Poultry Science Journal
ISSN: 2345-6604 (Print), 2345-6566 (Online)
http://psj.gau.ac.ir

Blood Profiles and Gut Microbial Communities in Broiler Chickens: Are There Any Associations?

Galimzhan Duskaev[1], Lyudmila Vlasenko[2]*, Ilshat Karimov[2,3], Alexander Zatevalov[2,4], Dmitry Deryabin[2]

[1] Department of Feeding for Farm Animals and Feed Technology named after S.G. Leushin, Federal Research Centre of Biological Systems and Agrotechnologies of the Russian Academy of Sciences, Orenburg, Russia
[2] Laboratory of Breeding and Genetic Research in Animal Husbandry, Federal Research Centre of Biological Systems and Agrotechnologies of the Russian Academy of Sciences, Orenburg, Russia
[3] Department of Epidemiology and Infectious Diseases, Orenburg State Medical University of the Ministry of Health of Russia, Orenburg, Russia
[4] G.N. Gabrichevsky Research Institute for Epidemiology and Microbiology, Moscow, Russia

Poultry Science Journal 2026, 14(2): 223-242

Keywords
Blood profile
Broiler chicken
Gut microbiome

Corresponding author
Ludmila Vlasenko
lv.efremova@yandex.ru

Article history
Received: November 13, 2025
Revised: July 9, 2026
Accepted: September 17, 2026

Abstract

The general concept of a gut-bone marrow axis, which describes the communication between the microbial community and the hematopoietic system, still has little experimental support in poultry. The goal of this study was to evaluate the hematological values and gut microbial communities in broiler chickens belonging to the globally used Arbor Acres strain and the domestic Smena 8 strain, and to assess the associations between these parameters. The study design included a group-level meta-analysis of homogeneous quantitative hematological and microbiological datasets obtained from 40 independent chicken groups using an automatic 5-diff hematology analyzer and metagenomic sequencing technology performed on the Illumina MiSeq platform. Comparison of blood profiles between Arbor Acres and Smena 8 broiler chicken strains revealed significant ($P< 0.001$) differences in red blood cells (RBC) and white blood cells (WBC) counts, complemented by less expressed ($P= 0.002$) differences in platelet (PLT) counts. In turn, a comparison of gut microbiomes showed a common core, represented by 46 bacterial genera and equivalent taxonomic ranks, as well as specific components that are predominantly found (21 genera) or are exclusively characteristic (93 genera) for a particular broiler chicken strain. Subsequent analysis of the associations between blood profiles and microbial communities identified 23 bacterial genera that were strongly positively associated with the WBC and PLT counts or negatively associated with the RBC and WBC counts. Overall, the present study explained 12.39% of RBC and 22.28% of WBC count variability, and the most pronounced 55.65% PLT variability in blood profiles of broiler chickens as microbiome-related, which should be considered when these parameters are jointly assessed in poultry farming.

Introduction

Hematological examination of poultry provides valuable information for assessing health and physiological status, as well as the ability to fight infectious diseases and respond to various environmental factors (Thrall *et al.*, 2022). The classical hematological approach involves the quantitative analysis of key blood components such as red blood cells (RBC), white blood cells (WBC), and platelets (PLT), as well as different WBC types, by measuring their number within a fixed blood volume (El Brihi and Pathak, 2024). In turn,

Please cite this article as Galimzhan Duskaev, Lyudmila Vlasenko, Ilshat Karimov, Alexander Zatevalov, Dmitry Deryabin. 2026. Blood Profiles and Gut Microbial Communities in Broiler Chickens: Are There Any Associations?. Poult. Sci. J. 14(2): 223-242.

DOI: 10.22069/psj.2026.24279.2453

subsequent comparison of experimental blood test data and established reference intervals is essential for diagnosing health issues where deviations from these ranges can indicate anemia, infection, or physiological stress (Nwaigwe *et al.,* 2020).

An in-depth analysis performed for *Gallus gallus domesticus* showed that different morphotypes of this species (chicken breeds or strains) can exhibit significant variations in their normal blood profiles, including remarkable differences in most RBC-related and WBC-related parameters (Bilkova *et al.,* 2017). Such variations are thought to be determined by genetic factors that reflect a combination of artificial and natural selection, which may influence the production of blood components. As a result, different chicken breeds/strains have evolved original adaptation mechanisms specific to external stressors (Nawaz *et al.,* 2024) or pathogen invasion (Idowu *et al.,* 2025) to which the bird needs to respond.

A novel factor influencing hematopoiesis is the microbial community that inhabits the host and is termed the "microbiome" (Berg *et al.,* 2020). The recently identified relationship between the gut microbiome and the hematopoietic system has been coined the gut-bone marrow axis (Wells *et al.,* 2024). Initially considered important for leukopoiesis (Fernandez Sanchez *et al.,* 2024), this concept was later extended to erythropoiesis (Lee *et al.,* 2021) and thrombocytopoiesis (Gurumurthy *et al.,* 2026), and currently describes communication pathways between the microbial community and hematopoietic stem cells by modifying the bone marrow microenvironment, including mechanical properties, inflammatory signals, and metabolites (Liu *et al.,* 2024).

Having been found in humans and experimental mammals, the links between the gut microbiome and hematopoiesis in poultry are confirmed but less clear. The interactions between microbial community, chicken's immune system development and immune homeostasis were summarized by Diaz Carrasco et al. (Diaz Carrasco *et al.,* 2019), and the impact of the chicken gut microbiome on cellular innate immune system components was described in Al Hakeem et al.'s study (Al Hakeem *et al.,* 2023). Notably, the germ-free chickens exhibit altered hematopoiesis, since the absence of promoter signals from the gut microbiome does not allow granulocyte-macrophage progenitors to optimally develop and differentiate (Khosravi *et al.,* 2014). The results obtained on conventionally reared and germ-free chickens estimated microbiome-related plasticity for the immune tissue maturation rate parameter to be 70–90%, and the impact on the blood leukocyte, neutrophil, and lymphocyte counts to be 5–15% (Cowieson, 2022).

Against this background, the goal of this study was to evaluate the hematological values and gut microbiomes in broiler chickens belonging to the globally used Arbor Acres strain and the domestic Smena 8 strain, and to identify associations between these datasets that are important for understanding the interactions of the microbial community and the hematopoietic system.

Materials and Methods

Study design and ethical statement

The study design was based on a group-level meta-analysis of homogeneous quantitative data sets from 40 independent chicken groups, previously described in (Ryazanov *et al.,* 2021; Atlanderova *et al.,* 2021; Duskaev *et al.,* 2021; Shajahmetova et al., 2021; Deryabin *et al.,* 2023; Bagirov *et al.,* 2020; Duskaev *et al.,* 2022; Duskaev *et al.,* 2022; Duskaev *et al.,* 2022; Duskaev *et al.,* 2023), aimed at identifying patterns that were not evident in each experiment. The working hypothesis that is provisionally accepted as a basis for current research was that the variability of the examined microbiomes was a consequence of the use of dietary supplements (antibiotic, probiotic, plant extract or chemically synthesized analogues of plant-derived compounds) specifically targeting the microbial community in the chicken gut, while the supplements themselves had no direct effect on hematopoiesis or their effect was not obvious.

A total of 28 groups (5 control and 23 experimental) were represented by the Arbor Acres strain (Aviagen LLC, Tula, Russia), while 3 control and 9 experimental groups belonged to the Smena 8 strain, bred using genetic material from two crosses: the domestic Smena 7 and the globally used Ross 308 (Emanuylova *et al.,* 2021). All research series were conducted between September 2016 and February 2024. The complete datasets containing both hematological parameters and gut microbiome compositions were gathered from different groups and included in a meta-analysis to find shared trends and conclusions.

The keeping of chicken groups was carried out in accordance with the general requirements of the "European Convention for the Protection of Vertebrate Animals used for Experimental and other Scientific Purposes" of 18 March 1986. The study protocols details were approved by the local ethics committee of the Federal Research Center for Biological Systems and Agrotechnologies (see Institutional Review Board Statement).

Broiler chicken management and diets

Seven-day-old broiler chickens were randomly divided into groups of 15-30 birds and labeled with plastic foot tags indicating their assignment to the control or experimental series. Each group was housed together in specialized, well-ventilated cages with mesh floors at temperatures and relative humidity regimes appropriate for growing broilers.

The photoperiod program complied with the European Council Directive (2007/43/EU), which regulates the protection of chickens kept for meat production. The control groups received commercial standard broiler meal, represented by pellets of 2.5–3.0 mm, while the experimental groups were fed a same basic diet supplemented with antibiotic, probiotic, plant extract or chemically synthesized analogues of plant-derived compound (Ryazanov *et al.*, 2021; Atlanderova *et al.*, 2021; Duskaev *et al.*, 2021; Shajahmetova *et al.*, 2021; Deryabin *et al.*, 2023; Bagirov *et al.*, 2020; Duskaev *et al.*, 2022; Duskaev *et al.*, 2022; Duskaev *et al.*, 2022; Duskaev *et al.*, 2023), which led to variability in hematological and microbiological datasets in finisher broilers and supplemented the genetically determined differences between these parameters in the compared chicken strains.

Sampling collection

In 42-day-old broiler chickens of each control and experimental group, sets of blood samples were drawn by puncturing the axillary vein into 6 ml disposable vacuum-sealed tubes internally coated with spray-dried anticoagulant K2EDTA (Greiner Bio-One International AG, Kremsmünster, Austria). Immediately after blood collection, the sample tubes were gently shaken to prevent hemolysis. This standardized method ensured that the blood remained in a liquid, non-clotted state, which was crucial for the accurate hematological analysis, which was performed within 60 min of sample collection.

Chickens were randomly selected from each group and humanely slaughtered, after which a ventral midline incision was performed to provide maximum access to the abdominal cavity. The gut (cecal) contents were extruded into sterile cryogenic tubes and rapidly frozen at -80°C in a Thermo Fisher Scientific 803CV freezer (Waltham, MA, USA).

