ANNALES
UNIVERSITATIS MARIAE CURIE-SKŁODOWSKA
LUBLIN – POLONIA
VOL. LXI, 9 SECTIO DD 2006

Zakład Mikrobiologii Weterynaryjnej Instytutu Chorób Zakaźnych i Inwazyjnych
Akademii Rolniczej w Lublinie

GRAŻYNA ZIÓŁKOWSKA, STANISŁAW TOKARZEWSKI,
ANETA NOWAKIEWICZ, ANNA KOSTRUBA

Bacteriological flora isolated from geese reproductive flocks

Flora bakteryjna występująca w stadach gęsi reprodukcyjnych

SUMMARY

The objective of the experiments was to determine the bacteria species isolated from the ontocenoses of the beak cavity and cloaca in the reproductive geese flocks as well as to recognize the potential dependence of the microbial spectrum on bird age, environmental conditions and season. The studies covered 17 farms of reproductive geese white Italian breed reared under differentiated conditions. The experimental material was constituted by the beak cavity and cloaca swabs (920 samples). Isolation and identification of every bacteria species was performed according to the conventional bacteriological methods with commercial tests. The obtained results were analysed statistically by t-Student test. Regardless of a sampling site (beak cavity, cloaca) the isolated bacterial flora composition included: *Escherichia coli, Proteus* spp., *Staphylococcus* spp., *Streptococcus* spp. and *Enterococcus* spp. Moreover, in single cases *Bacillus* spp., *Citrobacter* spp., *Yersinia* spp., *Enterobacter* spp. and *Klebsiella* spp. were identified. Each microbial species incidence was mainly contingent on the environmental conditions and the examined bird age, while to a smaller extent on the ontocenosis.

Key words: geese, bacterial flora, cloaca, beak cavity

INTRODUCTION

In recent years the growth of breeding geese population in Poland [Gaweł *et al.* 2001, Lis 2002] and in other countries [Cattaneo *et al.* 2002, Kozak *et al.* 2002] has been marked, which arouses interest in this relatively less known waterfowl species. An increased flock number, high stock density of birds and the introduction of intensive rearing methods constitute a potential threat to flock health status, despite the appropriate feeding and permanent medical and veterinarian care.

There is a distinct infection increase noted where the etiological factors. Besides, currently isolated pathogens like, *Salmonella* spp., *Pasteurella* spp., *Campylobacter* spp. and *Listeria* spp. [Wieliczko and Mazurkiewicz 1995, Samorek-Salamonowicz *et al.* 1998, Karakolev *et al.* 2003] can be opportunistic bacteria [Tankson *et al.* 1999] or even commensalic ones [DeBoer *et al.* 2001]. An etiological factor of infection has the endogenous source – the microflora of bird's organism. The physiological bacterial flora harboured on the digestive system in particular exerts a very significant impact on the animal health state through its influence on the intestinal mor-

phology, protection from their colonization by pathogens as well as immune response stimulation [Mead 2000]. Under conducive conditions, like stress or disturbances in the immune system function, the microbes change their commensalic status and penetrate the natural protective barrier of organism to induce infection [Tankson *et al.* 2002].

In many countries recent intensive methods of birds rearing, including feeds supplemented with antibiotics for prophylaxis and to promote nutrients convertion into body weight, appeared to affect the growth of antibiotic-resistant bacterial strains [Gong *et al.* 2002]. A high percentage of antibiotic-resistant strains, among others from *Enterococcus faecium* and *E. faecalis* genera constituting the microflora of most animals, poultry and people suggest that resistance genes can be transmitted between the strains originating from various hosts and generate serious medical and veterinarian problems [Baele *et al.* 2002].

The natural microflora of birds makes a direct contamination source of poultry meat and its products, thus being a causative agent of man's diseases [Panisello *et al.* 2000]. The bacterial microflora composition, both qualitative (every species) and quantitative, is differentiated, subject to a bird species first of all as well as feeding and management conditions. The hen's microflora is relatively well known [Gong *et al.* 2002, Lu *et al.* 2003] just like that of turkey [Bielke *et al.* 2003] and pigeon [Baele *et al.* 2002]; however, there is scarce information concerning the bacteria species present in a waterfowl representative – water goose. The objective of the work was to determine bacteria species occurring in the ontocenoses of beak cavity and cloaca in the reproductive geese flocks as well as establishing the potential dependences of the microbe spectrum on bird age, environmental conditions and season.

MATERIAL AND METHODS

Animals

The studies included 17 farms of reproductive geese white Italian breed from the south-eastern Poland. The flocks of 190–800 birds were kept at differentiated environmental conditions (wooden or brick buildings), while the feeding and management conditions met the general standards for this kind of breeding. The farms were provided with permanent veterinary control and a prophylactic programs including the protective immunization against Derzsy disease as well as seasonal disinfestations of birds.

