Microbiological screening of bacterial infections in Russian duck breeding enterprises

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Abstract. One of the factors for the development and spread of antibacterial resistance of bacteria is untimely or incorrectly performed laboratory diagnostics, which results in randomly prescribed antibacterial therapy aimed at containing the infection and ensuring the safety of the livestock. This phenomenon is common in many industrial poultry and livestock enterprises, but at the same time, it is difficult to blame the veterinary service of these farms, since they must ensure safety which sometimes cannot be achieved without antibiotics. The use of advanced microbiological screening of all microbiological risks to which enterprises are exposed is proposed as means of solving the indicated problem. The results of such work done in a number of duck breeding enterprises in Russia, in which at least 192 species of cultivated bacteria are circulated, are presented as an example. Most of the isolated microbes are representatives of the normal or transient flora, but a certain part of the bacteria has an obvious pathogenic or conditionally pathogenic role. From the selected bacteria, we emphasize the relevance of the following pathogens for the duck breeding industry: Bordetella avium, Campylobacter coli, Campylobacter concisus, Campylobacter jejuni, Clostridium colinum, Clostridium perfringens, Myroides odoratimimus, Pasteurella multocida, Riimerella anatipestifer, Salmonella typhimurium, Staphylococcus aureus, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus entericus, Streptococcus gallolyticus, Shigella sonnei, which are typical pathogens of poultry infections. Information from the literature about the remaining bacteria were analyzed and structured in the form of a table with the description of the possible clinical and morphological manifestations of the diseases that they cause.

1. Introduction

The control of bacterial infections is one of the most important tasks for the veterinary service of any livestock or poultry enterprise. Against the background of modern realities, this control should focus not only on ensuring the safety and productivity of the livestock, but also on careful monitoring of the safety of manufactured products. Of course, the mechanism of this work has already been carefully established with respect to some epidemiologically significant pathogens of human infectious pathologies and their toxic infections, in particular, Salmonella sp., Escherichia coli, Listeria monocytogenes, Staphylococcus aureus, but this control is not always enough [1-3]. The widespread and often unreasonable use of antibiotics in industrial poultry and other livestock industries contributes to the formation and spread of bacteria multi-resistance to antibiotics [4-6]. The consequences of this phenomenon are often published in news portals in the form of the reports of...
people deaths due to infectious complications that are not amenable to antibiotic therapy. It should be recognized that it is impossible to avoid and/or prevent the development of resistance, since for bacteria this is a natural evolutionary path [7]. The high degree of resistance of such microorganisms as Pseudomonas, Klebsiella, Pasteurella, Mannheimia, etc., isolated from birds and animals in the Russian Federation, was determined by us earlier, which shows stable dynamics to the multiresistance spread in all sectors of agricultural activity [8-11]. It is also impossible to completely abandon antibiotics. However, this “evolution” can be slowed down. There are several ways to solve this problem:

- prevent infections, including using specific prophylaxis;
- use antibacterial drugs alternative to antibiotics, such as organic acids, bacteriophages, probiotics with antagonistic properties;
- improve laboratory diagnostic methods used in the diagnosis, before prescribing antibiotic therapy.

The last way, in our opinion, is so far more realistic in execution in comparison with the first two. Since vaccines against the large number of bacterial species have not been developed or registered and alternative to antibiotics preparations often cannot demonstrate the desired effect (for example, with respiratory and septic infections). That is why more advanced laboratory diagnostic methods or approaches to diagnosing bacterial infections make it possible to rationalize the tactics of antibacterial therapy during outbreaks of infections. This way has its drawbacks, in particular, a number of regulatory documents governing the conduct of certain studies are missing or existing regulations require updating. In the fight against bacterial pathologies, it is worth taking into account such important factors as the intensity of reproduction, as well as the introduction of infections due to newly imported livestock or breeding material. In this case, the quarantine of animals is mainly aimed at identifying especially dangerous diseases or infected animals, which during the furlough period will show clinical signs of pathology. But a number of factor infections will not be detected in this way, since for them there is a dependence on the presence of certain trigger mechanisms. In order to effectively deal with these problems, it is necessary to broaden the horizons of veterinary and laboratory specialists regarding the possible microbiological risks to which their enterprises are exposed [12]. The use of only routine bacteriological methods for diagnosis is often not enough to obtain the correct result, since these methods are limited. For example, identification of microorganisms with commercial biochemical kits is possible only for a small number of species, which in turn are primarily of medical importance. In addition, biochemical identification will not be effective in differentiating closely related bacterial species. The purpose of this investigation was to study the current epizootological situation, using the industrial duck breeding enterprises of Russia as an example, through expanded microbiological screening using modern diagnostic methods and approaches.