Hematological analysis

In the individual blood samples, cell counting was performed using a DF50 Vet (Shenzhen Dymind Biotechnology Co., Ltd., Shenzhen, P.R. China) automatic hematology analyzer with a throughput of 60 samples per hour. Diluent, detergent and lyse reagents provided by the device manufacturer were used. Based on the principle of electrical impedance, absolute values of the white blood cell (WBC), red blood cell (RBC), and platelet (PLT) counts were determined as the number of cells per 1 L. In addition, a 5-part differentiation of WBC types was performed, representing lymphocytes (LYM), monocytes (MONO), heterophils (HPH), eosinophils (EOS), and basophils (BAS) as a percentage of the total leukocyte count.

This instrumental approach ensured high efficiency, accuracy, reliability and reproducibility of the analytical procedure, as well as comparability of the hematological data both within and between experimental series. Since the use of hematological analyzers for blood testing in poultry is still controversial, randomly selected samples were re-examined using manual hematological methods, and a 5% deviation was considered acceptable.

Gut microbiome analysis

The chicken's gut microbial community was analyzed using the V3-V4 hypervariable regions of the 16S rRNA gene, which is the most widely adopted target offering an optimal balance between broad bacterial coverage and taxonomic resolution (Tong *et al.*, 2022).

Total DNA extraction from cecal samples was performed using commercial Fast DNA SPIN Kit for Feces (MP Biomedicals Inc., Irvine, CA, USA) and QIAamp Fast DNA Stool Mini Kit (Qiagen GmbH, Hilden, Germany).

A two-step Illumina protocol (Part #15044223, Rev. B) was implemented to prepare the 16S rRNA library, including amplification of target V-regions using the forward primer S-D-Bact-0341-b-S-17 and the reverse primer S-D-Bact-0785-a-A-21. The QIAxcel Advanced system (Qiagen GmbH, Hilden, Germany) was used to assess the quality of the obtained DNA libraries.

Finally, Illumina's second-generation MiSeq high-throughput short-read sequencing platform was used to sequence the V3–V4 regions. The high-throughput paired-end sequencing of 2 × 250 bp was performed using the V.2 reagent kit (Illumina Inc., San Diego, CA, USA).

After quality filtering using USEARCH v11.0.667 with the –fastq filter option (-minlen 400, -maxee 1.0), a total of 334,832 reads were retained. The number of reads per sample ranged from 11,131 to 31,809, with a mean of 20,927 ± 5,079.51 reads per sample. Rarefaction curves reached a plateau at the selected sampling depth, indicating sufficient sequencing coverage for downstream analyses.

The raw sequencing data were clustered into operational taxonomic units (OTUs) using the USEARCH V.10.0.240 software and the RDP classifier (Wang *et al.*, 2007) against the SILVA 16S rRNA database (SILVA, 2025). The OTUs' affiliation to specific taxa was determined according to the NCBI taxonomy browser (Schoch *et al.*, 2020).

Statistical analysis

Data for each broiler chicken group were pre-calculated as separate units and stored using the Microsoft Excel 2019 package (Microsoft Corporation, Redmond, Washington, DC, USA). Advanced data processing was performed using Statistica 13.0 software (TIBCO Software Inc., Palo Alto, CA, USA).

Since the Shapiro–Wilk test rejected the normal distribution hypothesis of the original data with 95% confidence level, nonparametric methods for subsequent statistical analysis were justified. In accordance with this approach, quantitative data were presented as median values [Q1–Q3], and differences between chicken strains were assessed using the Mann–Whitney test, where the significance threshold was considered to be $P<0.001$.

A multivariate principal component analysis (PCA) was used to identify the largest variation in hematological data, and the distribution of chicken strain datasets was visualized using the F1 × F2 factor plane. Associations between blood cell counts and bacterial genera in chicken gut microbiomes were assessed by correlation analysis corrected for multiple comparisons and visualized using a "heat map" chart. The impact of host genetics and gut microbiome composition on blood cell counts in the compared broiler chicken strains was investigated using regression analysis and represented by the R^2 coefficient of determination.

Results

Broiler chicken's hematology

Comparison of blood profiles between Arbor Acres commercial broiler chickens and Smena 8 domestic broiler chickens revealed numerous differences, as presented in Table 1.

Table 1: Hematological parameters in Arbor Acres and Smena 8 broiler chicken strains.

Parameters	Arbor Acres (n=28)	Smena 8 (n=12)	P-value
RBC, 10^{12} cell/L	3.56 [3.28–3.73]	1.97 [1.80–2.01]	<0.001
WBC,10^9 cell/L	46.25 [36.42–50.03]	21.45 [17.14–26.35]	<0.001
LYM, %	42.48 [41.87–43.45]	41.76 [40.50–42.62]	0.108
MONO, %	8.38 [7.79–8.64]	6.98 [6.55–8.14]	0.016
HPH, %	39.97 [38.14–40.72]	40.22 [39.64–41.48]	0.323
EOS, %	8.71 [7.95–9.62]	9.97 [9.55–10.40]	0.009
BAS, %	0.60 [0.53–0.67]	0.55 [0.50–0.67]	0.425
PLT, 10^9 cell/L	104.17 [73.52–123.42]	67.50 [65.01–68.00]	0.002

Note: data are presented as median value [Q1–Q3]. P-value between groups were calculated using the Mann–Whitney U test. Abbreviations: RBC – red blood cells, WBC – white blood cells, LYM – lymphocytes, MONO – monocytes, HPH – heterophils, EOS – eosinophils, BAS – basophils, PLT – platelets.

First, the Arbor Acres strain was characterized by an increased RBC count (3.56 [3.28–3.73] × 10^{12} cells/L), which was higher than that of the Smena 8 strain (1.97 [1.80–2.01] × 10^{12} cells/L) with statistical significance at $P<$ 0.001. Second, total WBC counts also differed significantly (46.25 [36.42–50.03] × 10^9 cell/L vs 21.45 [17.14–26.35] × 10^9 cell/L; $P<$ 0.001), although fluctuations between the proportions of leukocyte types were less pronounced or absent. Third, a moderate increase was recorded for Arbor Acres strain compared with the Smena 8 strain in PLT counts (104.17 [73.52–123.42] × 10^9 cell/L vs 67.50 [65.01–68.00] × 10^9 cell/L; $P=$ 0.002), which are often considered the most abundant type of "white blood cell" in chickens due to their involvement in the innate immune response.

The subsequent principal component analysis transformed the observed hematological data into a new coordinate system and represented the most characteristic variations in the blood profiles as individual factors (F). As a result of this processing, the first weigh F1 was described, showing the correlation matrix eigenvalue to be 2.640989, and the total variance to be 33.0124%. The F1 structure included significant unrotated factor loadings (>0.07) for three hematological parameters, namely, RBC count (0.802755), WBC count (0.891060), and PLT count (0.756546), which were characteristic of the Arbor Acres strain compared to the Smena 8 strain (see above). In turn, F2 had an eigenvalue of 1.613283 with a total variance of 20.1660 %, showing only one significant unrotated factor loading found for the "eosinophils" parameter (0.726711), which was not associated with any of the compared broiler chicken strains.

The following factor scores calculation made it possible to link each analyzed groups with the F1 factor directly or inversely, while projection of the observed data sets onto the F1 × F2 factor plane revealed clearly separated blood profiles that differed significantly between the Arbor Acres and Smena 8 strains (Figure 1).

Chicken gut microbiomes: common and strain-specific components

Based on the analysis of a subset of 16S rRNA gene reads, 11 bacterial phyla, represented by 160 bacterial genera and equivalent taxonomic ranks, were found in the chicken gut microbiomes (Table S1 in the Supplement).

The phylum *Bacillota* was dominant, occurring in all groups, showing relative abundances from 28.66 to 90.12% and being represented by 113 genera or equivalent taxonomic ranks. The phylum *Bacteroidota* (represented by 12 genera) was also found everywhere, but its relative abundance was lower, ranging from 4.19 to 69.10%. The resident community of the chicken gut microbiomes also

included the phyla *Actinomycetota*, *Cyanobacteriota*, *Pseudomonadota*, and *Thermodesulfobacteriota*, which were present in at least two-thirds of the analyzed groups with an abundance of less than 1% and were represented by 12, 1, 14, and 3 genera, respectively. In turn, another 5 phyla (*Chloroflexota*, *Chlamydiota*, *Mycoplasmatota*, *Spirochaetota* and *Verrucomicrobiota*), each represented by one genus only, were discovered sporadically.

Comparison of microbial communities in Arbor Acres and Smena 8 chicken strains revealed several common genera that make up the core microbiome (CM) of *Gallus gallus domesticus*, as well as bacterial taxa associated with a particular chicken strain (Figure 2).

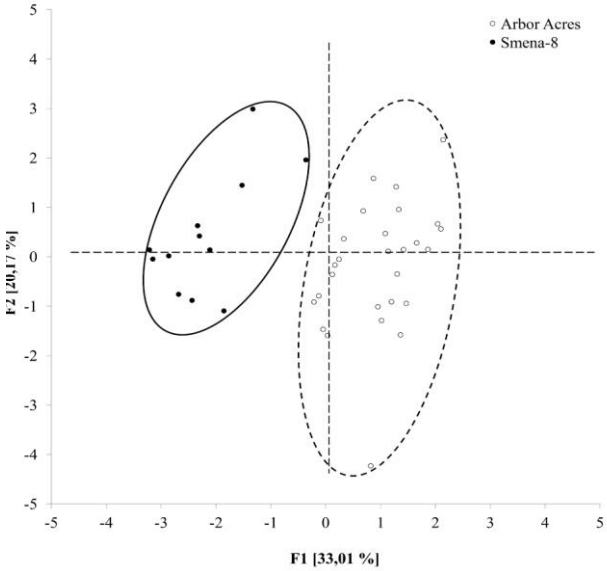


Figure 1. Projection of blood profiles in the Arbor Acres and Smena 8 broiler chicken strains onto the F1 × F2 factor plane, assessed using principal component analysis. The abscissa and ordinate axes indicate F1 and F2 factors with the percentage variance explained.