The scope of investigations regarded the assessment of bacterial flora present in geese subject to bird age, flock size, type of building and season (January 2003, 2004 and April 2003]. The beak cavity and cloaca swabs constituted the experimental material sampled randomly every time from the chosen animals from each flock. Totallly, 920 samples were examined.

Bacterial isolation and identification

The swabs were inoculated directly on blood agar and McConkey medium. The bacteriological examinations for *Salmonella* rods presence were performed after the recommendations enclosed [Instrukcja 1999]. After 24 h growth period the preliminary evaluation of the bacterial flora was made on the grounds of colony appearance and preparation staining after Gram method. In the case of Gram-positive cocci, the catalase test was performed with 3% hydrogen peroxide solution. The Gram-positive and catalase-positive strains were inoculated on Chapman medium followed by the clumping factor test made by the diagnostic kit ST-80 (Cormay, Lublin, Poland).

The Gram-positive and catalase-negative bacterial strains of spherical shape were inoculated simultaneously on TKT and Slanetz media.

The strains isolated on the McConkey medium were defined as Gram-negative rods and then identified with commercial tests (Cormay, Lublin, Poland).

Statistical analysis

The data obtained in the study were analyzed statistically using t-Student test (Statistica 6.0). The differences were considered significant at $p<0.05$.

RESULTS

The present authors' observations and the veterinary documentation proved the absence of the clinical signs of the bacterial diseases over the experimental period. The isolation of *Salmonella* rods were negative in all the examined cases.

The results of inoculations made from the beak cavity and cloaca are presented in Fig. 1. It is noteworthy that irrespective of a sampling site (beak cavity, cloaca) the composition of isolated bacterial flora was very similar and its main representatives were identified as *Escherichia coli*, *Proteus* spp., *Staphylococcus* spp., *Streptococcus* spp., *Enterococcus* spp. Besides, in some single cases *Bacillus* spp., *Citrobacter* spp., *Yersinia* spp., *Enterobacter* spp. and *Klebsiella* spp. were reported.

However, in the examined birds no presence of Gram-positive rods of *Listeria* genus or coagulase-positive bacteria *Staphylococcus* genus was recorded.

Regardless of a flock size the coagulase-negative strains *Staphylococcus* were obtained from each bird (around 80–90%) from both beak cavity and cloaca (Tab. 1) and the percentage was significantly lower in the big flocks (over 500 units) when the examinations concerned cloaca samples.

Table 1. Bacteria isolated in reproductive geese flocks in relation to flock size
Tabela 1. Bakterie izolowane w stadach gęsi reprodukcyjnych w zależności od wielkości stada

	Flock size – Wielkość stada			
	Beak cavity – Jama dziobowa		Cloaca – Kloaka	
	< 500 (n =300)	> 500 (n = 160)	< 500 (n =300)	> 500 (n = 160)
Escherichia coli	52.67±3.30 *	66.87±2.44 *	59.33±2.41*	78.12±2.23 *
Proteus spp.	15.00±1.93	18.12±2.61	13.33±1.47	19.37±2.21
Staphylococcus coagulase-negative	87.00±1.68	89.37±1.52	90.33±1.45 *	80.62±2.64 *
Streptococcus spp.	60.33±4.54	66.25±4.53	60.67±4.59	68.12±4.49
Enterococcus spp.	61.00±2.86	73.12±2.30	60.33±2.49 *	75.62±2.92*
Bacillus spp.	10.00±0.40	-	0.67±0.25	0.62±0.25
Citrobacter spp.	2.33±0.68	1.25±0.50	1.67±0.65 *	6.25±1.20 *
Yersinia spp.	2.00±0.48	0.62±0.25	-	1.25±0.50
Enterobacter spp.	0.67±0.36	-	-	-
Klebsiella spp.	-	-	-	0.62±0.25

*p<0.05

Bacteria *Streptococcus* and *Enterococcus* species were recorded slightly rarely (about 60–70%) and their incidence depended on bird stocking rate. At the farms of over 500 animals the contaminated birds percentage has gone up significantly (Tab. 1).

Similar dependences were found for *E. coli*. Microbes appeared in 50–60% of geese; however, this number increased significantly when the examinations concerned the cloaca material collected from birds from the large sized farms (over 500 animals).

The other microbes like *Proteus* spp., *Bacillus* spp. and *Citrobacter* spp. were isolated more seldom or occasionally (*Klebsiella* spp., *Yersinia* spp. and *Enterobacter spp*., Tab. 1) so it is difficult to establish any potential regularities of their occurrence.