2. Materials and methods
The scientific work was performed in the period of 2016-2019 on the basis of Federal State Budget Scientific Institution “Federal Scientific Centre VIEV” (FSC VIEV).

To achieve this goal, 120 heads of birds under the age of 4 weeks (10 birds from each enterprise) from 12 duck breeding enterprises of various regions of Russia, namely the Krasnodar Krai, Altai Krai, the Republics of Bashkortostan, Chuvashia and Tatarstan, Orenburg, Rostov, Ryazan, Tambov, Astrakhan, Nizhny Novgorod and Kurgan regions, was subjected to a comprehensive laboratory diagnosis. The enterprises from which the birds were obtained for this study will remain anonymous. The bird was delivered to the laboratory as a whole carcass, and the autopsy and selection of pathological material was carried out already in place. For the study, the following samples were taken from each bird: intestine, liver, lungs, oviducts, heart.
Bacteriological studies, as well as the study of the morphological, tinctorial, cultural, pathogenic and serological properties of microorganisms isolates, were carried out in the Microbiology Laboratory with the Museum of Typical Cultures of FSC VIEV and on the experimental base on Lisy Island, Vyshnevolotsky District, Tver Region.

During performing scientific work, we used: Collection and museum strains of bacteria from the collection of the FSC VIEV; reference cultures for monitoring culture media and diagnostics. Differential diagnostic and elective culture media. Complex bacteriological diagnostics was carried out using the following solid nutrient media: Bile Esculin Agar (Modified), MacCo nkey Agar, Phenol Red Agar, Columbia Agar, Brain Heart Infusion, Trypticase Soy Agar, Meat Peptone Agar, Cystine Tryptone Agar, Tryptone Soy Agar; as well as using the following broth media: Nitrate Broth, Trypticase Soy Broth, Andrade Peptone Water, Tryptone Soy Broth, Meat Peptone Broth, Hottinger Broth from “Himedia” (India) and “Oxoid” (UK) companies. Species identification of microorganisms was carried out using MALDI-ToF analysis. Additionally, to study the proteolytic and saccharolytic properties of bacteria isolates with the aim of their generic and specific identification, Hiss media with carbohydrates: adonite, arabinose, galactose, D-glucose, dulcite, inositol, inulin, xylose, maltose, mannitol, mannose, raffinose, rhamnose, salicit, sorbitol, sucrose, trehalose, fructose, cellobiose from "Himedia" company (India) were used.

3. Results and discussion

The results of microbiological screening are shown in table 1.