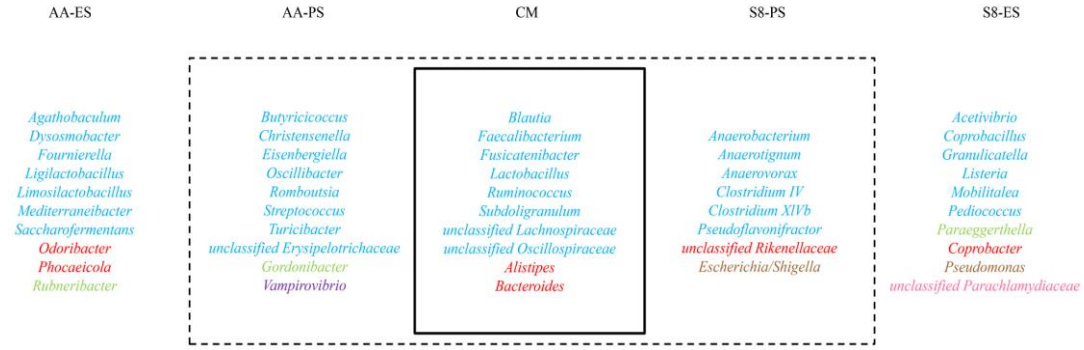


Figure 2. Top bacterial genera and equivalent taxonomic ranks common for chicken gut microbiomes or specific for Arbor Acres and Smena 8 strains.

Note: central part, solid line – bacterial taxa found in both strains (core microbiome – CM); intermediate parts, dotted line – bacterial taxa predominantly specific (PS) for Arbor Acres (AA) or Smena 8 (S8) strains; exclusively specific (ES) placed in the lateral parts are not outlined.

Taxa belonging to phylum *Bacillota* are highlighted in blue, those belonging to phylum *Bacteroidota* are highlighted in red, to phylum *Actinomycetota* – in green, to phylum *Cyanobacteriota* – in purple, to phylum *Pseudomonadota* – in brown, to phylum *Chlamydiota* – in pink.

The CM list (Figure 2, central part) included the genera *Blautia*, *Faecalibacterium*, *Fusicatenibacter*, *Lactobacillus*, *Ruminococcus*, *Subdoligranulum*, and also unclassified *Lachnospiraceae and Oscillospiraceae*, all belonging to the phylum *Bacillota*, as well as the genera *Alistipes* and *Bacteroides*, belonging to the phylum *Bacteroidota*,

which occurred in 75-100%, without differences in the abundance between the compared chicken strains. Another 36 genera and equivalent taxonomic ranks were also not statistically different between Arbor Acres and Smena 8 strains, but showed a lower occurrence and abundance.

Subsequent analysis identified strain-specific bacterial genera, subdivided into two categories: predominantly specific (PS) and exclusively specific (ES) for Arbor Acres or Smena 8 gut microbiomes. In this case, the PS category included taxa that occurred in both chicken strains but differed significantly ($P<$ 0.001) in abundance, whereas the ES category was represented by bacterial genera that were found in one strain's microbiomes only but were absent in the other.

According to these criteria, the PS component of the Arbor Acres microbiomes included the *Butyricicoccus*, *Christensenella*, *Eisenbergiella*, *Oscillibacter*, *Romboutsia*, *Streptococcus*, *Turicibacter*, and unclassified *Erysipelotrichaceae*, all within belonging to the phylum *Bacillota*. In addition, the criteria for predominant specificity were met by frequently occurring genera *Gordonibacter* (belonging to the phylum *Actinomycetota*) and *Vampirovibrio* (belonging to the phylum *Cyanobacteriota*). In turn, the ES genera were *Agathobaculum*, *Dysosmobacter*, *Fournierella*, *Ligilactobacillus*, *Limosilactobacillus*, *Mediterraneibacter*, *Saccharofermentans* (all belonging to the phylum *Bacillota*), *Odoribacter*, *Phocaeicola* (belonging to the phylum *Bacteroidota*) and *Rubneribacter* (belonging to the phylum *Actinomycetota*), which were found in 78,57% Arbor Acres groups, but were absent in the Smena 8 strain (Figure 2, left part).

The PS taxa for Smena 8 microbiomes were *Anaerobacterium*, *Anaerotignum*, *Anaerovorax*, *Clostridium IV*, *Clostridium XIVb*, *Pseudoflavonifractor* (all belonging to the phylum *Bacillota*), unclassified *Rikenellaceae* (belonging to the phylum *Bacteroidota*), and *Escherichia/Shigella* sp. (belonging to the phylum *Pseudomonadota*). At last, exclusively Smena 8 strain-specific taxa included *Acetivibrio*, *Coprobacillus*, *Granulicatella*, *Listeria*, *Mobilitalea*, *Pediococcus* (belonging to the phylum *Bacillota*), *Paraeggerthella* (phylum *Actinomycetota*), *Coprobacter* (phylum *Bacteroidota*), *Pseudomonas* (phylum *Pseudomonadota*), and unclassified *Parachlamydiaceae* (phylum *Chlamydiota*), accompanied with other 38 bacterial genera that were not found in any of the Arbor Acres groups (Figure 2, right part).

Associations between hematological profiles and gut microbiome communities

Since numerous hematological and microbiological characteristics of the Arbor Acres and Smena 8 strains differed significantly, these facts justified subsequent analysis of possible links between observed blood parameters and gut microbial communities. To test this hypothesis, associations between blood cell counts and bacterial taxa abundance were assessed using correlation analysis, and relationships between significant genera and hematological profiles were visualized in a two-dimensional heat map.

According to this approach, 1280 correlation coefficients were calculated between 8 blood parameters and 160 bacterial taxa, among which 36 values were significant at a threshold of $P<0.001$. The RBC count was positively correlated with unclassified *Erysipelotrichaceae* only (r=+0.56782; $P=$ 0.00013), while significant negative links were found with 7 bacterial genera and equivalent taxonomic ranks. The WBC counts were strongly associated with the abundance of 11 bacterial genera in gut microbiomes, including positive links ($r \geq +0.5$) with 7 taxa and negative links ($r \leq -0.5$) with 4 taxa. In turn, the PLC counts were positively correlated with 14 bacterial genera, while it was negatively correlated with the abundance of the genus *Bacteroides* only (r=–0.56471; $P=$ 0.00015). In total, 23 bacterial genera and equivalent taxonomic ranks significantly associated with hematological profiles in Arbor Acres and Smena 8 strains were established and listed in Figure 3.

When a heat map was subsequently constructed, these data were clustered, and two robust clusters were found for both blood profiles and gut microbiome composition. Notably, cluster I, negatively associated with the observed hematological parameters, showed multiple links with RBC and WBC counts, whereas cluster II was predominantly positively associated with WBC and PLT counts.

In terms of biodiversity, cluster I included 8 bacterial taxa belonging to 3 bacterial phyla (*Bacillota* – 5 genera and equivalent taxonomic ranks; *Bacteroidota* – 2 and *Pseudomonadota* – 1), while cluster II, comprising 15 bacterial taxa, consisted of 9 genera belonging to the phylum *Bacillota*, 2 each to the phyla *Pseudomonadota* and *Thermodesulfobacteriota*, and 1 each to the phyla *Actinomycetota* and *Bacteroidota*.

In terms of specificity for the compared broiler chicken strains, both clusters contained components of the core microbiome as well as taxa predominantly or exclusively specific to the Arbor Acres and Smena 8 strains. Bacterial cluster I, associated with decreased RBC and WBC values, included the genus *Bacteroides*, classified as a CM member; *Anaerobacterium* and unclassified *Rikenellaceae*, assessed as PS for Smena 8 microbiomes; and also *Acetivibrio*, *Coprobacillus*, *Paraeggerthella*,

Peptococcus, and unclassified *Clostridiales* Family XIII, recognized as ES for this broiler chicken strain. In turn, cluster II, linked with elevated WBC and PLT values, consisted of the genera *Anaerofustis*, *Bilophila*, *Parasutterella* and *Roseburia*, which did not have significant differences in occurrence and abundance among the compared chicken strains, while *Butyricicoccus*, *Romboutsia*, *Turicibacter* and unclassified *Erysipelotrichaceae* were found predominantly in the Arbor Acres microbiomes, and *Abyssivirga*, *Aestuariispira*, *Agathobaculum*, *Ihubacter*, *Mailhella*, *Phocaeicola* and *Rubneribacter* were exclusively specific for this strain.

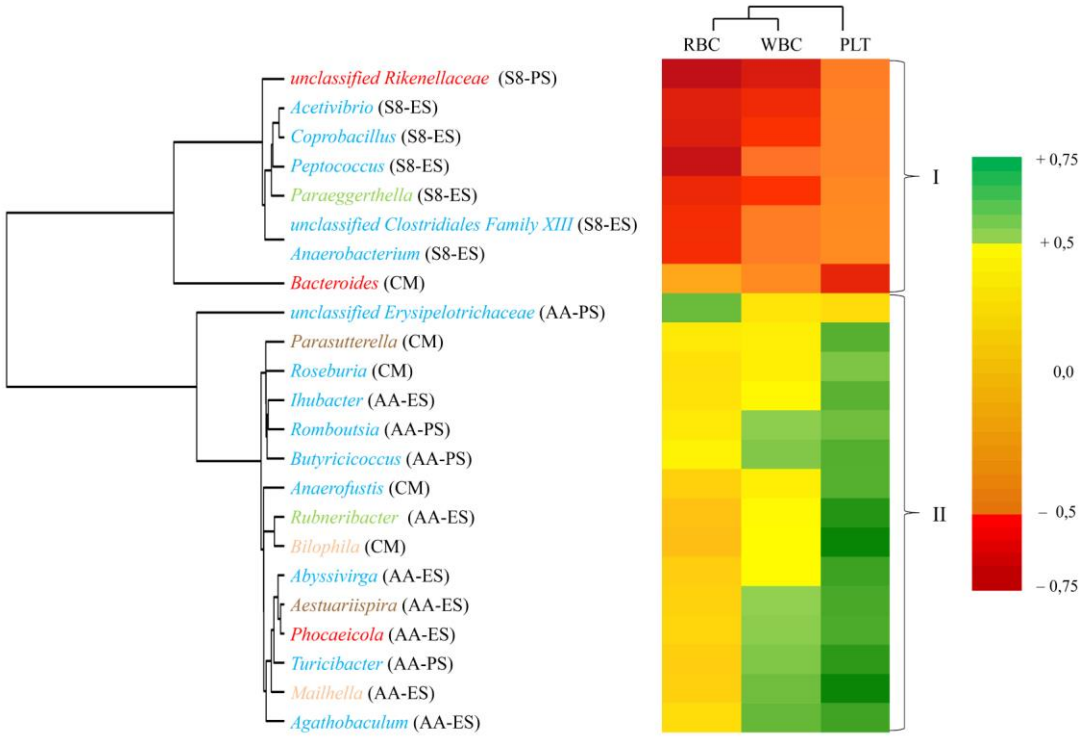


Figure 3. Hierarchical cluster heat map depicting the associations between blood cell counts and the relative abundance of the most influential bacterial genera in the chicken gut microbiome.
Note: The color highlighting of bacterial taxa and their belonging to the core or specific to Arbour Acres and Smena 8 microbiomes is similar to Figure 2.
The strength of associations is indicated by colors from red (negative) to green (positive) according to the right scale.

