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Pathogenic potential of ornithogenic *Escherichia coli* strains detected in the Earth's polar regions

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Abstract

Introduction. Pathogenic strains of *Escherichia coli* are an important object of surveillance within the One Health concept in the wild, agriculture and human society.

Migratory bird colonies and high latitude avian colonies may be points of active intraspecies and interspecies contact between different animal species, accompanied by the spread of pathogens. At the same time, the phylogeography of *E. coli* in relation to the presence of natural foci of colibacillosis in polar regions remains virtually unstudied.

The aim of this study was to assess the pathogenic potential of *E. coli* strains from the polar regions of the Earth, based on the analysis of the genomes of these bacteria from typical ornithogenic ecosystems of the Arctic and Antarctic.

Materials and methods. The study used collections of *E. coli* isolated from ornithogenic biological material during expeditions to high latitude areas of the Arctic (archipelagos of Novaya Zemlya, Franz Josef Land, Svalbard) and Antarctic (Haswell Archipelago). 16 cultures associated with avian *E. coli* (12 polar and 4 temperate strains) were selected for genome-wide sequencing using BGI technology. The annotation of the genomes focused on the identification of genes for pathogenicity factors and antimicrobial resistance, as well as the identification of strains belonging to individual genetic lineages using the cgMLST method.

Results. The annotation of the genomes allowed their assignment to different sequence types in the multilocus sequencing typing and genome-wide sequencing typing schemes. The analysis of the geographical distribution of the sequence types of polar *E. coli* strains determined by the cgMLST method showed their global representation in geographically distant regions of the planet. For example, cgST 133718 was observed in Antarctica (strain 17_1myr) and in the UK, and sequence 11903, to which strain 32-1 from the northernmost point of Novaya Zemlya belonged, was previously identified in the USA.

All strains studied were characterized by the presence of extensive virulence. Among the pathogenicity factors identified were haemolysins A, E, F, siderophores, including the yersiniabactin gene cluster, a number of adhesion, colonization and invasion factors, as well as the thermostable enterotoxin EAST-1 and genes that characterize enteroaggregative strains of *E. coli* (the virulence regulator gene *eilA* and enteroaggregative protein (air)). One of the Arctic strains (33-1) had determinants of antibiotic resistance, in particular the extended-spectrum beta-lactamase gene TEM-1b and the Tn1721 transposon, including tetracycline resistance genes (tetA-TetR), were detected in its genome.

Conclusion. The results of the study indicate the circulation of *E. coli* strains with strong pathogenic potential in high-latitude Arctic and Antarctic ornithogenic ecosystems. The analysis of genomic data indicates the presence of geographically widespread genetic lineages in these regions, which justifies the importance of monitoring epidemic clones of *E. coli*, along with monitoring for other pathogens, in bird colonies in high-latitude areas.

Keywords: *Arctic, Antarctica, Escherichia coli, genome sequencing, pathogenicity factors, ornithogenic ecosystems*

Ethics approval. The procedure of biological material sampling was carried out in accordance with generally accepted ethical normsю The research protocol was approved by the Ethics Committee of the which is confirmed by the decision of the Local Ethics Committee of North-Western State Medical University named after I.I. Mechnikov (Protocol No. 3, March 13, 2024).

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Оригинальное исследование
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Патогенный потенциал орнитогенных штаммов *Escherichia coli*, выявленных в полярных регионах Земли

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Аннотация

Введение. Патогенные штаммы *Escherichia coli* являются важным объектом мониторинга в природе, сельском хозяйстве и человеческом обществе в рамках концепции «Единого здоровья». Колонии мигрирующих птиц и птичьи базары в высоких широтах могут быть точками активных внутривидовых и межвидовых контактов между различными видами животных, сопровождающихся распространением микроорганизмов. В то же время филогеография *E. coli* в контексте наличия природных очагов колибактериозов в полярных регионах практически не изучалась.

Цель работы: оценка патогенного потенциала штаммов *E. coli*, распространённых в полярных регионах Земли, на основе анализа геномов данных бактерий из выборки, характеризующей типичные орнитогенные экосистемы Арктики и Антарктики.