| №  | Diagnostic result / Total number of isolates | Intestines % | Liver % | Lungs % | Oviduct % | Heart % |
|----|------------------------------------------|--------------|--------|--------|-----------|--------|
| 1  | Acinetobacter baumannii / 9              | 22.22        | 66.67  | 0.00   | 11.11     | 0.00   |
| 2  | Acinetobacter johnsonii / 4              | 50.00        | 50.00  | 0.00   | 0.00      | 0.00   |
| 3  | Acinetobacter 1wofii / 24                | 12.50        | 29.17  | 12.50  | 45.83     | 0.00   |
| 4  | Acinetobacter pittii / 3                 | 66.67        | 33.33  | 0.00   | 0.00      | 0.00   |
| 5  | Acinetobacter ursingii / 8               | 25.00        | 25.00  | 12.50  | 25.00     | 12.50  |
| 6  | Actinobacillus ureae / 17                | 0.00         | 5.88   | 35.29  | 58.82     | 0.00   |
| 7  | Actinomyces odontolyticus / 2            | 0.00         | 50.00  | 50.00  | 0.00      | 0.00   |
| 8  | Aerococcus urinae / 24                   | 4.17         | 12.50  | 29.17  | 41.67     | 12.50  |
| 9  | Aerococcus vaginalis / 6                 | 0.00         | 50.00  | 16.67  | 33.33     | 0.00   |
| 10 | Aerococcus viridans / 24                 | 0.00         | 12.50  | 62.50  | 12.50     | 12.50  |
| 11 | Aeromonas hydrophila / 30                | 60.00        | 40.00  | 0.00   | 0.00      | 0.00   |
| 12 | Aeromonas salmonicida / 11               | 54.55        | 27.27  | 0.00   | 18.18     | 0.00   |
| 13 | Aggregatibacter                        | 100.00       | 0.00   | 0.00   | 0.00      | 0.00   |
|    | actinomycetemcomitans / 3               |              |        |        |           |        |
| 14 | Alcaligenes faecalis / 3                | 33.33        | 33.33  | 33.33  | 0.00      | 0.00   |
| 15 | Arcanobacterium haemolyticum / 22        | 0.00         | 0.00   | 22.73  | 50.00     | 27.27  |
| 16 | Bacillus amyloiquefaciens / 4            | 50.00        | 50.00  | 0.00   | 0.00      | 0.00   |
| 17 | Bacillus asahii / 4                     | 50.00        | 50.00  | 0.00   | 0.00      | 0.00   |
| 18 | Bacillus beijingensis / 7                | 42.86        | 28.57  | 0.00   | 28.57     | 0.00   |
| 19 | Bacillus cereus / 18                     | 66.67        | 22.22  | 5.56   | 5.56      | 0.00   |
| 20 | Bacillus licheniformis / 13              | 61.54        | 30.77  | 0.00   | 7.69      | 0.00   |
| 21 | Bacillus subtilis / 9                    | 33.33        | 66.67  | 0.00   | 0.00      | 0.00   |
| 22 | Bacillus thermoamylovoranor / 2          | 50.00        | 0.00   | 0.00   | 50.00     | 0.00   |
| 23 | Bacillus thuringiensis / 10              | 20.00        | 30.00  | 50.00  | 0.00      | 0.00   |
| 24 | Bacteroides fragilis / 13                | 53.85        | 46.15  | 0.00   | 0.00      | 0.00   |
| 25 | Bordetella avium / 5                     | 0.00         | 20.00  | 40.00  | 0.00      | 40.00  |
| 26 | Branhamella catarrhalis / 3              | 0.00         | 0.00   | 100.00 | 0.00      | 0.00   |
| 27 | Brevibacterium casei / 13                | 7.69         | 15.38  | 15.38  | 38.46     | 23.08  |
| 28 | Brevundimonas diminuta / 11              | 0.00         | 54.55  | 9.09   | 36.36     | 0.00   |
29. Burkholderia cenocepacia / 11 0,00 9,09 81,82 9,09 0,00
30. Burkholderia cepacia / 8 12,50 0,00 25,00 37,50 25,00
31. Campylobacter coli / 5 80,00 20,00 0,00 0,00 0,00
32. Campylobacter concisus / 1 100,00 0,00 0,00 0,00 0,00
33. Campylobacter jejuni / 9 100,00 0,00 0,00 0,00 0,00
34. Chromohalobacter beijerinckii / 1 0,00 0,00 0,00 0,00 100,00
35. Chryseobacterium endophyticum / 9 0,00 0,00 44,44 22,22 33,33
36. Chryseobacterium hominis / 7 0,00 14,29 42,86 14,29 28,57
37. Citrobacter braakii / 6 83,33 16,67 0,00 0,00 0,00
38. Citrobacter diversus / 10 60,00 40,00 0,00 0,00 0,00
39. Citrobacter freundii / 5 60,00 40,00 0,00 0,00 0,00
40. Citrobacter sedlakii / 14 28,57 21,43 28,57 21,43 0,00
41. Clostridium baratii / 1 0,00 100,00 0,00 0,00 0,00
42. Clostridium bif ermentans / 16 43,75 56,25 0,00 0,00 0,00
43. Clostridium colinum / 4 75,00 25,00 0,00 0,00 0,00
44. Clostridium difficile / 9 88,89 11,11 0,00 0,00 0,00
45. Clostridium perfringens / 56 44,64 55,36 0,00 0,00 0,00
46. Clostridium ramosum / 3 66,67 33,33 0,00 0,00 0,00
47. Clostridium septicum / 9 55,56 44,44 0,00 0,00 0,00
48. Clostridium sordellii / 4 75,00 25,00 0,00 0,00 0,00
49. Clostridium sporogenes / 13 38,46 61,54 0,00 0,00 0,00
50. Corynebacterium cystitidis / 1 0,00 0,00 100,00 0,00 0,00
51. Corynebacterium durum / 5 20,00 20,00 20,00 20,00 20,00
52. Corynebacterium xerosis / 17 0,00 58,82 0,00 35,29 5,88
53. Elizabethkingia meningoseptica / 8 12,50 25,00 25,00 12,50 25,00
54. Enterobacter asburiae / 3 33,33 33,33 33,33 0,00 0,00
55. Enterobacter cancerogenus / 17 29,41 41,18 11,76 11,76 5,88
56. Enterobacter cloacae / 30 33,33 26,67 23,33 10,00 6,67
57. Enterobacter cowanii / 3 33,33 33,33 0,00 33,33 0,00
58. Enterococcus asini / 2 0,00 100,00 0,00 0,00 0,00
59. Enterococcus avium / 8 37,50 50,00 0,00 0,00 12,50
60. Enterococcus casseliflavus / 4 25,00 0,00 0,00 75,00 0,00
61. Enterococcus columbae / 8 12,50 12,50 12,50 50,00 12,50
62. Enterococcus durans / 32 25,00 21,88 6,25 43,75 3,13
63. Enterococcus faecalis / 20 45,00 20,00 10,00 20,00 5,00
64. Enterococcus faecium / 40 37,50 35,00 5,00 20,00 2,50
65. Enterococcus gallinarum / 25 32,00 44,00 4,00 20,00 0,00
66. Enterococcus hirae / 23 13,04 8,70 17,39 0,00 60,87
67. Enterococcus plantarum / 5 20,00 60,00 0,00 0,00 20,00
68. Escherichia coli / 172 46,51 39,53 4,65 8,72 0,58
69. Escherichia fergusoni / 8 62,50 12,50 0,00 25,00 0,00
70. Escherichia harnannii / 13 38,46 38,46 0,00 7,69 15,38
71. Facklamia sourekii / 7 0,00 14,29 0,00 57,14 28,57
72. Flavobacterium aquatilis / 16 18,75 37,50 25,00 12,50 6,25
73. Fusobacterium necrophorum / 16 43,75 56,25 0,00 0,00 0,00
74. Fusobacterium nucleatum / 5 40,00 60,00 0,00 0,00 0,00
75. Gemella haemolytica / 1 0,00 0,00 0,00 100,00 0,00
76. Klebsiella mobilis / 13 15,38 7,69 69,23 7,69 0,00
77. Klebsiella oxytoca / 14 64,29 28,57 7,14 0,00 0,00
78. Klebsiella pneumonia / 8 37,50 37,50 12,50 12,50 0,00
79. Klebsiella varicella / 7 42,86 0,00 14,29 42,86 0,00
80. Kocuria rosea / 12 25,00 33,33 8,33 33,33 0,00
81. Kyococcus shoereteri / 3 0,00 33,33 0,00 33,33 33,33
82. Kyococcus sedentarius / 7 14,29 57,14 14,29 14,29 0,00