Assessment of host- related and microbiome-related plasticity of blood profiles in broiler chickens

To estimate the host-related and microbiome-related influences on the variability of blood profiles in broiler chickens, a series of regression analyses were performed. For this purpose, outcome variables (WBC, RBC and PLT endpoint values) were presented as a function of strain specificity, gut microbiome composition or both these independent parameters. Once the regression models had been constructed, the statistical significance of the estimated parameters was assessed via R-squared and checked by an F-test criterion. A summary of the possible plasticity of blood profiles in broiler chickens, depending on host genetics and gut microbial composition, is presented in Figure 4.

The calculated regressions and regression summary showed an essential dependence of the cell count in the blood of broiler chickens on the host genetics. The most significant influence of chicken strain specificity (Arbor Acres vs. Smena 8) was found for the RBC count: adjusted R^2=0.84631777 and F[1.38]=215.77; while this effect on the WBC count was characterized as adjusted R^2=0.57012022 and F[1,38]=52.723; being minimal for the PLT outcome: adjusted R^2=0.30781213 and F[1,38]=18.343.

Multiple regressions based on both chicken strain specificity and microbiome composition data showed an increase in R-squared values, confirmed by the F-test significance. For the RBC count variability, the adjusted R^2 value was 0.97027866 (F[10.29]=128.32), for the WBC it became 0.79300847 (F[5.34]=30.883) and increased most noticeably for the PLT outcome to 0.86440169 (F[7.32]=36.516), which assumes from 12.39% and 22.28% to 55.65% plasticity of these blood parameters in broiler chickens as microbiome-related (Figure 4).

To eliminate multicollinearity, numerous highly correlated variables were removed from these multiple regression models, after which the final lists of genera most significant for determining the RBC, WBC and PLT counts included 9, 4, and 6 bacterial taxa, respectively. However, due to the large number of remaining variables, the regression models appear unstable and are not intended to be predictive without external verification, although they are of interest in the context of describing the most relevant bacterial taxa influencing blood profile outcomes.

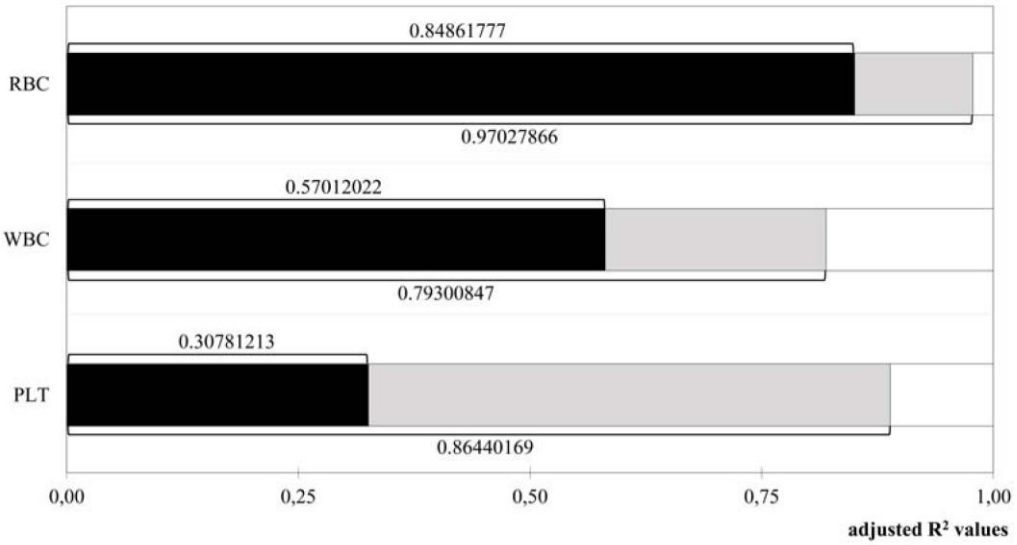


Figure 4. The impact of host-related (black) and microbiome-related (grey) factors on the variability of blood cell counts in broiler chickens, represented by the adjusted R^2 coefficient of determination.
Note: Values above the bars show R^2 for regression models based on the host factor only; values below the bars represent R^2 for regression models accounting for both the host and microbiome parameters.

Thus, in the multiple regression for the RBC count, positive structure coefficients were found for the genera Butyricicoccus (P= 0.009849), Parasutterella (P= 0.000053), Phocaeicola (P< 0.000001) and Romboutsia (P= 0.000672), while negative structure coefficients were established for Abyssivirga (P= 0.000003), Acetivibrio (P= 0.012151), Aestuariispira (P< 0.000001), Anaerofustis (P= 0.000445) and Turicibacter (P< 0.000001). In the WBC regression model, the independent variables were the genera Anaerofustis (P= 0.00538), Phocaeicola (P= 0.0000249), Roseburia (P= 0.0000288) and Rubneribacter (P= 0.00001). In turn, the complex associations between gut microbiome composition and PLT outcomes included the abundance of genera Aestuariispira (P= 0.022696), Agathobaculum (P= 0.001513), Anaerobacterium (P= 0.000012), Bilophila (P< 0.000001), Paraeggerthella (P= 0.020828) and unclassified Clostridiales Family XIII (P= 0.008856).

According to $(1 – R^2)$ criteria, about 2.97%, 20.69% and 13.56% of the RBC, WBC and PLT variability remained unclear in the constructed multiple regressions and could be explained by other factors not included in the model, namely, environmental effects and management differences.

Discussion

The study contributes to current knowledge on the variability of blood profiles in broiler chickens, which influence their resistance to infectious diseases, response to various environmental factors, and physiological state during performance. In contrast to several studies (Talebi et al., 2005; Kongpechr et al., 2021), which found similarities in hematological parameters among major broiler chicken breeds (Ross 308, Cobb 500, Arbor Acres, and Arian), we described differences between the compared commercial Arbor Acres and domestic Smena 8 strains, which included variations in RBC, WBC and PLT counts and manifested in significantly different blood profiles. On the other hand, the obtained results are in good agreement with observations about the differences between local (indigenous) chickens and commercial broiler strains (Baudouin et al., 2021; Dutta et al., 2013), in which improved hemogram and leukogram characteristics are apparently the result of genetic selection.

To assess non-genetic factors that may also determine variations in hematological profiles, we analyzed the composition of gut microbiomes, which, according to current concepts, are involved in the gut-bone marrow regulatory axis (Wells et al., 2024; Liu et al., 2024).

Based on the results of a series of metagenomic analyses and subsequent integrative analysis, we have established two principal points: (i) the gut microbiome of Gallus gallus domesticus has a common core, represented by bacterial genera, the occurrence and abundance of which are relatively stable in the various chicken strains; (ii) the microbial communities of individual chicken strains contain specific components that are exclusively characteristic or are predominantly found in a particular strain. In this study, the core microbiome was represented by 46 bacterial genera and equivalent taxonomic ranks, while the predominantly specific component in the Arbor Acres strain included 13 taxa and in the Smena 8 included 8 taxa, while the exclusively specific components were represented by 45 and 48 taxa, respectively. Thus, the current study is in line with several observations that also support the presence of breed-specific and across-breed core gut microbiomes in native and commercial broilers (Paul et al., 2021), as well as between modern and slower-growing broiler breeder lines (Shterzer et al., 2023), which are important for growth performance and other physiological aspects accelerating growth. It is possible that due to the different numbers of Arbor Acres and Smena 8 groups included in the study, some exclusively specific taxa were overestimated and should be clarified in further studies.

A comparison of hematological values and microbial communities revealed significant associations of RBC, WBC and PLT counts with the abundance of 23 bacterial taxa out of 160 included in the study. This analysis took into account both inter-strain differences and intra-strain distribution, which allowed us to discover three fundamental facts: (i) typical was a combined change in two hematological parameters - a decrease in in RBC and WBC counts or an increase in WBC and PLT counts; (ii) the influencing bacterial taxa were divided into two robust clusters associated with these variations in blood profiles; (iii) the influencing taxa belonged to both exclusively or predominantly strain-specific genera and the core microbial communities. Thus, the present study demonstrates a more comprehensive effect of the chicken gut microbiome on hematopoiesis than has been previously described in terms of impact on the cellular immune system alone (Diaz Carrasco et al., 2019; Khosravi et al., 2014).