Материалы и методы. В работе были использованы штаммы *E. coli*, выделенные из орнитогенного биологического материала в ходе экспедиций на высокоширотные территории Арктики (архипелаги Новая Земля, Земля Франца-Иосифа, Шпицберген) и Антарктики (архипелаг Хасуэлл). Из них 16 штаммов, ассоциированных с птицами (12 полярных штаммов и 4 штамма, выделенных в умеренных широтах), были отобраны для полногеномного секвенирования с использованием технологии BGI. Аннотирование геномов было сфокусировано на идентификации генов, кодирующих факторы патогенности и устойчивости к антимикробным препаратам, а также на определении принадлежности штаммов к отдельным серотипам и генетическим линиям, в том числе на основе использования метода cgMLST.

Результаты. Проведённое аннотирование геномов *E. coli* позволило установить их принадлежность к различным сиквенс-типам в схемах мультилокусного секвенирования-типирования и полногеномного секвенирования-типирования. Анализ географического распространения сиквенс-типов «полярных» штаммов *E. coli*, определённых методом cgMLST, продемонстрировал их глобальную представленность. Так, например, cgST 133718 был отмечен в Антарктиде (штамм 17_1myr) и ранее — в Великобритании, а сиквенс-тип 11903, к которому принадлежал штамм 32-1 из самой северной точки Новой Земли, был ранее выявлен в США. Все изученные штаммы характеризовались наличием обширного вирулома. В числе выявленных генов факторов патогенности обнаружены гены гемолизинов A, E, F, сидерофоры, включая иерсиниабактиновый кластер генов, ряд генов факторов адгезии, колонизации и инвазии, а также ген термостабильного энтеротоксина EAST-1 и гены, маркирующие энтероаггрегативные штаммы *E. coli*: ген регулятора вирулентности *eilA* и энтероаггрегативный белок (air). Один из «арктических» штаммов (33-1) характеризовался наличием детерминант устойчивости к антибиотикам, в частности, в его геноме был детектирован

ген бета-лактамазы расширенного спектра TEM-1b и транспозон Tn1721, включающий гены устойчивости к тетрациклинам (tetA-tetR).

Заключение. Результаты исследования свидетельствуют о циркуляции в орнитогенных экосистемах высокоширотной Арктики и Антарктики штаммов *E. coli*, обладающих выраженным патогенным потенциалом. Анализ геномных данных свидетельствует о распространении в этих регионах генетических линий, широко географически представленных, что обосновывает значимость мониторинга эпидемических клонов кишечной палочки, наряду с мониторингом других патогенов, в колониях массовых видов птиц на высокоширотных территориях.

Ключевые слова: *Арктика, Антарктика, Escherichia coli, полногеномное секвенирование, факторы патогенности, орнитогенные экосистемы*

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Introduction

Escherichia coli is a unique microorganism capable of causing infections in a wide range of clinical manifestations in humans and various animals, which determines the importance of monitoring the spread of its main pathotypes in nature, agriculture and human society [1].

One of such pathotypes monitored under the One Health concept is avian pathogenic *E. coli* (avian pathogenic *E. coli* — APEC), which belongs to the group of pathogens of extraintestinal localization (extraintestinal pathogenic *E. coli* — ExPEC) [2, 3].

Although the possibility of direct zoonotic transmission of APEC from birds to humans is debatable [4], numerous studies show that APEC are genetically similar to human ExPEC (uropathogenic *E. coli* (UPEC) and *E. coli* associated with neonatal meningitis (NMEC)). There are studies supporting the commonality of pathogenicity factors in human APEC and ExPEC isolates. For example, the virulence genes *iroN*, *traT*, *iucD*, *cvi/cva*, *ibeA*, *gimB*, *tia*, *neuC*, *kpsMTII*, *tsh*, *iss*, *sitD*, *chuA*, *fyuA*, *irp2*, *vat*, *malX* and *pic* are present in the genomes of both APEC, UPEC and NMEC [5].

