella*. Only six *Salmonella* strains were isolated from geese and these

Salmonellae are excreted intermittently often in low numbers and sometimes cloacal swabbing is not usually sufficient to detect *Salmonella*[8]. Nevertheless, examination of both cloacal and faecal samples for detecting *Salmonellae* can increase the chance of isolation. In this study, both cloacal and faecal samples were used as materials for isolation of *Salmonellae.*

Salmonella enterica is a major cause of intestinal disease in humans and animals worldwide[3,14,22]. One hundred and ten *Salmonella* serovar have been identified from different sources up to 1997 in Turkey[23]. *Salmonella enterica* serovar Enteritidis and serovar Typhimurium have been identified as the prime etiologic agents of human salmonellosis in Turkey. In this study, we have also found *S.* Typhimurium in geese.

Geese are kept on small-scale family farms and the industry is economically important in the district of Kars in Turkey and no vaccine is used to immunise the animals in the vicinity. Poultry, cows and equides are housed together. The poultry are free range and thus may contaminate feedstuffs, drinking water and the surrounding area. Therefore, poultry may be potential risk for *Salmonella* infections especially for children and elderly people and for other animal species housed together. In our previous study, *S.* Enteritidis and *S.* Typhimurium serovars were identified from cattle and sheep in the same district[24]. Therefore, epidemiological studies related with poultry should be combined with farm animals to find the exact source of the infection. In addition, new genotyping tools should be combined with phenotyping data in order to obtain discriminative

Kafkas Üniv. Vet. Fak. Derg.
2005, 11(1): 25-27

patterns of the isolated strains. This may also help track down the exact source of the infection.

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