The contamination level of the examined flocks with the defined bacteria species was also related to a type of building where breeding took place (Tab. 2). The microflora of beak cavity and cloaca of geese from both building types was dominated with coagulase-negative bacteria *Staphylococcus* species (80–90%). In the brick buildings a clear contamination level of flocks with *E. coli* and *Enterococcus* spp. was detected, while *Streptococcus* spp. appeared in the wooden buildings more frequently. The above regularity concerned both the microflora of beak cavity and cloaca, whereas the statistically significant differences ($p<0.05$) were noted for *E. coli* and *Enterococcus* spp. The *Proteus* spp. presence was recorded in a relatively low percentage of birds (12–18%) and its level was very close irrespective of the environmental conditions.

Table 2. Bacteria isolated in reproductive geese flocks in relation to a building type
Tabela 2. Bakterie izolowane w stadach gęsi reprodukcyjnych w zależności od rodzaju budynku

	Building type – Rodzaj budynku			
	Beak cavity – Jama dziobowa		Cloaca – Kloaka	
	Brick (n = 160) Murowany	Wooden (n = 300) Drewniany	Brick (n = 160) Murowany	Wooden (n = 300) Drewniany
Escherichia coli	63.00±2.95 *	47.50±3.15 *	69.33±2.84	59.37±1.53
Proteus spp.	18.00±2.47	12.50±1.44	15.67±1.85	15.00±1.63
Staphylococcus coagulase-negative	88.33±1.49	86.87±1.89	84.00±2.33	92.50±0.86
Streptococcus spp.	60.33±4.52	66.25±4.56	61.67±4.52	66.25±4.65
Enterococcus spp.	75.00±2.37 *	49.37±2.74 *	68.33±2.83	61.25±2.47
Bacillus spp.	0.67±0.36	0.62±0.25	-	1.87±0.40
Citrobacter spp.	1.67±0.53	2.50±0.77	3.67±0.99	2.50±0.68
Yersinia spp.	1.67±0.46	1.25±0.34	-	1.25±0.50
Enterobacter spp.	0.67±0.36	-	-	-
Klebsiella spp.	-	-	0.33±0.18	-

* $p<0.05$

The season also influenced the bird organism colonization by every bacteria species (Tab. 3). In spring the percentage of geese population with identified *Streptococcus* spp. ($p<0.05$), *Enterococcus* spp. ($p<0.05$) and *Proteus* spp. was evidently higher. These microbes were obtained from the microflora of beak cavity and cloaca. The coagulase-negative bacteria *Staphylococcus* were isolated from the majority of birds (up to 90%) and their incidence grew substantially in the spring period (from 85 to 91%).

Table 3. Bacteria isolated from reproductive geese flocks in relation to a season
Tabela 3. Bakterie izolowane w stadach gęsi reprodukcyjnych w zależności od pory roku

	Season – Pora roku			
	Beak cavity – Jama dziobowa		Cloaca – Kloaka	
	January (n = 300) Styczeń	April (n = 160) Kwiecień	January (n = 300) Styczeń	April (n = 160) Kwiecień
Escherichia coli	63.67±2.88 *	46.25±3.20 *	66.67±2.29	64.37±2.90
Proteus spp.	13.00±1.62	21.87±2.90	14.33±1.79	17.50±1.73
Staphylococcus coagulase-negative	85.67±1.81	91.87±1.11	85.33±2.24	90.00±1.37
Streptococcus spp.	44.67±4.64 *	95.62±0.89 *	46.00±4.75 *	95.62±0.72 *
Enterococcus spp.	58.00±2.92 *	81.25±1.67 *	58.00±2.66 *	80.62±2.17 *
Bacillus spp.	1.00±0.40	-	1.00±0.30	-
Citrobacter spp.	2.67±0.74	0.62±0.25	4.33±1.04	1.25±0.50
Yersinia spp.	2.33±0.50	-	0.67±0.37	-
Enterobacter spp.	-	1.25±0.50	-	-
Klebsiella spp.	-	-	-	0.62±0.25

*p<0.05

As for *E. coli* the percentage of birds with this bacteria species recognized depended on the origin of the studied material (beak cavity, cloaca). *E. coli* was detected in winter more often (63.6%) and in spring a statistically significant fall (p<0.05) of the infected geese number (46.2%) was observed; this regularity regarded only the microflora of the beak cavity.

Interrelation between bird age defined as egg-laying season and number of individuals contaminated with a fixed bacteria species is presented in Fig. 1 and 2.