The similarity between the virulomes of APEC strains and human ExPEC emphasizes the potential threat of avian-associated zoonotic infections. Importantly, wild birds may act as a facilitator of the spread of APEC-associated virulence and antimicrobial resistance genes. For example, it has been shown that antibiotic resistance determinants can be transmitted from wild geese and swan strains of *Enterobacteriaceae* to strains in domestic birds, and from the latter to humans [6, 7].

The circumpolar regions of the Earth represent a unique geographical environment in which, despite extreme climatic conditions, the high productivity of shelf seas [8] maintains a high level of faunal biodiversity. The coasts of the Arctic and Southern Oceans within the continental Antarctic, Antarctic and sub-Antarctic archipelagos are points of attraction for billions of migrating birds, a significant part of which make long, including transcontinental flights. For example, the Palaearctic-African migration system alone includes 2.1 billion migrating individuals [9]. Colonies of migrating birds in high latitudes can be points of active intraspecies and interspecies contacts between birds and other animals, accompanied by the exchange of microbiota, including the pathogenic part of it [10].

In this regard, it seems important to study the distribution of bird-associated pathogens in ornithogenic ecosystems formed around bird colonies on the coasts of the Arctic and Antarctic seas.

At the same time, phylogeography and genetic features of such an actual object of epidemiologic and epizootologic surveillance as *E. coli* remains virtually unstudied in polar regions.

The aim of the study is the assessment of the pathogenic potential of *E. coli* strains distributed in the polar regions of the Earth based on the analysis of the genomes of these bacteria from a sample characterizing typical ornithogenic ecosystems of the Arctic and Antarctica.

Materials and methods

Collections of *E. coli* strains isolated from ornithogenic biological material (droppings, feces and carcasses of fallen birds, nest substrates, microbial mats of water bodies contaminated with bird droppings) during several expeditions were used in this study.

In particular, during the implementation of the scientific program of the Russian Arctic expedition on the Svalbard archipelago in 2018, 28 samples of ornithogenic material were collected, from which 6 isolates were isolated, in the expedition of Arctic Floating University (2023) — 8 isolates from 38 samples, in the 68th Russian Antarctic expedition of 2022–2023 — 19 isolates from 29 samples.

The present study describes the *E. coli* cultures isolated in the bird colonies of the Svalbard archipelago (West Spitsbergen Island), Novaya Zemlya and Franz Josef Land archipelagos, as well as on the islands of the Haswell Archipelago, which became one of the key ornithological territories of East Antarctica due to many thousands colonies of Adelie and Emperor penguins.

Furthermore, five *E. coli* strains isolated from cloacal flushes during bird ringing in the spring-summer period of 2023 at the Ladoga ornithological station (Nizhne-Svirsky Reserve, Gumbaritsy tract, Leningrad region) were used as comparison strains. All Arctic and Antarctic cultures were isolated without the use of enrichment methods using dense nutrient media when cultured directly in the field, as described previously [11].

The procedure of biological material sampling was carried out in accordance with generally accepted ethical normsю The research protocol was approved by the Ethics Committee of the which is confirmed by the decision of the Local Ethics Committee of North-Western State Medical University named after I.I. Mechnikov (Protocol No. 3, March 13, 2024).

Species identification of the isolated strains was performed using time-of-flight mass spectrometry (MALDI-TOF) on a Bactoscreen instrument (Litech). Mass spectra were analyzed using Biotyper 3.1 software.

As a result of random sampling, 16 strains were selected for whole-genome sequencing (WGS), followed by annotation and evaluation of pathogenic potential.

Information on the sources of cultures whose genomes were sequenced is presented in **Table 1**.

Biolabmix kits were used for genomic DNA isolation. Genomic sequencing was performed using BGI technology at the Pasteur Research Institute of Epidemiology and Microbiology. Genome annotation was performed using the RAST server (https://rast.nmpdr.org/rast.cgi), drug resistance and virulence genes were searched using the ABRicate v 0.8 program (https://github.com/tseemann/abricate), and the MEGARes (https://megares.meglab.org/amrplusplus/latest/html), Comprehensive Antibiotic Resistance Database, CARD 3.0.2 (https://card.mcmaster.ca/analyze/rgi) and VFDB (https://www.mgc.ac.cn/VFs/) databases were used for this purpose.