In discussing the limitations of the present study, which do not allow us to unambiguously interpret the reported associations as causal, it should be noted that there is a lack of biological evidence confirming the influence of the gut microbiome on blood profiles, which was beyond the scope of the performed analysis. Based on current knowledge, these mechanisms can be explained by influences on hematopoietic stem cell differentiation through changes in the bone marrow microenvironment, including mechanical properties, inflammatory signals, and various metabolites (Liu et al., 2024). Thus, for several genera associated with RBC count (namely Parasutterella (Bush and Alfa, 2020), Romboutsia (Fan et al., 2024) and Turicibacter (Lynch et al., 2023), this effect may be determined by involvement in lipid metabolism, which is necessary for cell membrane biogenesis. Furthermore, the effect of the gut microbiome on erythropoiesis may be mediated by lactate, which induces the production of stem cell factors by niche cells expressing the leptin receptor (Lee et al., 2021). Another mechanism may be the influence of the microbial community on trace element metabolism (Deryabin et al., 2024), including iron metabolism, which is essential for effective hematopoiesis, especially for erythropoiesis. The association between genus Roseburia and WBC count may be explained by a decrease in pro-inflammatory mediators and an increase in anti-inflammatory cytokines (Nie et al., 2021). In turn, the apparent effect of the microbial community on PLT count variability is particularly interesting, which may be explained by the influence of circulating microbial metabolites on receptor-mediated platelet priming and reveals platelets as part of the immune system (Gurumurthy et al., 2026). Besides, the influence of Bilophila and Paraeggerthella (previously classified under Eggerthella) on PLT counts can be discussed in the context of the description of these bacterial genera as emerging pathogens causing bacteremia, a serious systemic infection (Kovacs et al., 2024; Salameh et al., 2012). The authors hope that further in-depth analysis of the influencing taxa will allow a more detailed explanation of the mechanisms of their involvement in the gut-bone marrow regulatory axis.

Conclusions

This study confirms and expands our understanding of the gut-bone marrow regulatory axis, which represents a communication pathway between the gut microbiome and the hematopoietic system and is one manifestation of host-microbiome interaction in poultry. Based on differences in blood profiles and gut microbial community between the globally used Arbor Acres strain and the domestic Smena 8 chicken strain, 23 bacterial genera belonging to 5 bacterial phyla were identified that were strongly positively associated with the WBC and PLT counts or negatively associated with the RBC and WBC counts. Overall, the present study explained 12.39% of RBC count variability, as well 22.28% WBC variability and 55.65% PLT variability in blood profiles of broiler chickens as microbiome-related, which should be considered when these parameters are jointly assessed in poultry farming and strain-specific reference intervals are proposed.

Acknowledgments
The study was supported by the Russian Science Foundation (grant No. 22-16-00036; https://rscf.ru /project/22-16-00036/).

Institutional Review Board Statement: The study protocol was approved by the local ethics committee in the Federal Research Center for Biological Systems and Agrotechnologies of the Russian Academy of Sciences (Resolution No. 1/2019 of March 25, 2019, as amended and clarified by Resolution No. 2/2022 of March 28, 2022).

Data Availability Statement: The data that support the findings of this study are available on request from the corresponding author. The raw sequencing data may be obtained upon request to the Center of Collective Scientific Equipment "Persistence of microorganisms" (Orenburg, Russia, e-mail: icis-ofrc@list.ru), which provided technical assistance in the analysis of the chicken gut microbiome.

References

Al Hakeem WG, Acevedo Villanueva KY & Selvaraj RK. 2023. The development of gut microbiota and its changes following *C. jejuni* infection in broilers. Vaccines, 11(3): 595. DOI: 10.3390/vaccines11030595.

Atlanderova KN, Duskaev GK, Rakhmatullin SG & Kvan OV. 2021. Metagenomic analysis of the broiler intestine microbiome against the background of plant extracts and probiotics. FEBS Open Bio, 11: 386. DOI: 10.1002/2211-5463.13205.

Bagirov VA, Ushakov AS, Duskaev GK, Kvan OV, Rakhmatullin SG, Yausheva EV & Vershinina IA. 2020. Metagenomic analysis of intestinal microbiome and biochemical composition of broiler meat upon use of *Quercus cortex* extract dietary additive. Agricultural Biology, 55(4): 682-696. DOI: 10.15389/agrobiology.2020.4.682eng.

Baudouin KA, Soualio K, Mathieu BN & Angoue Paul Y. 2021. Hematological profile of broilers and local chickens in Korhogo, Cote D'Ivoire. International Journal of Agriculture Environment and Bioresearch, 6(2): 14-23. DOI: 10.35410/IJAEB.2021.5618.

Berg G, Rybakova D, Fischer D, Cernava T, Vergès MC, Charles T, Chen X, Cocolin L, Eversole K, Corral GH, Kazou M, Kinkel L, Lange L, Lima N, Loy A, Macklin JA, Maguin E, Mauchline T, McClure R, Mitter B, Ryan M, Sarand I, Smidt H, Schelkle B, Roume H, Kiran GS, Selvin J, Souza RSC, van Overbeek L, Singh BK, Wagner M, Walsh A, Sessitsch A & Schloter M. 2020. Microbiome definition re-visited: old concepts and new challenges. Microbiome, 8(1): 103. DOI: 10.1186/s40168-020-00875-0.

Bilkova B, Bainova Z, Janda J, Zita L & Vinkler M. 2017. Different breeds, different blood: Cytometric analysis of whole blood cellular composition in chicken breeds. Veterinary Immunology and Immunopathology, 188: 71-77. DOI: 10.1016/j.vetimm.2017.05.001.

Bush JR & Alfa MJ. 2020. Increasing levels of *Parasutterella* in the gut microbiome correlate with improving low-density lipoprotein levels in healthy adults consuming resistant potato starch during a randomised trial. BMC Nutrition, 6(1): 72. DOI: 10.1186/s40795-020-00398-9.

Cowieson AJ. 2022. Comparative biology of germ-free and conventional poultry. Poultry Science, 101(10): 102105. DOI: 10.1016/j.psj.2022.102105.

Deryabin DG, Kosyan DB, Inchagova KS & Duskaev GK. 2023. Plant-derived quorum sensing inhibitors (quercetin, vanillin and umbelliferon) modulate cecal microbiome, reduces inflammation and affect production efficiency in broiler chickens. Microorganisms, 11(5): 1326. DOI: 10.3390/microorganisms11051326.

Deryabin D, Kosyan D, Vlasenko L, Lazebnik C, Zatevalov A, Karimov I & Duskaev G. 2024. Macro, trace and toxic element composition in liver and meat of broiler chicken associated with cecal microbiome community. Biology, 13(12): 975. DOI: 10.3390/biology13120975.

Diaz Carrasco JM, Casanova NA & Fernández Miyakawa ME. 2019. Microbiota, gut health and chicken productivity: what is the connection? Microorganisms, 7(10): 374. DOI: 10.3390/microorganisms7100374.

Dutta RK, Islam MS & Kabir MA. 2013. Haematological and biochemical profiles of *Gallus* indigenous, exotic and hybrid chicken breeds (*Gallus domesticus* L.) from Rajshahi, Bangladesh. Bangladesh Journal of Zoology, 41(2): 135-144. DOI: 10.3329/bjz.v41i2.23314.

Duskaev G, Kvan O, Kosyan D, Rakhmatullin S & Levakhin G. 2021. Coumarin derivative and *Bacillus cereus* change live weight and cecal ecology in broilers. AIMS Agriculture and Food, 6(1): 360-380. DOI: 10.3934/agrfood.2021022.

Duskaev GK, Rakhmatullin SG, Kosyan DB, Rusakova EA, Kvan OV & Levakhin GI. 2022. The effect of the combined use of gamma-octalactone and chlortetracycline in the broiler diet: live weight, feed efficiency and the microbiome of the caecum. Agrarian Science, (9): 47-53. DOI: 10.32634/0869-8155-2022-362-9-47-53.

Duskaev GK, Lazebnik KS & Klimova TA. 2022. Microbial diversity in the cecum of broiler chickens after introduction of coumarin and feed

antibiotic into the diet. RUDN Journal of Agronomy and Animal Industries, 17(4): 555-566. DOI: 10.22363/2312-797X-2022-17-4-555-566.

Duskaev GK, Rusakova EA & Deryabin DG. 2022. The using of gamma-octanolactone in the broiler diet: Intestinal microbiome. International Journal of Veterinary Medicine, (4): 152-158. DOI: 10.52419/issn2072-2419.2022.4.152.

Duskaev GK, Vlasenko LV, Kosyan DB & Kurilkina MY. 2023. The effect of small molecules of plant origin on the cecal microbial diversity in broilers. Ptitsevodstvo, 72(4): 46-51. DOI: 10.33845/0033-3239-2023-72-4-46-51.

El Brihi J & Pathak S. 2024. Normal and abnormal complete blood count with differential. In: StatPearls. StatPearls Publishing, Treasure Island, FL, USA.

Emanuylova ZhV, Egorova AV, Efimov DN & Komarov AA. 2021. New highly productive Russian cross of broiler chicken "Smena-9". Agrarian Science, (7-8): 33-36. DOI: 10.32634/0869-8155-2021-351-7-8-33-36.

Fan Z, Ke X, Jiang L, Zhang Z, Yi M, Liu Z, Cao J, Lu M & Wang M. 2024. Genomic and biochemical analysis reveals fermented product of a putative novel *Romboutsia* species involves the glycometabolism of tilapia. Aquaculture, 581(41): 740483. DOI: 10.1016/j.aquaculture.2023.740483.

Fernandez Sanchez J, Maknojia AA & King KY. 2024. Blood and guts: how the intestinal microbiome shapes hematopoiesis and treatment of hematologic disease. Blood, 143(17): 1689-1701. DOI: 10.1182/blood.2023021174.

Gurumurthy G, Gurumurthy J, Gurumurthy S, Reynolds L & Thachil J. 2026. Dysbiosis and immunothrombosis - How platelets and the gut microbiome interact. Blood Reviews, 101395. DOI: 10.1016/j.blre.2026.101395.

Idowu PA, Mpofu TJ, Zishiri OT, Oluwamayowa OJ, Nephawe KA & Mtileni B. 2025. Gene sequencing and in silico characterization of mannose-binding lectin in South African chicken breeds. Journal of Advanced Veterinary and Animal Research, 12(3): 941-955. DOI: 10.5455/javar.2025.l955.

Khosravi A, Yanez A, Price JG, Chow A, Merad M, Goodridge HS & Mazmanian SK. 2014. Gut microbiota promote hematopoiesis to control bacterial infection. Cell Host & Microbe, 15(3): 374-381. DOI: 10.1016/j.chom.2014.02.006.

Kongpechr S, Sukon P & Sohsuebngarm D. 2021. The study of hematology in commercial broiler chickens of Cobb 500, Ross 308, and Arbor Acres Plus. Journal of Mahanakorn Veterinary Medicine, 15(2): 209-221.