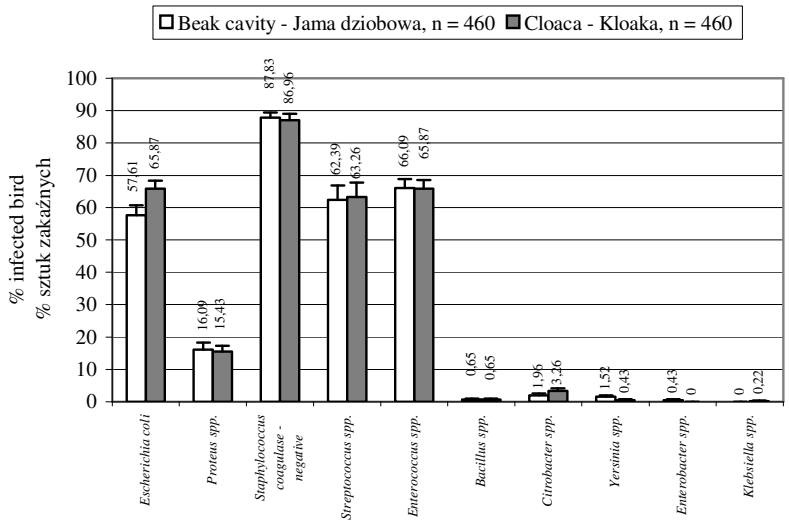

Fig. 1. Bacteria isolated from reproductive geese flocks in relation to a sampling site
Rys. 1. Bakterie izolowane w stadach gęsi reprodukcyjnych w zależności od miejsca pobrania materiału

The colonization dynamics of beak cavity and cloacae by the bacteria species isolates proceeds a bit differently. The bird beak cavity (Fig. 2) in the first laying period was colonized mostly by the coagulase-negative bacteria *Staphylococcus* (85.6% of the studied population) and then as following: *Enterococcus* spp. (74.4%), *E. coli* (69.4%), *Streptococcus* spp. (58.7%) and *Proteus* spp. (22.5%). The second season showed a decline of values for most bacteria isolated, i.e. *E. coli* (to 46.4%, $p<0.05$), *Enterococcus* spp. (to 57.3%) and *Proteus* spp. (8.2% $p<0.05$) as well as statistically significant growth for *Streptococcus* spp. (77.3%, $p<0.05$). In the third and fourth egg-laying season the percentage of birds colonized with the above mentioned bacteria generally increased or persisted at the near level (*E. coli, Enterococcus* spp., *Staphylococcus, Proteus* spp.) and only in the case of *Streptococcus* bacteria a statistically significant ($p<0.05$) fall (65.0 and 53.08%) was recorded.

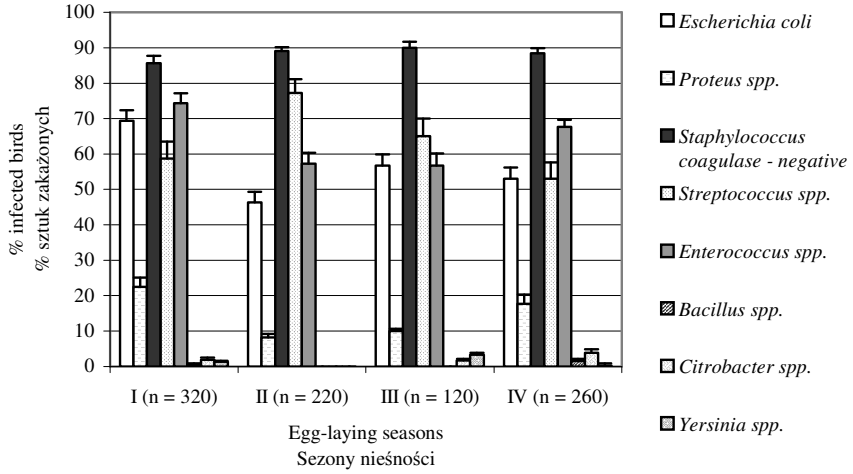

Fig. 2. Bacteria isolated in beak cavity in reproductive geese flocks in relation to age
Rys. 2. Bakterie izolowane z jamy dziobowej w stadach gęsi reprodukcyjnych w zależności od wieku

The microflora of cloaca (Fig. 3) in the first laying period showed the presence of coagulase-negative bacteria *Staphylococcus* species (86.2% of the examined bird population), then *E. coli* (69.4%), *Enterococcus* spp. (65.6%), *Streptococcus* spp. (58.1%) and *Proteus* spp. (20.6%). In the second season an increase of bird percentage was noted with the presence of each microbe (Fig. 3). The third egg-laying season was marked with distinct decline of contaminated birds percentage, predominantly regarding *E. coli* (to 50%, $p<0.05$), *Staphylococcus* spp. (to 91.7%), *Proteus* spp. (to 5.0%, $p<0.05$) and *Streptococcus* spp. (to 65.0%, $p<0.05$). The values maintained at a similar level exclusively for *Enterococcus* spp. The following season exhibited a further percentage decline of birds from which the discussed bacteria species isolates were taken. The only exception was reported for *E. coli*, whose presence was stated in 65.4% of the examined population and that value was statistically significantly higher ($p<0.05$) than this obtained in the second season (50.0%).