The antigenic structure of *E. coli* was determined using the online tool SerotypeFinder 2.0 (https://cge.food.dtu.dk/services/SerotypeFinder/). The MLST 2.0 resource (https://cge.food.dtu.dk/services/MLST/) was used to evaluate the results of multilocus sequencing-typing (MLST). The WGS typing results for bovine genes obtained using the online tool cgMLSTFinder 1.2 (https://cge.food.dtu.dk/services/cgMLSTFinder/) were compared with the data on the corresponding cgMLST types deposited in the EnteroBase database (https://enterobase.warwick.ac.uk/species/index/ecoli), allowing for differences (Max Number MisMatches) of no more than 20 single polymorphisms (SNPs).

Results

The annotation of genomes allowed us to determine their belonging to different STs in MLST and WGS-typing schemes. The main characteristics of the studied genomes and access numbers to their sequences are presented in **Table 2.**

Genes encoding AmpC-like beta-lactamases, the hyperproduction of which provides resistance to cephalosporins, were identified in all genomes studied [12]. In addition, the genome of the Arctic strain *E. coli* 33-1 was characterized by the presence of a plasmid of about 78,000 bp containing the gene for the extended-spectrum beta-lactamase TEM-1b and transposon Tn1721, which includes tetracycline resistance genes (*tetA-tetR*). Numerous pathogenicity factor genes associated with adhesion, invasion and iron capture were detected in the genomes of the studied microorganisms (**Table 3**).

The wide representation of ExPEC pathogenicity factor genes in the genomes of the strains under study raises the question of the potential association of these strains with cases of infectious diseases in humans.

Using the EnteroBase database (https://enterobase.warwick.ac.uk/species/index/ecoli), which accumulates global data on cgMLST genotyping results and currently includes information on more than 340,000 *E. coli* strains, a search was carried out for information on the geographical distribution of cgSTs identified in this study and their sources of isolation. The information was retrieved from the metadata provided in EnteroBase database for 11 STs (**Table 4**).

Discussion

In this study, an attempt was made to generate a sample of *E. coli* strains associated with high-latitude ornithogenic ecosystems typical of circumpolar regions in both the Northern and Southern Hemispheres.

In the Arctic, our studies focused on strains associated with marine colonial birds (Long-tailed Duck, Thick-billed Buzzards) and goose species (Bean Goose,

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Table 1. Characteristics of studied isolates

No.	Isolates	Place of isolation, coordinates	Source of isolation
		Isolates associated with bird ecosystems of the Arctic	
1	67Spits	Svalbard archipelago, Barentsburg, 78°03'N 14°16'E	Feces of *Rissa trydacyla*
2	70_2Spits	Svalbard archipelago, Gronfjorden Bay coast, N 78°00'36.2"N 14°18'09.7"E	Feces of *Rissa trydacyla*
3	89Spits	Svalbard archipelago, Barentsburg, 78°03'N 14°16'E	Feces of *Anser brachyrhynchus*
4	97Spits	Svalbard archipelago, Barentsburg, 78°03'N 14°16'E	Feces of *Anser brachyrhynchus*
5	AFU_2	Yugorsky Peninsula, White Nose Cape, 69°36'14.7"N 60°12'08.1"E	Feces of *Somateria mollissima*
6	AFU_32_1	Novaya Zemlya archipelago, Cape of Desire, 76°57'18.5"N 68°34'41.9"E	Feces of polar bear near the *Rissa trydacyla* bird spot
7	AFU_33_1	Novaya Zemlya archipelago, North Island, Cape of Desire, 76°57'18.5"N 68°34'41.9"E	Nests in the bird spot of *Rissa trydacyla*
8	AFU_43_1	Архипелаг Земля Франца-Иосифа, о-в Вильчека, 79°53'41.8"N 58°44'07.2"E Franz Josef Archipelago, Wilczek Island, 79°53'41.8"N 58°44'07.2"E	Egg shell of *Uria lomvia*
9	AFU_55_1	Franz Josef Archipelago, Komsomolskie islands (South Island), 80°34'48.3"N 58°32'40.2"E	Pond near the *Sterna paradisaea* bird spot
		Isolates associated with bird ecosystems of the Antarctic	
10	15myr	West Antarctica, Queen Mary Land, Haswell Archipelago, Haswell Island, 66°31'36.6"S 93°00'20.8"E	Adelie penguin (*Pygoscelis adeliae*), cloaca sample
11	17_1myr	West Antarctica, Queen Mary Land, Haswell Archipelago, Haswell Island, 66°31'36.6"S 93°00'20.8"E	Stomach sample from *Fulmarus glacialoides*
12	28myr	West Antarctica, Queen Mary Land, Haswell Archipelago, Tokareva Island, 66°32'06.1"S 92°58'25.8"E	Feces of *Adelie penguin* (*Pygoscelis adeliae*)
		Isolates form birds in European region of Russia, Ladoga Ornithological Station (LOS)	
13	LOS_49	Nizhne-Svirskiy Reserve, LOS, 60°40'35.0"N 32°56'27.2"E	Cloaca sample from *Poecile palustris*
14	LOS_51	Nizhne-Svirskiy Reserve, LOS, 60°40'35.0"N 32°56'27.2"E	*Anas crecca* feces
15	LOS_52	Nizhne-Svirskiy Reserve, LOS, 60°40'35.0"N 32°56'27.2"E	Cloaca sample from *Turdus pilaris*
16	LOS_54	Nizhne-Svirskiy Reserve, LOS, 60°40'35.0"N 32°56'27.2"E	Cloaca sample from *Turdus pilaris*