Kovacs R, Arokszállási T, Bozo A, Jakab A, Babel KS, Heja M, Kovacs KB, Balazs B, Vitalis E, Majoros L & Tóth Z. 2024. Bacteraemia associated with *Bilophila wadsworthia*: A rare case presentation from Hungary. Pathogens, 13(9): 749. DOI: 10.3390/pathogens13090749.

Lee YS, Kim TY, Kim Y, Kim S, Lee SH, Seo SU, Zhou BO, Eunju O, Kim KS & Kweon MN. 2021. Microbiota-derived lactate promotes hematopoiesis and erythropoiesis by inducing stem cell factor production from leptin receptor+ niche cells. Experimental & Molecular Medicine, 53(9): 1319-1331. DOI: 10.1038/s12276-021-00667-y.

Liu X, Zhang H, Shi G, Zheng X, Chang J, Lin Q, Tian Z & Yang H. 2024. The impact of gut microbial signals on hematopoietic stem cells and the bone marrow microenvironment. Frontiers in Immunology, 15: 1338178. DOI: 10.3389/fimmu.2024.1338178.

Lynch JB, Gonzalez EL, Choy K, Faull KF, Jewell T, Arellano A, Liang J, Yu KB, Paramo J & Hsiao EY. 2023. Gut microbiota *Turicibacter* strains differentially modify bile acids and host lipids. Nature Communications, 14(1): 3669. DOI: 10.1038/s41467-023-39403-7.

Nawaz AH, Setthaya P & Feng C. 2024. Exploring evolutionary adaptations and genomic advancements to improve heat tolerance in chickens. Animals, 14(15): 2215. DOI: 10.3390/ani14152215.

Nie K, Ma K, Luo W, Shen Z, Yang Z, Xiao M, Tong T, Yang Y & Wang X. 2021. *Roseburia intestinalis*: a beneficial gut organism from the discoveries in genus and species. Frontiers in Cellular and Infection Microbiology, 11: 757718. DOI: 10.3389/fcimb.2021.757718.

Nwaigwe CU, Ihedioha JI, Shoyinka SV & Nwaigwe CO. 2020. Evaluation of the hematological and clinical biochemical markers of stress in broiler chickens. Veterinary World, 13(10): 2294-2300. DOI: 10.14202/vetworld.2020.2294-2300.

Paul SS, Chatterjee RN, Raju MVLN, Prakash B, Rama Rao SV, Yadav SP & Kannan A. 2021. Gut microbial composition differs extensively among Indian native chicken breeds originated in different geographical locations and a commercial broiler line, but breed-specific, as well as across-breed core microbiomes, are found. Microorganisms, 9(2): 391. DOI: 10.3390/microorganisms9020391.

Ryazanov V, Duskaev G, Rakhmatullin S, Nurzhanov B & Rysaev A. 2021. Effects of joint and separate uses of the *Quercus cortex* extract and antibiotics on the microbiome of the broiler intestine. FEBS Open Bio, 11: 385-386. DOI: 10.1002/2211-5463.13205.

Salameh A, Klotz SA & Zangeneh TT. 2012. Disseminated infection caused by *Eggerthella lenta* in a previously healthy young man: a case

report. Case Reports in Infectious Diseases, 2012: 517637. DOI: 10.1155/2012/517637.

Schoch CL, Ciufo S, Domrachev M, Hotton CL, Kannan S, Khovanskaya R, Leipe D, Mcveigh R, O'Neill K, Robbertse B, Sharma S, Soussov V, Sullivan JP, Sun L, Turner S & Karsch-Mizrachi I. 2020. NCBI Taxonomy: a comprehensive update on curation, resources and tools. Database, 2020: baaa062. DOI: 10.1093/database/baaa062.

Shajahmetova E, Deryabin D & Duskaev G. 2021. Gamma lactone and vanillic acid change the microbiome of broiler blind appendage. Biotechnology and Biotechnological Equipment, 35(S1): S74. DOI: 10.1080/13102818.2020.1871545.

Shterzer N, Sbehat Y, Poudel B, Rothschild N, Oloko OE, Headrick J, Petersen E, Druyan S & Mills E. 2023. Differences in gut bacterial community composition between modern and slower-growing broiler breeder lines: Implications of growth selection on microbiome composition. Frontiers in Physiology, 14: 1151151. DOI: 10.3389/fphys.2023.1151151.

SILVA. 2025. SILVA rRNA database project. Available online:

Talebi A, Asri-Rezaei S, Rozeh-Chai R & Sahraei R. 2005. Comparative studies on haematological values of broiler strains (Ross, Cobb, Arbor-acres and Arian). International Journal of Poultry Science, 4: 573-579. DOI: 10.3923/ijps.2005.573.579.

Thrall MA, Weiser G, Allison RW & Campbell TW. 2022. Veterinary Hematology, Clinical Chemistry, and Cytology, 3rd ed. Wiley Blackwell, Hoboken, NJ, USA. 1042 Pages.

Tong L, Wang W, Ren S, Wang J, Wang J, Qu Y, Addoma Adam FE, Li Z & Gao X. 2022. The 16S rRNA gene sequencing of gut microbiota in chickens infected with different virulent Newcastle disease virus strains. Animals, 12(19): 2558. DOI: 10.3390/ani12192558.

Wang Q, Garrity GM, Tiedje JM & Cole JR. 2007. Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. Applied and Environmental Microbiology, 73(16): 5261-5267. DOI: 10.1128/AEM.00062-07.

Wells C, Robertson T, Sheth P & Abraham S. 2024. How aging influences the gut-bone marrow axis and alters hematopoietic stem cell regulation. Heliyon, 10(12): e32831. DOI: 10.1016/j.heliyon.2024.e32831.

Supplementary data:

Table S1: Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains.

Table S1: (Supplement). Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains

Genus	Arbor Acres (n=28)		Smena-8 (n=12)		*p* value
	Occurrence (%)	Abundance (%)	Occurrence (%)	Abundance (%)	
Belonging to the phylum *Actinomycetota*					
Adlercreutzia	64.29	0.054 [0.021–0.126]	16.67	0.006 [0.006–0.006]	2.307×10^{-3}
Bifidobacterium	17.86	0.321 [0.172–0.435]	50.00	0.244 [0.184–0.335]	5.816×10^{-2}
Eggerthella	14.29	0.062 [0.022–0.101]	33.33	0.019 [0.008–0.031]	4.896×10^{-1}
Enterorhabdus	0.00	0.00 [0.00–0.00]	41.67	0.005 [0.002–0.005]	1.408×10^{-1}
Gardnerella	0.00	0.00 [0.00–0.00]	16.67	0.002 [0.002–0.002]	$<10^{-6}$
Gordonibacter	78.57	0.028 [0.016–0.102]	41.67	0.004 [0.003–0.009]	2.242×10^{-4}
Paraeggerthella	0.00	0.00 [0.00–0.00]	75.00	0.016 [0.015–0.028]	1.365×10^{-5}
Parvibacter	0.00	0.00 [0.00–0.00]	25.00	0.002 [0.002–0.003]	$<10^{-6}$
Rubneribacter	78.57	0.585 [0.147–1.757]	0.00	0.00 [0.00–0.00]	4.667×10^{-5}
Slackia	39.29	0.020 [0.009–0.022]	8.33	0.004 [0.004–0.004]	1.380×10^{-2}
unclassified Coriobacteriaceae	10.71	0.559 [0.505–0.663]	75.00	0.030 [0.014–0.152]	6.163×10^{-4}
unclassified Eggerthellaceae	50.00	0.055 [0.022–0.13]	0.00	0.00 [0.00–0.00]	3.761×10^{-3}
Belonging to the phylum *Bacillota*					
Abyssivirga	35.71	0.027 [0.019–0.075]	0.00	0.00 [0.00–0.00]	2.087×10^{-2}
Acetanaerobacterium	0.00	0.00 [0.00–0.00]	8.33	0.003 [0.003–0.003]	$<10^{-6}$
Acetatifactor	0.00	0.00 [0.00–0.00]	16.67	0.004 [0.004–0.004]	$<10^{-6}$
Acetivibrio	0.00	0.00 [0.00–0.00]	100.00	0.017 [0.005–0.04]	6.079×10^{-8}
Agathobacter	17.86	0.194 [0.177–0.227]	0.00	0.00 [0.00–0.00]	1.297×10^{-1}
Agathobaculum	60.71	1.221 [0.984–2.273]	0.00	0.00 [0.00–0.00]	8.704×10^{-4}
Anaerobacillus	0.00	0.00 [0.00–0.00]	8.33	0.011 [0.011–0.011]	1.408×10^{-1}