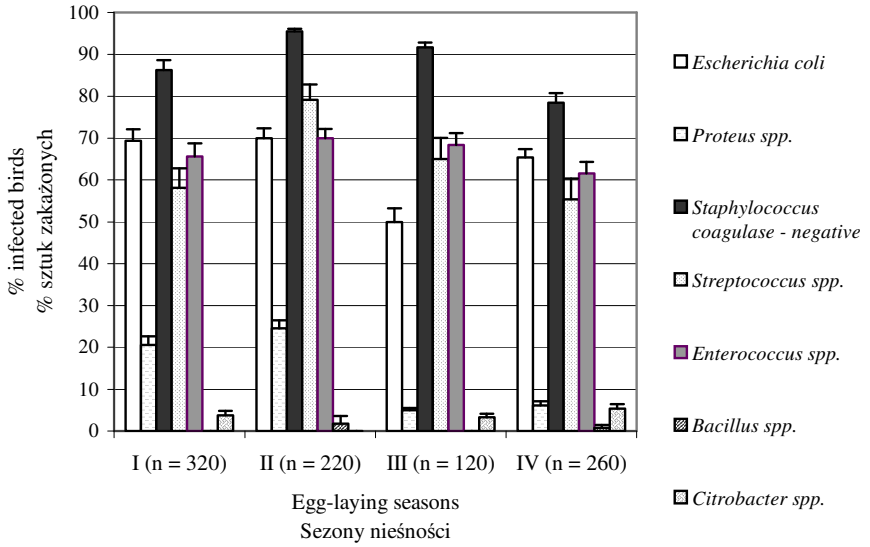

Fig. 3. Bacteria isolated in cloaca in reproductive geese flocks in relation to age
Rys. 3. Bakterie izolowane z kloaki w stadach gęsi reprodukcyjnych w zależności od wieku

Summing up, the conclusion is that the microflora composition in the studied geese population was close on the whole and every microbial species incidence depended mainly on the environmental conditions and the age of the examined birds, while less so on ontocenosis (beak cavity, cloaca).

DISCUSSION

Besides the viral and mycotic diseases, the bacterial infections are responsible for high economic losses in the breeding geese flocks. In Poland in the 90's bacterial diseases caused about 24–30% of the total fall number at the breeding geese farms [Samorek-Salamonowicz *et al.* 1998]. The agent isolated most frequently appeared to be *Salmonella* rods [Wieliczko and Mazurkiewicz 1995, Samorek-Salamonowicz *et al.* 1998]. The monitoring of reproductive geese flocks performed after 2000 at the Lublin Province area (current studies), in Wielkopolska and the Lower Silesia [Gaweł *et al.* 2001] did not exhibit *Salmonella* rods presence in any of the examined farms. The studied bird population, however, cannot be considered completely free from salmonellosis for two reasons. Firstly, in both examinations the cloaca swabs were used as the material for isolation and it is known that *Salmonella* rods occurrence in the contaminated birds' faeces may be seasonal [Hafez *et al.* 1997]. Secondly, the culturing methods of microbe identification, especially in carrier state, do not always provide a sufficient level of sensitivity and specificity [Carli *et al.* 2001].

Table 4. Bacteria isolated from reproductive geese flocks in relation to age
Tabela 4. Bakterie izolowane w stadach gęsi reprodukcyjnych w zależności od wieku

	Beak cavity – Jama dziobowa				Cloaca – Kloaka			
	Egg-laying seasons – Sezony nieśności				Egg-laying seasons – Sezony nieśności			
	I	II	III	IV	I	II	III	IV
Escherichia coli	69.38±2.98 *	46.36±2.98 *	56.67 ± 314	53.08±3.12	69.38±2.67	70.00±2.36 *	50.00±3.16 * **	65.38±1.98 **
Proteus spp.	22.5±2.59 *	8.18±0.98 *	10.00±0.63	17.69±2.62	20.63±1.98 *	24.55±1.92 ** ***	5.00±0.55 * **	6.15±0.96 ***
Staphylococcus coagulase-negative	85.63±2.10	89.09±1.04	90.00±1.67	88.46±1.46	86.25±2.33	95.45±0.69 *	91.67±1.17 **	78.46±2.30 * **
Streptococcus spp.	58.75±4.76	77.27±3.9 *	65.00±5.05 *	53.08±4.57	58.13±4.65	79.09±3.7 * **	65.00±5.05 *	55.38±4.93 **
Enterococcus spp.	74.38±2.78	57.27±3.1	56.67±3.5	67.69±1.96	65.63±3.12	70.00±2.14	68.33±2.86	61.54±2.76
Bacillus spp.	0.63±0.25	-	-	1.54±0.55	-	1.81±0.4	-	0.77±0.28
Citrobacter spp.	1.88±0.54	-	1.67±0.41	3.85±0.96	3.75±1.09	-	3.33±0.82	5.38±1.05
Yersinia spp.	1.25±0.34	-	3.33±0.52	0.23±0.6	-	-	3.33±0.82	-
Enterobacter spp.	1.25±0.5	-	-	-	-	-	-	-
Klebsiella spp.	-	-	-	-	0.63±0.25	-	-	-