83. Lactobacillus sakei / 25 40,00 52,00 4,00 4,00 0,00
84. Lactobacillus salivarius / 9 88,89 11,11 0,00 0,00 0,00
| Microorganism                          | Percent (%) | Number |
|---------------------------------------|-------------|--------|
| Lactococcus lactis                    | 41.18       |        |
| Lelliottia ammigena                   | 50.00       |        |
| Leminorella richardi                 | 25.00       |        |
| Listeria innocua                      | 0.00        |        |
| Lysinibacillus sphaericus            | 33.33       |        |
| Macroccocus caroucelicus             | 25.00       |        |
| Macroccocus caseolyticus             | 28.57       |        |
| Microccocus cohnii                    | 18.18       |        |
| Microccocus flavus                    | 9.09        |        |
| Microccocus luteus                    | 4.00        |        |
| Microccocus lyiae                     | 14.29       |        |
| Moraxella caprae                      | 25.00       |        |
| Moraxella lacunata                   | 0.00        |        |
| Morganella morgani                   | 33.33       |        |
| Myroides odoratimimus                | 0.00        |        |
| Neisseria bacilliformis              | 0.00        |        |
| Nocardiosis alba                     | 0.00        |        |
| Oligella ureolytica                   | 0.00        |        |
| Paenibacillus amylolyticus           | 25.00       |        |
| Pantoea agglomerans                  | 42.86       |        |
| Pantoea septica                      | 75.00       |        |
| Pasteurella aerogenes                 | 0.00        |        |
| Pasteurella multocida                 | 0.00        |        |
| Pediococcus argentinicus             | 40.00       |        |
| Pediococcus pentosaceus              | 27.27       |        |
| Peptococcus simiae                   | 100.00      |        |
| Plesiomonas shigelloides             | 62.50       |        |
| Porphyromonas gingivalis             | 100.00      |        |
| Pragia fontium                       | 44.44       |        |
| Prevotella aurantiaca                | 50.00       |        |
| Prevotella copri                      | 33.33       |        |
| Prevotella intermedia                | 50.00       |        |
| Prevotella oralis                    | 50.00       |        |
| Prevotella oris                      | 69.23       |        |
| Propionibacterium acnes              | 0.00        |        |
| Proteus mirabilis                    | 30.56       |        |
| Proteus penneri                      | 50.00       |        |
| Proteus vulgaris                     | 63.16       |        |
| Providencia alcalifiaciens           | 22.22       |        |
| Pseudomonas aeruginosa               | 43.75       |        |
| Pseudomonas flavescens               | 70.00       |        |
| Pseudomonas marginalis               | 33.33       |        |
| Pseudomonas putida                   | 52.94       |        |
| Pseudomonas taetrolens               | 40.00       |        |
| Raoultella planticola                | 75.00       |        |
| Riemerella antitasiifera             | 0.00        |        |
| Riemerella columbica                 | 0.00        |        |
| Rothia endophytica                   | 0.00        |        |
| Rothia nasimurium                    | 0.00        |        |
| Salimicrobium halophilum             | 20.00       |        |
| Salmonella typhimurium               | 55.56       |        |
| Serratia marcescens                 | 42.86       |        |
| Serratia plymuthica                  | 100.00      |        |
| Shigella boydii                      | 66.67       |        |
| Shigella sonnei                       | 57.14       |        |
| Staphylococcus agnetis               | 28.57       |        |
As can be seen from the data presented in table 1, the species composition of bacterial agents, isolated from waterfowl which bred under industrial conditions in various regions of the Russian...
Federation, is represented by at least 192 species of cultivated bacteria, isolated from various parenchymal organs and tissues of the bird, belonging to 75 different genera which in turn belong to 37 different families, namely (the number of species of the designated genus is indicated in parentheses): Actinomycetaceae (3) – Actinomyces, Arcanobacterium, Trueperella; Aerococcaceae (2) – Aerococcus, Facklamia; Aeromonadaceae (1) – Aeromonas; Alcaligenaceae (3) – Alcaligenes, Bordetella, Oligella; Bacillaceae (3) – Bacillus, Lysinibacillus, Salimicrobium; Bacteroidaceae (1) – Bacteroides; Brevibacteriaceae (1) – Brevibacterium; Burkholderiaceae (1) – Burkholderia; Campylobacteraceae (1) – Campylobacter; Caulobacteraceae (1) – Brevundimonas; Clostridiaceae (1) – Clostridium; Corynebacteriaceae (1) – Corynebacterium; Dermacoccaceae (1) – Kyctococcus; Enterobacterales (1) – Lelliottia; Enterobacteriaceae (16) – Citrobacter, Enterobacter, Escherichia, Klebsiella, Leminorella, Morganella, Pantoea, Pragia, Plesiomonas, Proteus, Providencia, Raoulattles, Salmonella, Serratia, Shigella, Yersinia; Enterococccaceae (2) – Enterococcus, Vagococcus; Flavobacteriaceae (5) – Chryseobacterium, Elizabethkingia, Flavobacterium, Myroides, Riemerella; Fusobacteriaceae (1) – Fusobacterium; Halomonadaceae (1) – Chromohalobacter; Lactobacillaceae (2) – Lactobacillus, Pediococcus; Listeriaceae (1) – Listeria; Lysobacteraceae (1) – Stenotrophomonas; Micrococcaceae (3) – Kocuria, Micrococcus, Rothia; Moraxellaceae (3) – Acinetobacter, Branhamella, Moraxella, Neisseriaceae (1) – Neisseria; Nocardiopsaceae (1) – Nocardiosis; Paenibacillaceae (1) – Paenibacillus; Pasteurellaceae (3) – Actinobacillus, Aggregatibacter, Pasteurella; Peptococcaceae (1) – Peptococcus; Porphyromonadaceae (1) – Porphyromonas; Prevotellaceae (1) – Prevotella; Propionibacteriaceae (1) – Propionibacterium; Pseudomonasaceae (1) – Pseudomonas; Staphylococcaceae (2) – Staphlococcus, Staphylococcus, Streptococcaceae (2) – Lactococcus, Streptococcus; Streptomyctecae (1) – Streptomyces; Veillonellaceae (1) – Veillonella, as well as genera of an undefined by classifier family (namely: Family unassigned (2) - Gemella, Tissierella). Some isolates of these microorganisms are stored in the collection of the institute for further study.