Table S1: (Supplement). Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains

Genus	Arbor Acres (n=28)		Smena-8 (n=12)		*p* value
	Occurrence (%)	Abundance (%)	Occurrence (%)	Abundance (%)	
Anaerobacterium	71.43	0.034 [0.03–0.168]	100.00	0.602 [0.251–0.785]	3.899×10^{-5}
Anaerobutyricum	64.29	0.043 [0.022–0.069]	0.00	0.00 [0.00–0.00]	5.049×10^{-4}
Anaerofilum	78.57	0.046 [0.033–0.148]	91.67	0.1 [0.051–0.106]	1.812×10^{-1}
Anaerofustis	50.00	0.031 [0.014–0.06]	33.33	0.007 [0.005–0.009]	6.298×10^{-2}
Anaeromassilibacillus	78.57	0.217 [0.183–0.678]	0.00	0.00 [0.00–0.00]	4.654×10^{-5}
Anaerorhabdus	17.86	0.098 [0.015–0.098]	0.00	0.00 [0.00–0.00]	1.296×10^{-1}
Anaerostipes	53.57	0.025 [0.013–0.064]	50.00	0.015 [0.008–0.021]	3.422×10^{-1}
Anaerotignum	78.57	0.689 [0.603–1.541]	8.33	1.892 [1.892–1.892]	8.565×10^{-4}
Anaerotruncus	82.14	0.225 [0.086–0.381]	100.00	0.027 [0.022–0.041]	5.811×10^{-3}
Anaerovorax	10.71	0.048 [0.045–0.122]	91.67	0.069 [0.041–0.146]	3.685×10^{-6}
Asaccharospora	0.00	0.00 [0.00–0.00]	33.33	0.005 [0.002–0.009]	3.160×10^{-2}
Bacillus	0.00	0.00 [0.00–0.00]	16.67	0.002 [0.002–0.002]	$<10^{-6}$
Beduinibacterium	75.00	0.137 [0.069–0.466]	0.00	0.00 [0.00–0.00]	8.814×10^{-5}
Blautia	100.00	0.232 [0.154–0.283]	100.00	0.712 [0.402–0.85]	5.001×10^{-3}
Butyricicoccus	100.00	1.025 [0.695–1.473]	100.00	0.213 [0.152–0.275]	1.980×10^{-5}
Butyrivibrio	7.14	0.039 [0.031–0.047]	0.00	0.00 [0.00–0.00]	3.689×10^{-1}
Caecibacterium	3.57	0.081 [0.081–0.081]	0.00	0.00 [0.00–0.00]	5.484×10^{-1}
Caproicibacter	3.57	0.194 [0.194–0.194]	0.00	0.00 [0.00–0.00]	$5.484\times\text{-}10^{-1}$
Catellicoccus	0.00	0.00 [0.00–0.00]	8.33	0.003 [0.003–0.003]	$<10^{-6}$
Catenibacterium	0.00	0.00 [0.00–0.00]	8.33	0.004 [0.004–0.004]	$<10^{-6}$
Cellulosilyticum	0.00	0.00 [0.00–0.00]	25.00	0.003 [0.003–0.007]	1.408×10^{-1}
Christensenella	100.00	2.445 [1.188–4.271]	91.67	0.023 [0.022–0.056]	2.394×10^{-6}
Clostridium	14.29	0.059 [0.046–0.089]	0.00	0.00 [0.00–0.00]	1.828×10^{-1}

Table S1: (Supplement). Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains

Genus	Arbor Acres (n=28)		Smena-8 (n=12)		*p* value
	Occurrence (%)	Abundance (%)	Occurrence (%)	Abundance (%)	
Clostridium IV	96.43	0.157 [0.085–0.431]	100.00	1.126 [0.864–1.397]	9.124×10^{-5}
Clostridium XlVa	82.14	0.064 [0.037–0.78]	91.67	0.155 [0.059–0.218]	7.221×10^{-1}
Clostridium XlVb	42.86	0.038 [0.025–0.198]	100.00	0.142 [0.062–0.328]	1.847×10^{-4}
Clostridium sensu stricto	14.29	0.016 [0.015–0.04]	33.33	0.010 [0.009–0.015]	2.626×10^{-1}
Coprobacillus	0.00	0.00 [0.00–0.00]	66.67	0.041 [0.021–0.065]	2.463×10^{-6}
Coprococcus	85.71	0.054 [0.034–0.075]	83.33	0.012 [0.005–0.024]	1.090×10^{-3}
Desulfotomaculum	21.43	0.370 [0.057–0.705]	0.00	0.00 [0.00–0.00]	1.297×10^{-1}
Dielma	64.29	0.197 [0.148–0.362]	0.00	0.00 [0.00–0.00]	5.097×10^{-4}
Dorea	3.57	0.015 [0.015–0.015]	66.67	0.006 [0.005–0.01]	5.119×10^{-4}
Dysosmobacter	78.57	0.999 [0.721–1.66]	0.00	0.00 [0.00–0.00]	4.637×10^{-5}
Eisenbergiella	100.00	1.929 [0.537–4.942]	75.00	0.057 [0.021–0.06]	2.097×10^{-6}
Enterococcus	3.57	0.09 [0.09–0.09]	58.33	0.015 [0.008–0.02]	3.213×10^{-3}
Erysipelotrichaceae Incertae sedis	7.14	0.620 [0.602–0.637]	83.33	0.010 [0.004–0.015]	5.638×10^{-3}
Ethanoligenens	3.57	4.248 [4.248–4.248]	25.00	0.008 [0.006–0.008]	1.852×10^{-1}
Eubacterium	7.14	0.034 [0.028–0.04]	41.67	0.005 [0.002–0.005]	9.742×10^{-1}
Faecalibacillus	35.71	0.072 [0.051–0.164]	8.33	0.008 [0.008–0.008]	5.810×10^{-2}
Faecalibacterium	100.00	4.500 [2.469–5.772]	100.00	7.302 [4.926–8.6]	4.627×10^{-2}
Flavonifractor	71.43	0.525 [0.415–0.756]	100.00	0.258 [0.089–0.498]	6.143×10^{-1}
Fournierella	78.57	0.685 [0.408–0.942]	0.00	0.00 [0.00–0.00]	4.667×10^{-5}
Frisingicoccus	64.29	0.073 [0.057–0.088]	0.00	0.00 [0.00–0.00]	5.004×10^{-4}
Fusicatenibacter	100.00	0.401 [0.162–0.545]	91.67	0.402 [0.009–0.553]	3.446×10^{-1}
Gemmiger	17.86	0.293 [0.285–0.326]	58.33	0.015 [0.006–0.033]	1.486×10^{-1}
Granulicatella	0.00	0.00 [0.00–0.00]	8.33	0.017 [0.017–0.017]	1.408×10^{-1}

Table S1: (Supplement). Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains

Genus	Arbor Acres (n=28)		Smena-8 (n=12)		*p* value
	Occurrence (%)	Abundance (%)	Occurrence (%)	Abundance (%)	
Harryflintia	67.86	0.021 [0.018–0.042]	0.00	0.00 [0.00–0.00]	2.782×10^{-4}
Hespella	28.57	0.025 [0.015–0.028]	25.00	0.091 [0.05–0.096]	9.252×10^{-1}
Holdemania	3.57	0.013 [0.013–0.013]	8.33	0.005 [0.005–0.005]	5.484×10^{-1}
Hungatella	17.86	0.370 [0.317–0.407]	8.33	0.004 [0.004–0.004]	1.297×10^{-1}
Hydrogeniiclostridium	78.57	0.070 [0.053–0.280]	0.00	0.00 [0.00–0.00]	4.650×10^{-5}
Ihubacter	75.00	0.060 [0.031–0.134]	0.00	0.00 [0.00–0.00]	8.769×10^{-5}
Intestinibacter	42.86	0.053 [0.021–0.067]	0.00	0.00 [0.00–0.00]	9.171×10^{-3}
Intestinimonas	67.86	1.670 [1.001–2.541]	91.67	0.029 [0.013–0.291]	1.182×10^{-1}
Isobaculum	0.00	0.00 [0.00–0.00]	25.00	0.009 [0.007–0.019]	3.166×10^{-2}
Lachnospira	35.71	0.075 [0.037–0.147]	0.00	0.00 [0.00–0.00]	2.093×10^{-2}
Lachnospiracea incertae sedis	75.00	0.050 [0.026–0.065]	100.00	0.056 [0.033–0.141]	1.188×10^{-1}
Lacrimispora	32.14	0.027 [0.016–0.052]	0.00	0.00 [0.00–0.00]	3.078×10^{-2}
Lactobacillus	100.00	2.225 [0.744–4.189]	100.00	4.915 [2.193–11.595]	1.368×10^{-2}
Lawsonibacter	32.14	0.117 [0.041–0.140]	0.00	0.00 [0.00–0.00]	3.079×10^{-2}
Ligilactobacillus	75.00	0.920 [0.251–2.246]	0.00	0.00 [0.00–0.00]	8.829×10^{-5}
Limosilactobacillus	78.57	0.608 [0.2–1.297]	0.00	0.00 [0.00–0.00]	4.667×10^{-5}
Listeria	0.00	0.00 [0.00–0.00]	25.00	0.031 [0.019–0.073]	7.328×10^{-3}
Massiliimalia	67.86	0.053 [0.034–0.072]	0.00	0.00 [0.00–0.00]	2.888×10^{-4}
Massilimicrobiota	78.57	0.060 [0.044–0.150]	0.00	0.00 [0.00–0.00]	4.596×10^{-5}
Mediterraneibacter	78.57	1.931 [1.268–2.913]	0.00	0.00 [0.00–0.00]	4.667×10^{-5}
Merdimonas	78.57	0.125 [0.085–0.327]	0.00	0.00 [0.00–0.00]	4.650×10^{-5}
Mobilitalea	0.00	0.00 [0.00–0.00]	8.33	0.015 [0.015–0.015]	1.408×10^{-1}
Monoglobus	78.57	0.291 [0.104–0.438]	0.00	0.00 [0.00–0.00]	4.663×10^{-5}