*p<0.05, **p<0.05, ***p<0.05

Since 1980 there has been an increasing threat to the public health due to *Listeria monocytogenes*, a pathogen transmitted with food, in that of poultry origin as well [Farber and Peterkin 1991, Lawrence and Gilmour 1994]. *Listeria* spp. was regularly detected in the fresh carcasses of various poultry species, among others in France and Belgium at 32% level, Norway 62% [Rørvik *et al.* 2003], while in Bulgaria microbes were identified in muscle tissues and goose liver in 35.7% of the examined samples [Karakolev *et al.* 2003]. Owing to the fact that birds are contaminated mainly through the alimentary tract together with water, soil or vegetation, the present research attempted at microbe isolation from faeces. In the 17 studied reproductive geese flocks no single case of *Listeria* spp. rods recognition was recorded.

The progressing number of the opportunistic infections of man and animal, a matter of primary importance proves to be the qualitative composition of their microflora (a potential reservoir of infections). In birds the spectrum of bacteria most often isolated in their ontocenoses varies and depends on host species to a great measure. The relatively thoroughly known microflora of chicken alimentary tract is composed *E. coli, Enterococcus* spp., *Lactobacillus* spp., *Bacillus* spp., *Clostridium* spp. [Gong *et al.* 2002, Lu *et al.* 2003]. On the other hand, the respiratory system ontocenosis harbored, among others, *Staphylococcus* spp., *Micrococcus* spp., *Escherichia* spp., *Sarcina* spp., *Corynebacterium* spp. [Tankson *et al.* 2002]. The studies on the beak cavity and cloacae microflora of reproductive geese showed that the qualitative bacteria spectrum of both ontocenoses is similar. The following were identified most frequently: *Staphylococcus* spp., *Streptococcus* spp., *Enterococcus* spp., *Escherichia* spp., *Proteus* spp., while *Citrobacter* spp., *Bacillus* spp., *Yersinia* spp., *Klebsiella* spp., *Enterobacter* spp. more rarely.

Although the percentage of every bacteria isolation was variable and depended on age, season and bird breeding conditions, the contribution of the first four species (*Staphylococcus* spp., *Streptococcus* spp., *Enterococcus* spp., *E. coli*) was high enough (>40%) to constitute a permanent potential threat to goose health and indirectly to man.

In recent years there has been noted an increasing share of coagulase-negative species *Staphylococcus* in the disease processes, the species believed to be a commensalic component of the physiological microflora of man and animal. *Staphylococcus lentus, S. sciuri* and *S. gallinarum* were obtained from various types of infections [Adegoke 1986]. *S. lentus*, e.g., a bacteria dominating the turkey alimentary tract [DeBoer *et al.* 2001] being a potential inductor of IL-6 expression by pulmonary macrophages was responsible for the inflammatory responses of the human respiratory system [Larsson *et al.* 1999].

In the chickens subjected to stress some chronic diseases of the respiratory system were recognized as well as endocarditis induced by *Enterococcus faecalis*, a microbe harboured naturally on the ontocenoses of the respiratory and alimentary systems [Tankson *et al.* 1999].

The next component of the geese bacterial microflora isolated in about 50–60% of birds appeared to be *E. coli* strains, which could also include the strains pathogenic for fowl. The APEC strains connected mostly with the diseases of the alimentary tract, respiratory system or sepsis are responsible for the economic losses in bird breeding [La Ragione and Woodward 2002]. There are more and more records on the conversion of so far non-pathogens *E. coli* strains into pathogenic bacteria that as a secondary factor follow a primary bacterial e.g. *Mycoplasma* spp. or viral infection e.g. Newcastle Disease Virus [La Ragione and Woodward 2002]. What is more, *E. coli* strains were isolated in pure culture in over 20% cases of sinus inflammation in breeding geese [Ibrahim *et al.*

2000]. Owing to the endangered public health, special attention should be paid to the reports on isolation of enterohaemorrhagic strains *E. coli* $O_{157}H_7$ from slaughter poultry carcasses [Samadpour *et al.* 1994] and Canadian geese excrements [Kullas *et al.* 2002].

The commensalic bird microflora can comprise a relatively high percentage of antibiotic resistant strains, which mainly refers to breeding species not living free [Baele *et al.* 2002]. The coagulase-negative strains *Staphylococcus* obtained from the alimentary tract of hens may demonstrate resistance to methicillin as well as lowered sensitivity to vancomicin [DeBoer *et al.* 2001]. *Enterococcus* species, *E. faecium* and *E. faecalis* in particular, exhibit resistance to a broad spectrum of antibiotics [Schouten *et al.* 1999]. In Denmark, e.g. in hen, faeces up to 92% of the vancomicin resistant strains were isolated [Bager *et al.* 1997]. Out of *E. coli* strains obtained from the alimentary tract tetracycline resistance was detected in 47% hens and 31% geese [Bryan *et al.* 2004], while the resistance genes established in the strains coming form broiler chickens [Bass *et al.* 1999]. A high percentage of breeding geese, in which *Staphylococcus* spp., *Streptococcus* spp. and *E. coli* were isolated in the present studies, indicates that their microflora may constitute a substantial reservoir of antibiotic-resistant bacterial strains.