Eiders). These bird species differ both in the ecological niches they occupy and in the duration and directions of migration, which may influence the structure of their microbiota, determining the probability of colonization by different *E. coli* genotypes.

At the same time, it is necessary to take into account the possibility of forming a single reservoir for populations of this microorganism along the entire coast of the Arctic Ocean, determined by bird migrations in the meridional direction. Thus, it was recently found out that a significant part of the kittiwake population migrates from the South Island of Novaya Zemlya to the wintering grounds on the coast of the North Pacific Ocean [13]. The spread of pathogens with Arctic migratory birds (predominantly from the goose group) simultaneously in latitudinal and meridional directions was previously shown for influenza viruses [14]. It should be noted that bean geese, the strains from which were studied in this research, make seasonal migrations from the Svalbard archipelago to wintering grounds in Belgium and the Netherlands, and against the background of global climate change in the Arctic, these birds are actively exploring Novaya Zemlya as well [15].

Three Antarctic strains, whose genomes were characterized in the present study, were isolated in the territory of Adelie penguin colonies on the islands of the Haswell Archipelago in East Antarctica. In spite of the fact that penguins of this species are endemic to Antarctica, in the territories of the colonies they neighbor also with long-distance migratory species of birds. For example, a frequent inhabitant of the Haswell Archipelago, the south polar skua, is able to make long seasonal migrations and reach the North Pacific and the North Atlantic [16]. Thus, the populations of Antarctic birds are not isolated from the global circulation of pathogens, as evidenced, in particular, by the circula-

Table 2. Genetic characteristics of isolated *E. coli* strains

Strain	Region of isolation	Serotype	Sequence type (ST)	ST by core genome (cgST)	GenBank access number
67Spits	Arctic	O4:H5	12	10054	JAYEAG010000000
70_2Spits	Arctic	O43:H2	937	28072	JAYEAE000000000.1
89Spits	Arctic	O83:H1	135	87221	JAYEAD000000000.1
97Spits	Arctic	O166:H49	1246	162	JAYEAC000000000.1
AFU_2	Arctic	O93:H16	8097	132840	JAYEAJ000000000
AFU_32_1	Arctic	O54:H45	491	11903	JAYEAI000000000
AFU_33_1	Arctic	O15:H2	69	189219	JAYEAH000000000
AFU_43_1	Arctic	O9:H49	6163*	1429	JBIQXY000000000
AFU_55_1	Arctic	O39:H4	1155	196482	JBIQXZ000000000
15myr	Antarctic	O8:H7	127	196780	JBIQXV000000000
17_1myr	Antarctic	O6:H31	196	133718	JBIQXW000000000
28myr	Antarctic	O182:H38	1632	94237	JBIQXX000000000
LOS_49	European Russia	O8:H5	2594*	47119	JBIQYA000000000
LOS_51	European Russia	O85:H8	297	114487	JBIQYB000000000
LOS_52	European Russia	N/i	1333*	119313	JBIQYC000000000
LOS_54	European Russia	N/i	58	126100	JBIQYD000000000