Figure 1. Graphic reflection of the results of the generic determination of bacterial microflora in various organs and tissues of waterfowl contained in industrial environment.
According to the data shown in table 1, the maximum number of bacterial species was isolated from samples of the studied liver, the value of this indicator was 158 species. A slightly smaller number of microorganisms species was isolated from the digestive system of birds - 142 species. 109 types of bacteria were isolated from oviducts and 97 species from lung tissue. The smallest species composition was determined in the heart muscle, namely 68 species. It is worth noting here that as a result of the work done, it is possible to analyze data only on cultivated types of bacterial agents, therefore, this bacterial composition of various organs and tissues of the bird’s organism cannot be considered complete, and for the full disclosure of the microbiome it is necessary to use molecular biological methods, in particular metagenomic analysis. For clarity, data on the excretion of various genera of bacterial agents isolated from different organs and tissues of waterfowl were reflected in the form of graphic figure 1. Figure 1 indicates that the main bacterial flora isolated from the studied samples turned out to be coccal microorganisms of the genera Staphylococcus, Enterococcus, Streptococcus, as well as enterobacteria Escherichia, spore-forming bacteria of the genus Clostridium, etc. Despite the high incidence of the isolation of these bacteria, we cannot confirm their participation in the development of infectious pathologies of birds, since most of the isolated bacteria species are representatives of normal or transient flora.