It appears from the presented studies that intensive poultry rearing, including geese, providing suitable conditions for the simultaneous horizontal transmission of bacterial strains onto large bird populations requires the most frequent and oriented monitoring of flocks. It would be advisable to apply probiotics more commonly as well as harboring preparations instead of antibiotics often employed in excess.

REFERENCES

Adegoke G.O. 1986. Comparative characteristics of *Staphylococcus sciuri*, *Staphylococcus lentus* and *Staphylococcus gallinarum* isolated from healthy and sick hosts. Vet. Microbiol. 11, 185–189.

Baele M., Devriese L.A., Butaye P., Haesebrouck F., 2002. Composition of enterococcal and streptococcal flora from pigeon intestines. J. Appl. Microbiol. 92, 348–351.

Bager F., Madsen M., Christensen J., Aerestrup F.M. 1997. Avoparcin used as a growth promoter is associated with the occurrence of vancomycin-resistant *Enterococcus faecium* on Danish poultry and pigs farms. Prev. Vet. Med. 31, 95–112.

Bass L., Liebert C.A., Lee M.D., Summers A.D., White D.G., Thayer S.G., Maurer J.J. 1999. Incidence and characterization of integrons, genetic elements mediating multiple-drug resistance in avian Escherichia coli. Antimicrob. Agents Chemother. 43, 2925–2929.

Bielke L.R., Elwood A.L., Donoghue D.J., Donoghue A.M., Newberry L.A., Neighbor N.K., Hargis B.M. 2003. Approach for selection of individual enteric bacteria for competitive exclusion in turkey poults. Poult. Sci. 82, 1378–1382.

Bryan A., Shapir N., Sadowsky M.J. 2004. Frequency and distribution tetracycline resistance genes in genetically diverse, nonselected, and nonclinical *Escherichia coli* strains isolated from diverse human and animal sources. Appl. Environ. Microbiol. 70, 2503–2507.

Cattaneo P., Balzaretti C., Stella S. 2000. Goose meat and products derived from it. Ingegneria Alimentare, Le Conserve Animali 16, 36–40.

DeBoer L.R., Slaughter D.M., Applegate R.D., Sobieski R.J., Crupper S.S. 2001. Antimicrobial susceptibility of staphylococci isolated from the faeces of wild turkeys (*Meleagris gallopavo*). Letters in Appl. Microbiol. 33, 382–386.

Carli K.T., Unal C.B., Caner V., Eyigor A. 2001. Detection of Salmonellae in chicken feces by a combination of tetrathionate broth enrichment, capillary PCR and capillary gel electrophoresis. J. Clin. Microbiol. 39, 1871–1876.

Farber J.M., Peterkin P.I. 1991. *Listeria monocytogenes,* a food-borne pathogen. Microbiol. Rev. 55, 476–511.

Gaweł A., Mazurkiewicz M., Tomczyk G., Bartczak R., Jurowski J. 2001. Ocena stanu zdrowotnego stad reprodukcyjnych gęsi. Medycyna Wet. 57, 335–337.

Gong J., Forster R. J., Yu H., Chambers J. R., Sabour P. M., Wheatcroft R., Chen S. 2002. Diversity and phylogenetic analysis of bacteria in the mucosa of chicken ceca and comparison with bacteria in the cecal lumen. FEMS Microbiol. Lett. 208, 1–7.

Hafez H.M., Stadler A., Kosters J. 1997. Surveillance on *Salmonella* in turkey flocks and processing plants. Dtsch. Tierarztl. Wochenschr. 104, 33–35.

Ibrahim R. S., Sohair, Hussein Z., 2000. Bacterial agents associated with sinusitis in waterfowls and turkeys in Assiut and El-Minia Governorates. Assiut Vet. Med. J. 44, 185–195.

Instrukcja Nr 10/99 Głównego Lekarza Weterynarii, dotycząca diagnostyki laboratoryjnej zakażeń pałeczkami *Salmonella* u drobiu z dnia 21 lipca 1999 r.

Karakolev R., Monov G., Doktorova M., Boteva M., 2003. Findings of *Listeria monocytogenes* in duck and goose meat and liver. Bulgarian J. Vet. Med. 6, 233–236.

Kozak A., Vecerek V., Steinhauserova I., Chloupek P., Pistekova V. 2002. Results of slaughterhouse carcass classification (capable for human consumption, capable for processing and condemned) in selected species of food animals. Vet. Med. 47, 26–31.