Note. *Genotypes with single nucleotide polymorphisms in genes for which sequencing-typing was performed, distinguishing them from the specified sequence types. N/I — not identified.

tion in the Antarctic of influenza virus strains identical to those isolated in other geographical regions [17].

Analysis of the geographical distribution of ST *E. coli* determined by the cgMLST method demonstrated their cosmopolitanism, which was manifested by the detection of identical cgST in geographically distant regions of the planet. For example, cgST 133718 was detected in Antarctica (strain 17_1myr) and Great Britain, and cgST 11903, to which strain 32-1 from the northernmost point of the New Earth belonged, was previously detected in the USA.

Despite the fact that all the strains studied belong to different genetic lineages (ST and serotypes), they are all united by the presence of an extensive virulome. As shown in Table 3, all strains from polar regions have a set of virulence factors that allow them to be considered as potential agents of human infections. In this respect, in general, they do not differ from the strains isolated from birds in the Leningrad Region.

Thus, 10 out of 12 polar strains contained genes or combinations of genes determining the synthesis of hemolysins A, E and F, which together with siderophores of the enterobactin, aerobactin and yersinibactin clusters participate in iron capture during the infection process [18]. It should be noted that the genes of the yersinibactin operon, found in half of the Arctic and Antarctic cultures, are part of the high pathogenicity island. This mobile genetic element is associated, as previously shown, with virulent UPECs [19].

The identified virulence factors for which localization in mobile genetic elements has been described include the uropathogenicity protein. The importance of this factor in damaging mammalian cells has been demonstrated, which is essential in the development of urinary tract infections [20].

In the studied sample, strains marking the enteroaggregative *E. coli* (EAEC) pathotype were also identified, in particular, the eilA virulence regulator gene (Salmonella HilA homolog) and the enteroaggregative protein gene (air), common in EAEC, were detected in the genomes of strains AFU-33-1 and AFU-43-1 from Novaya Zemlya and Franz Josef Land. The strain AFU-33-1 belongs to ST 189219 according to cgMLST results, which is widely represented in a number of European countries, USA and Brazil as a pathogen of generalized human infections. Thus, the spread of a peculiar epidemic clone of *E. coli* was observed in territories where there were no permanent human settlements.

In general, the spread of global genetic lineages of *E. coli* in high latitudes is consistent with the notion that the Rapoport Rule is observed for human pathogens, which states that as one moves from the equator to the poles, the distribution ranges of species or other taxonomic groupings increases [21].

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Table 3. Pathogenic determinants in studied *E. coli* strains