The full structure of the microbiome of various organs and tissues of the bird (by family), defined in the framework of the study, is shown in figures 2-6.
According to the data reflected in graphic figures 2-6, the following conclusions can be made:

In the structural composition of bacterial agents located in the intestines of waterfowl, the Enterobacteriaceae family prevails, the percentage of which was 34.22 %; then, by the incidence of excretion, bacteria of the Staphylococcaceae family were found to be 11.56 %; anaerobic microorganisms of the Clostridiaceae family were in third place by excretion – 9.06 %; the following place in the overall structure was occupied by microorganisms of the Enterococcaceae family – 7.66 %; Bacillaceae – 5.94 %; Pseudomonadaceae and Streptococcaceae – 4.22 %; Aeromonadaceae – 3.75 %; Lactobacillaceae – 3.59 %; Prevotellaceae – 2.97 %; Campylobacteraceae – 2.19 %; Moraxellaceae – 1.88 %; Micrococcaceae – 1.72 %; Fusobacteriaceae – 1.42 %; Bacteroidaceae – 1.09 %; Lysobacteraceae – 0.78 %; Flavobacteriaceae – 0.63 %; Paenibacillaceae, Pasteurellaceae and bacteria of indefinite families – 0.47 %; Enterobacterales – 0.31 %, as well as Aerococcaceae.
Alcaligenaceae, Brevibacteriaceae, Burkholderiaceae, Corynebacteriaceae, Dermacoccaceae, Peptococcaceae, Porphyromonadaceae, Veillonellaceae – 0.16 %, respectively.

**Figure 6.** Graphic reflection of the structure of bacterial microflora isolated from the heart of waterfowl contained in industrial enterprises.

In the structural composition of bacterial agents located in the liver of waterfowl, the Enterobacteriaceae family prevails, the percentage of which was 27.60 %; then, by the incidence of excretion, bacteria of the Staphylococcaceae family were found to be 10.88 %; anaerobic microorganisms of the Clostridiaceae family were in third place by excretion – 8.99 %; the following place in the overall structure was occupied by microorganisms of the Enterococcaceae family – 7.73 %; Streptococcaceae – 6.78 %; Bacillaceae – 4.57 %; Micrococcaceae – 3.94 %; Lactobacillaceae and Moraxellaceae – 3.00 %; Pseudomonadaceae – 2.84 %; Prevotellaceae – 2.52 %; Aeromonadaceae – 2.37 %; Flavobacteriaceae – 2.21 %; Fusobacteriaceae – 1.89 %; Corynebacteriaceae – 1.74 %; Aerococcaceae – 1.58 %; bacteria of undefined families (Family unassigned) – 1.26 %; Paenibacillaceae – 1.10 %; Bacteroidaceae and Caulobacteraceae – 0.95 %; Dermacoccaceae and Lysobacteraceae – 0.79 %; Alcaligenaceae, Pasteurellaceae and Veillonellaceae – 0.47 %, Brevibacteriaceae – 0.32 %; Actinomycetaceae, Burkholderiaceae, Campylobacteraceae, Listeriaceae and Propionibacteriaceae – 0.16 %, respectively.