Kullas H., Coles M., Rhyan J., Clark L. 2002. Prevalence of *Escherichia coli* serogroups and human virulence factors in faeces of urban Canada geese (*Branta canadensis*). Int. J. Environ. Health Res. 12, 153–162.

La Ragione R.M., Woodward M.J. 2002. Virulence factors of *Escherichia coli* serotypes associated with avian colisepticaemia. Res. Vet. Sci. 73, 27–35.

Larsson B.M., Larsson K., Malmberg P., Palmberg L. 1999. Gram positive bacteria induce IL-6 and IL-8 production in human alveolar macrophages and epithelial cells. Inflammation 23, 217–230.

Lawrence L. M., Gilmour A. 1994. Incidence of Listeria spp. and Listeria monocytogenes in a poultry processing environment and in poultry products and their rapid confirmation by multiplex PCR. Appl. Environ. Microbiol. 60, 4600–4604.

Lis H. 2002. Wyniki badania sanitarno-weterynaryjnego drobiu rzeźnego w Polsce w 2000 r. Medycyna Wet. 58, 112–113.

Lu J., Idris U., Harmon B., Hofacre Ch., Maurer J. J., Lee M. D. 2003. Diversity and succession of the intestinal bacterial community of the maturing broiler chicken. Appl. Environ. Microbiol. 69, 6816–6824.

Mead G. C., 2000. Prospects for 'competitive exclusion' treatment to control salmonellas and other foodborne pathogens in poultry. Vet. J. 159, 111–123.

Panisello P.J., Rooney R., Quantick P.C., Stanwell-Smith R. 2000. Application of foodborne disease outbreak data in the development and maintenance of HACCP system. Int. J. Food Microbiol. 59, 221–234.

Rørvik L.M., Aase B., Alvestad T., Caugant D. A. 2003. Molecular epidemiological survey of *Listeria monocytogenes* in broilers and poultry products. J. Appl. Microbiol. 94, 633–640.

Samadpour M., Ongerth J. E., Liston J., Tran N., Nguyen D., Whittam T.S., Wilson R.A., Tarr P.I. 1994. Occurrence of Shiga-like toxin-producing *Escherichia coli* in retail fresh seafood, beef, lamb, pork and poultry from grocery stores in Seattle, Washington. Appl. Environ. Microbiol. 60, 1038–1040.

Samorek-Salamonowicz E., Czekaj H., Kozdruń W. 1998. Choroby zakaźne występujące u drobiu wodnego. Medycyna Wet. 54, 305–308.

Schouten M.A., Voss A., Hoogkamp-Korstanje J.A. 1999. Antimicrobial susceptibility patterns of enterococci causing infectious in Europe. The European VRE Study Group. Antimicrob. Agents Chemother. 43, 2542–2546.

Tankson J.D., Thaxton J.P., Vizzier-Thaxton Y. 2002. Bacteria in heart and lungs of young chicks. J. Appl. Microbiol. 92, 443–450.

Tankson J.D., Vizzier-Thaxton Y., Thaxton J.P. 1999. Enterococcus faecalis and cardiovascular anomalies in broilers. Poult. Sci. 78 (Suppl.), S48.

Wieliczko A., Mazurkiewicz M. 1995. Choroby bakteryjne drobiu wodnego. Mat. Konf. Nauk. „Choroby gęsi i kaczek" Puławy, pp. 16–25.

STRESZCZENIE

Celem badań było określenie gatunków bakterii występujących w ontocenozach jamy dziobowej i kloaki w stadach gęsi reprodukcyjnych oraz ustalenie ewentualnych zależności spektrum drobnoustrojów od wieku ptaków, warunków środowiska oraz pory roku. Badaniami objęto 17 ferm reprodukcyjnych gęsi rasy biała włoska hodowanych w zróżnicowanych warunkach.

Materiał do badań stanowiły wymazy z jamy dziobowej oraz kloaki (920 próbek). Izolację i identyfikację poszczególnych gatunków bakterii wykonano według klasycznych metod bakteriologicznych z zastosowaniem testów komercyjnych, a uzyskane wyniki poddano analizie statystycznej testem t-Studenta.

Niezależnie od miejsca pobrania materiału (jama dziobowa, kloaka), skład izolowanej flory bakteryjnej stanowiły: *Escherichia coli*, *Proteus* spp., *Staphylococcus* spp., *Streptococcus* spp. i *Enterococcus* spp. Ponadto w pojedynczych przypadkach izolowano *Bacillus* spp., *Citrobacter* spp., *Yersinia* spp., *Enterobacter* spp. oraz *Klebsiella* spp. Częstotliwość występowania poszczególnych gatunków drobnoustrojów zależała głównie od warunków środowiska oraz od wieku badanych ptaków, w mniejszym zaś stopniu od ontocenozy (jama dziobowa, kloaka).

Słowa kluczowe: gęsi, flora bakteryjna, kloaka, jama dziobowa