Pathogenic determinants	17myr	15myr	28myr	67Spits	70_2Spits	89Spits	97Spits	AFU_2	AFU_32_1	AFU_33_1	AFU_43_1	AFU_55_1	LOS_49	LOS_51	LOS_52	LOS_54
Hemolysins																
Hemolysin A (hlyA)	+	–	–	+	–	–	–	–	–	–	–	–	–	–	–	–
Bird hemolysin E (hlyE)	–	+	+	–	+	–	+	+	–	+	+	–	–	+	–	+
Hemolysin F (hlyF)	+	+	–	–	–	–	–	–	–	+	–	+	+	–	–	+
Siderophores																
Enterobactin operon	+	–	–	–	–	–	–	–	–	–	–	+	+	–	–	+
Yersiniabactin operon	+	–	–	+	–	+	–	–	+	+	–	+	–	+	+	–
Aerobactin operon	+	+	–	–	–	–	–	–	–	+	–	+	–	–	–	–
Toxins																
Heat-stable enterotoxin EAST-1	–	–	–	–	–	–	+	–	+	–	–	–	–	–	+	+
Subtilase	–	–	–	–	–	–	–	–	+	–	–	–	–	–	–	–
Cytolethal distending toxin (cdt)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	+	–
Adhesion, invasion and biofilm formation determinants																
Adhesin AIDA-I	–	–	–	+	–	–	–	–	–	–	–	–	+	–	–	+
Aggregation substance Tia	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	+
Gen *eilA* homologue (*Salmonella* HilA homolog)	–	–	–	–	–	–	–	–	–	+	+	–	–	–	–	–
Enteroaggregative protein (air)	–	–	–	–	–	–	–	–	–	+	+	–	–	–	–	–
Factor of invasion of brain endothelium (ibeA)	–	–	–	–	–	+	–	–	–	–	–	+	+	–	+	–
Serum survival gene (iss)	+	–	+	–	+	–	+	–	–	+	–	+	+	–	–	+
Arylsulfatase AslA	+	–	+	+	–	+	–	–	–	–	–	–	+	–	+	–
Heat-resistant agglutinin (hra)	+	–	–	+	+	–	+	–	–	–	–	–	–	–	–	+
Cytotoxic necrotizing factor (cnf)	+	–	–	+	–	–	–	–	–	–	–	–	–	–	–	–
Uropathogenic specific protein (usp)	+	–	–	+	–	+	–	–	–	–	–	+	–	–	–	–
Curlin CsgA	+	+	+	+	+	+	+	+	+	–	+	+		+	+	+
Homologue of the *Shigella flexneri* SHI-2 pathogenicity island gene *shiA*	+	–	+	+	–	–	–	–	–	–	–	–	–	–	–	+
Intimin-like adhesin FdeC	+	+	–	+	+	+	+	+	+	–	+	–	–	–	+	+
Serine protease autotransporters of *Enterobacteriaceae* (SPATE)	+	–	–	+	–	+	–	–	+	+	–	+	+	–	+	–

The search for antimicrobial resistance genes in the genomes of *E. coli* strains carried out in this study indicates the absence (within our sample) of critical determinants of drug resistance. Nevertheless, the presence of genetic determinants of resistance to cephalosporins and tetracycline in the genome of the Arctic strain AFU 33-1 indicates the possibility of circulation of mobile genetic elements carrying these genes in the wild and their preservation in the microbiome of Arctic animals in the absence of antibiotic pressure.

Conclusion

The results of the study indicate the circulation of *E. coli* strains with strong pathogenic potential in high-latitude Arctic and Antarctic ornithogenic ecosystems. The analysis of the genomic data indicates the presence of genetic lineages that are geographically widespread in these regions, highlighting the importance of monitoring for epidemic clones of *E. coli*, together with monitoring for other pathogens, in high-latitude bird colonies.

Table 4. Geographical distribution and isolation sources of sequence types (cgST) of the identified strains

Sequence type by core genome (cgST)	Region (regions) of isolation	Source of isolation	Reference number of the Sequence Read Archive (SRA) for strains most similar to the identified STs
10054	Europe, Anand Islands	Human (blood culture)	ERR434967
28072	USA	Livestock (cows)	SRR3972294
162	Australia	*Chroicocephalus novaehollandiae*	SRR24017969
132840	USA	Livestock (calves)	SRR26082289
11903	USA	Human (patient with urinary tract infection)	SRR1314409
189219	USA, Spain, Brazil, Denmark, UK	Chicken, human (blood culture and urine during urinary tract infection)	SRR17774295, ERR13306341, ERR4014451, SRR21849316 SRR21846782
196780	USA	Livestock (cows)	SRR19171807
133718	UK	Wild birds (Anseriformes)	SRR11410512
114487	USA	Beef	SRR10156198
119313	Netherlands	Human (blood culture)	ERR3650458
126100	Sweden	Poultry	SRR14477383

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организация обработки биологического материала, написание и редактирование рукописи. Все авторы подтверждают соответствие своего авторства критериям Международного комитета редакторов медицинских журналов, внесли существенный вклад в проведение поисково-аналитической работы и подготовку статьи, прочли и одобрили финальную версию до публикации.

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