In the structural composition of bacterial agents located in the lungs of waterfowl, the Flavobacteriaceae family prevails – 15.90 %; Streptococcaceae – 11.56 %; Enterobacteriaceae – 11.27 %; Micrococcaceae – 9.54 %; Staphylococcaceae – 8.96 %; Aerococcaceae – 6.65 %; Pasteurellaceae – 5.20 %; Actinomycetaceae – 4.91 %; Streptomycetaceae – 4.62 %; Enterococcaceae – 4.34 %; Burkholderiaceae and Moraxellaceae – 3.18 %; Bacillaceae – 2.31 %; Lysobacteraceae – 2.02 %; Nocardiopsaceae – 1.16 %; Alcaligenaceae and Lactobacillaceae – 0.87 %; Brevibacteriaceae, Corynebacteriaceae, Neisseriaceae and Pseudomonadaceae – 0.58 %; Caulobacteraceae, Dermacoccaceae, Paenibacillaceae and Veillonellaceae – 0.29 %, respectively.

In the structural composition of bacterial agents located in the oviduct of waterfowl, the Enterobacteriaceae family prevails – 13.69 %; Enterococcaceae and Staphylococcaceae – 12.10 %; Streptococcaceae – 11.46 %; Micrococcaceae – 7.01 %; Actinomycetaceae – 6.37 %; Aerococcaceae – 6.05 %; Moraxellaceae – 5.73 %; Flavobacteriaceae – 4.14 %; Pasteurellaceae – 3.18 %; Bacillaceae – 2.78 %; Lysobacteraceae – 2.55 %; Corynebacteriaceae – 2.23 %; Pseudomonadaceae – 1.91 %; Brevibacteriaceae – 1.59 %; Burkholderiaceae, Caulobacteraceae and Lactobacillaceae – 1.27 %; Aeromonadaceae and Dermacoccaceae – 0.64 %; Alcaligenaceae, Enterobacteriales, bacteria of
undefined families (Family unassigned), Paenibacillaceae, Propionibacteriaceae and Veillonellaceae – 0.32 %, respectively.

In the structural composition of bacterial agents located in the heart of waterfowl, the Flavobacteriaceae family prevails – 28.85 %; Enterococcaceae – 13.94 %; Streptococcaceae – 13.46 %; Actinomycetaceae – 10.59 %; Enterobacteriaceae – 5.29 %; Micrococcaceae – 4.81 %; Staphylococcaceae – 4.33 %; Aerococcaceae – 3.85 %; Pasteurellaceae – 2.88 %; Alcaligenaceae, Brevibacteriaceae, Moraxellaceae and Veillonellaceae – 1.44 %; Burkholderiaceae, Corynebacteriaceae and Lysobacteraceae – 0.96 %; Dermacoccaceae, Enterobacterales, Halomonadaceae, Lactobacillaceae, Listeriaceae, Neisseriaceae, Pseudomonadaceae – 0.48 %, respectively.

To summarize the data obtained during bacteriological screening and analysis of literature, we compiled a table describing the possible forms and signs of the manifestation of an infectious disease in birds, manifested by various types of microorganisms (table 2). The summary table shows information on the most significant bacterial pathogens for poultry farming.

As can be seen from the data shown in table 2, bacterial isolates are able to provoke the development of many different clinical signs of diseases, both in the form of monoinfection and associated pathologies.