Table S1: (Supplement). Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains

Genus	Arbor Acres (n=28)		Smena-8 (n=12)		*p* value
	Occurrence (%)	Abundance (%)	Occurrence (%)	Abundance (%)	
Negativibacillus	60.71	0.423 [0.286–0.579]	0.00	0.00 [0.00–0.00]	8.686×10^{-4}
Neglectibacter	78.57	0.504 [0.369–0.689]	0.00	0.00 [0.00–0.00]	4.654×10^{-5}
Oscillibacter	100.00	0.409 [0.276–0.479]	91.67	0.129 [0.105–0.144]	3.135×10^{-4}
Papillibacter	0.00	0.00 [0.00–0.00]	16.67	0.004 [0.004–0.004]	$<10^{-6}$
Pediococcus	0.00	0.00 [0.00–0.00]	16.67	0.017 [0.017–0.017]	3.160×10^{-2}
Pelospora	0.00	0.00 [0.00–0.00]	8.33	0.003 [0.003–0.003]	$<10^{-6}$
Peptacetobacter	3.57	0.018 [0.018–0.018]	0.00	0.00 [0.00–0.00]	5.484×10^{-1}
Peptococcus	0.00	0.00 [0.00–0.00]	75.00	0.008 [0.006–0.014]	2.186×10^{-6}
Petroclostridium	35.71	0.023 [0.021–0.061]	0.00	0.00 [0.00–0.00]	2.056×10^{-2}
Phascolarctobacterium	7.14	0.072 [0.072–0.072]	25.00	0.006 [0.006–0.139]	1.431×10^{-1}
Phocea	67.86	0.046 [0.026–0.109]	0.00	0.00 [0.00–0.00]	2.888×10^{-4}
Pilibacter	0.00	0.00 [0.00–0.00]	8.33	0.011 [0.011–0.011]	1.408×10^{-1}
Pseudobutyrivibrio	0.00	0.00 [0.00–0.00]	16.67	0.005 [0.005–0.005]	$<10^{-6}$
Pseudoclostridium	17.86	0.033 [0.032–0.137]	0.00	0.00 [0.00–0.00]	1.297×10^{-1}
Pseudoflavonifractor	21.43	0.364 [0.307–0.480]	91.67	0.994 [0.577–1.975]	2.148×10^{-6}
Robinsoniella	0.00	0.00 [0.00–0.00]	8.33	0.004 [0.004–0.004]	$<10^{-6}$
Romboutsia	100.00	0.552 [0.366–1.163]	91.67	0.023 [0.012–0.029]	7.474×10^{-7}
Roseburia	78.57	0.266 [0.193–0.410]	75.00	0.008 [0.006–0.017]	1.264×10^{-3}
Ruminococcus	100.00	0.685 [0.227–1.481]	100.00	0.531 [0.309–1.290]	7.677×10^{-1}
Ruthenibacterium	75.00	0.225 [0.18–0.307]	0.00	0.00 [0.00–0.00]	8.821×10^{-5}
Saccharofermentans	3.57	0.609 [0.609–0.609]	0.00	0.00 [0.00–0.00]	5.484×10^{-1}
Solibacillus	0.00	0.00 [0.00–0.00]	8.33	0.003 [0.003–0.003]	$<10^{-6}$
Sporobacter	57.14	0.021 [0.014–0.046]	58.33	0.009 [0.008–0.012]	4.175×10^{-1}

Table S1: (Supplement). Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains

Genus	Arbor Acres (n=28)		Smena-8 (n=12)		*p* value
	Occurrence (%)	Abundance (%)	Occurrence (%)	Abundance (%)	
Staphylococcus	0.00	0.00 [0.00–0.00]	8.33	0.003 [0.003–0.003]	$<10^{-6}$
Streptococcus	78.57	0.334 [0.082–0.684]	58.33	0.005 [0.002–0.011]	9.284×10^{-4}
Subdoligranulum	100.00	1.433 [0.478–2.232]	91.67	0.23 [0.158–1.050]	6.579×10^{-3}
Terrisporobacter	0.00	0.00 [0.00–0.00]	25.00	0.012 [0.008–0.012]	3.160×10^{-2}
Thomasclavelia (Clostridium XVIII)	78.57	0.088 [0.050–0.267]	100.00	0.181 [0.037–0.423]	1.375×10^{-1}
Tindallia	0.00	0.00 [0.00–0.00]	16.67	0.002 [0.002–0.002]	$<10^{-6}$
Turicibacter	100.00	0.514 [0.157–6.202]	58.33	0.006 [0.002–0.006]	1.078×10^{-6}
unclassified Carnobacteriaceae	3.57	0.017 [0.017–0.017]	83.33	0.009 [0.003–0.035]	5.494×10^{-4}
unclassified Clostridiales Family XIII	0.00	0.00 [0.00–0.00]	75.00	0.008 [0.008–0.028]	2.366×10^{-6}
unclassified Erysipelotrichaceae	100.00	0.431 [0.263–0.690]	100.00	0.053 [0.033–0.078]	1.087×10^{-6}
unclassified Lachnospiraceae	100.00	3.738 [3.137–4.528]	100.00	3.272 [2.393–3.757]	1.360×10^{-1}
unclassified Oscillospiraceae	100.00	18.268 [15.237–21.440]	100.00	11.543 [7.605–14.222]	2.046×10^{-2}
unclassified Peptostreptococcaceae	42.86	0.065 [0.031–0.123]	58.33	0.099 [0.010–0.151]	5.024×10^{-1}
unclassified Planococcaceae	0.00	0.00 [0.00–0.00]	16.67	0.007 [0.007–0.007]	3.160×10^{-2}
Belonging to the phylum *Bacteroidota*					
Alistipes	64.29	14.014 [5.451–39.300]	100.00	28.818 [10.372–36.235]	2.282×10^{-2}
Bacteroides	100.00	4.611 [0.217–20.676]	100.00	16.118 [2.841–35.647]	5.313×10^{-2}
Chishuiella	3.57	0.01 [0.01–0.01]	25.00	0.002 [0.002–0.035]	5.319×10^{-1}
Coprobacter	0.00	0.00 [0.00–0.00]	58.33	0.061 [0.036–0.673]	1.385×10^{-5}
Odoribacter	10.71	0.523 [0.382–0.610]	0.00	0.00 [0.00–0.00]	2.581×10^{-1}
Parabacteroides	0.00	0.00 [0.00–0.00]	16.67	0.003 [0.003–0.003]	$<10^{-6}$
Paramuribaculum	21.43	0.015 [0.010–0.020]	0.00	0.00 [0.00–0.00]	9.153×10^{-2}
Petrimonas	0.00	0.00 [0.00–0.00]	16.67	0.002 [0.002–0.002]	$<10^{-6}$

Table S1: (Supplement). Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains

Genus	Arbor Acres (n=28)		Smena-8 (n=12)		*p* value
	Occurrence (%)	Abundance (%)	Occurrence (%)	Abundance (%)	
Phocaeicola	42.86	2.319 [1.513–4.678]	0.00	0.00 [0.00–0.00]	9.211×10^{-3}
Prevotella	0.00	0.00 [0.00–0.00]	8.33	0.007 [0.007–0.007]	1.408×10^{-1}
unclassified Porphyromonadaceae	7.14	0.036 [0.025–0.047]	33.33	0.012 [0.010–0.015]	1.430×10^{-1}
unclassified Rikenellaceae	10.71	0.021 [0.015–0.078]	100.00	0.198 [0.084–0.240]	3.808×10^{-8}
Belonging to the phylum *Chloroflexota*					
Candidatus Chloroploca	0.00	0.00 [0.00–0.00]	16.67	0.002 [0.002–0.002]	$<10^{-6}$
Belonging to the phylum *Cyanobacteriota*					
Vampirovibrio	96.43	0.446 [0.165–0.558]	41.67	0.018 [0.009–0.024]	6.792×10^{-6}
Belonging to the phylum *Chlamydiota*					
unclassified Parachlamydiaceae	0.00	0.00 [0.00–0.00]	8.33	0.013 [0.013–0.013]	1.408×10^{-1}
Belonging to the phylum *Mycoplasmatota*					
Anaeroplasma	35.71	0.068 [0.048–0.117]	25.00	0.02 [0.012–0.044]	2.090×10^{-1}
Belonging to the phylum *Pseudomonadota*					
Aestuariispira	42.86	0.042 [0.017–0.055]	0.00	0.00 [0.00–0.00]	9.091×10^{-3}
Escherichia/Shigella sp.	17.86	0.154 [0.048–0.339]	91.67	0.233 [0.152–0.942]	1.819×10^{-4}
Parasutterella	53.57	0.428 [0.327–0.692]	50.00	0.01 [0.006–0.019]	1.144×10^{-1}
Perlucidibaca	0.00	0.00 [0.00–0.00]	8.33	0.003 [0.003–0.003]	$<10^{-6}$
Propionivibrio	0.00	0.00 [0.00–0.00]	8.33	0.003 [0.003–0.003]	$<10^{-6}$
Pseudomonas	0.00	0.00 [0.00–0.00]	25.00	0.118 [0.065–0.18]	7.328×10^{-3}
Ralstonia	0.00	0.00 [0.00–0.00]	33.33	0.005 [0.004–0.006]	1.408×10^{-1}
unclassified Caulobacteraceae	0.00	0.00 [0.00–0.00]	16.67	0.004 [0.004–0.004]	$<10^{-6}$
unclassified Comamonadaceae	0.00	0.00 [0.00–0.00]	16.67	0.002 [0.002–0.002]	$<10^{-6}$
unclassified Enterobacteriaceae	3.57	0.083 [0.083–0.083]	41.67	0.024 [0.007–0.034]	3.224×10^{-3}

Table S1: (Supplement). Occurrence and relative abundance of bacterial genera and equivalent taxonomic ranks in the cecal microbiomes of Arbor Acres and Smena 8 broiler chicken strains

Genus	Arbor Acres (n=28)		Smena-8 (n=12)		*p* value
	Occurrence (%)	Abundance (%)	Occurrence (%)	Abundance (%)	
unclassified Oxalobacteraceae	0.00	0.00 [0.00–0.00]	33.33	0.008 [0.005–0.014]	3.166×10^{-2}
unclassified Pasteurellaceae	0.00	0.00 [0.00–0.00]	8.33	0.004 [0.004–0.004]	$<10^{-6}$
unclassified Rhodospirillaceae	0.00	0.00 [0.00–0.00]	8.33	0.005 [0.005–0.005]	1.408×10^{-1}
unclassified Sphingomonadaceae	0.00	0.00 [0.00–0.00]	25.00	0.003 [0.003–0.012]	1.408×10^{-1}
Belonging to the phylum *Spirochaetota*					
Leptospira	0.00	0.00 [0.00–0.00]	8.33	0.005 [0.005–0.005]	1.408×10^{-1}
Belonging to the phylum *Thermodesulfobacteriota*					
Bilophila	64.29	0.548 [0.267–1.438]	83.33	0.07 [0.054–0.098]	8.796×10^{-2}
Mailhella	39.29	0.078 [0.047–0.118]	0.00	0.00 [0.00–0.00]	1.397×10^{-2}
unclassified Desulfovibrionaceae	21.43	0.036 [0.022–0.083]	50.00	0.065 [0.039–0.095]	1.334×10^{-1}
Belonging to the phylum *Verrucomicrobiota*					
Akkermansia	39.29	0.125 [0.08–0.497]	8.33	0.005 [0.005–0.005]	1.400×10^{-2}

Note: Abundance data are presented as median values [Q1–Q3]; P-values between groups were calculated using the Mann–Whitney U test.