**Table 2.** Forms and signs of the manifestation of infectious pathologies in birds caused by various types of microorganisms (according to the literature data of domestic and foreign experts).

| Form of manifestation | Abscesses | Bacteremia | Septicemia | Dermatitis | Diarrhea | Conjunctivitis | Osteomyelitis | Otitis | Pericarditis | Omphalitis | Peritonitis | Pneumonia | Polyarthritis | Pharyngitis | Endocarditis | Enteritis | Cloacitis |
|-----------------------|----------|------------|------------|------------|----------|----------------|---------------|--------|--------------|-------------|--------------|-----------|----------------|--------------|--------------|-------------|-----------|
| Actinobacillus ureae  | +        | +          | +          | +          | +        | +              | +             | +      | +            |             | +            | +         | +              | +            | +            | +           | +         |
| Aeromonas hydrophila  | +        | +          |            | +          |          | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Aeromonas salmonicida| +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Aggregatibacter       | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| actinomycetemcomitans| +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Arcanobacterium       | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| haemolyticum          | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Brevibacterium casei  | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Campylobacter coli    | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Campylobacter jejuni  | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Citrobacter braakii   | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Citrobacter diversus  | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Citrobacter freundii  | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Citrobacter sedlakii  | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Clostridium colinum   | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Clostridium perfringens| +       | +          |            |            | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Clostridium sordellii | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Corynebacterium xerosis| +      | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Enterobacter cloacae  | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Enterococcus avium    | +        | +          |            |            | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Enterococcus gallinarum| +      | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Enterococcus hirae    | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Escherichia coli       | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Klebsiella oxytoca    | +        | +          | +          | +          | +        | +              |               | +      | +            |             | +            |           | +              |             | +            | +           | +         |
| Microorganism                                      | + | + | + | + | + |
|--------------------------------------------------|---|---|---|---|---|
| Klebsiella pneumonia                             |   |   |   |   |   |
| Leminorella richardi                             |   | + |   |   |   |
| Moraxella lacunata                               |   |   |   |   |   |
| Myroides odoratimimus                            | + |   | + |   |   |
| Pasteurella multocida                            |   | + |   | + | + |
| Proteus mirabilis                                |   | + |   | + |   |
| Proteus vulgaris                                 |   | + |   | + |   |
| Providencia alcalifaciens                        |   |   |   | + |   |
| Pseudomonas aeruginosa                           | + | + | + |   | + |
| Pseudomonas putida                               |   | + |   |   |   |
| Riemerella anatipestifer                         | + | + | + | + |   |
| Riemerella columbina                             |   | + |   |   |   |
| Salmonella typhimurium                           | + |   | + |   | + |
| Serratia marcescens                              | + | + | + | + | + |
| Staphylococcus aureus                            | + | + | + | + | + |
| Staphylococcus epidermidis                       | + | + |   |   |   |
| Staphylococcus haemolyticus                      | + | + | + | + | + |
| Staphylococcus sciuri                            | + |   |   |   | + |
| Streptococcus agalactiae                         | + | + |   |   | + |
| Streptococcus anginosus                          | + | + |   |   | + |
| Streptococcus galloyticus                        | + |   |   |   | + |
| Streptococcus mitis                              |   |   |   |   | + |
| Streptococcus pneumoniae                         | + |   | + | + | + |
| Trueperella pyogenes                             | + | + | + | + | + |
| Yersinia enterocolitica                          |   | + |   |   |   |

4. Conclusion
The obtained results indicate that the use of modern laboratory diagnostic tools such as MALDI-ToF mass spectrometric analysis allows microorganisms to be identified with high reliability, thereby increasing the effectiveness of subsequent treatment and prophylactic measures. The use of exclusively routine methods of bacteriology is not enough in the fight against the development and spread of antibiotic resistance. Thanks to a comprehensive laboratory diagnosis and the use of modern means of identification, we were able to discover wide range of microorganisms circulating in duck breeding enterprises of Russia. All types of bacteria that we have identified can be divided into various functional groups, such as: 1) the causative agents of the infectious pathologies of birds, including waterfowl: Bordetella avium, Campylobacter coli, Campylobacter jejuni, Clostridium colinum, Clostridium perfringens, Myroides odoratimimus, Pasteurella multocida, Riemerella anatipestifer, Salmonella typhimurium, Staphylococcus aureus, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus entericus, Streptococcus galloyticus, Shigella sonnei [13-17]. Some of these species are also causative agents of human toxic infections; 2) pathogens of nosocomial infections in humans, which include bacteria of the genera Acinetobacter, Pseudomonas, Klebsiella, Staphylococcus - which are most often multiresistant; 3) opportunistic and transient microorganisms - the remaining species.

Of course, this gradation is not universal, and in each individual case it is necessary to deal with it individually, including through the use of the data shown in table 2, where it is clearly seen that the same clinical manifestations of infections can be provoked by many types of bacteria. Thus, we
showed the real possibilities of laboratory diagnostic studies, which should be implemented as part of internal and state control at industrial poultry and livestock enterprises.

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