Gut microbiome and flight performance in racing pigeons: emerging evidence and mechanistic links

[1]Kouassi Elisee Kporou, [2,3,4,5]I. Valentin Petrescu-Mag

[1] Department of Biochemistry and Microbiology, Excellence Group of Research on products of Traditional Pharmacopoeia (GeRProPhaT), Jean Lorougnon Guédé University, Ivory Coast; [2] Department of Environmental Engineering and Protection, Faculty of Agriculture, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 400372 Cluj-Napoca, Romania; [3] Bioflux SRL, 400488 Cluj-Napoca, Romania; [4] University of Oradea, 410087 Oradea, Romania; [5] WABBA International Bodybuilding and Fitness LTD, E11 1HT London, United Kingdom; e-mail: ioan.mag@usamvcluj.ro

Abstract. This mini-review synthesizes current evidence on the relationship between the gut microbiome and flight performance in racing pigeons (*Columba livia*), with emphasis on emerging mechanistic links. The literature surveyed was identified through searches in major scientific databases (e.g., Web of Science, Scopus, and PubMed), focusing on studies published in the last two decades that address avian microbiomes, exercise physiology, and host–microbiome interactions. Available studies indicate that gut microbial communities in racing pigeons are closely associated with host health, energy metabolism, and endurance capacity, although direct causal relationships with flight performance remain insufficiently demonstrated. Observational data show that lower pathogen burdens and more stable microbiota profiles correlate with improved race consistency. Comparative insights from migratory birds and exercise models suggest that microbiome remodeling during sustained physical effort enhances metabolic pathways related to energy production, including fatty acid and carbohydrate metabolism. Mechanistically, the gut–muscle axis, microbial-derived short-chain fatty acids (SCFAs), and immune modulation appear central in mediating these effects. SCFAs contribute to intestinal integrity, energy supply, and systemic immune regulation, while dysbiosis may impair performance through inflammation and oxidative stress. However, experimental validation of these mechanisms in racing pigeons remains very limited, with most evidence derived from correlational studies or extrapolated from other species. Although pigeon-specific experimental evidence is still scarce, the integration of avian and broader animal research suggests a potential association between the gut microbiome and endurance flight. Future controlled intervention studies are required to establish causality and to develop microbiome-targeted strategies for optimizing racing pigeon performance.
Key Words: gut microbiome, racing pigeons, flight performance, endurance, gut-muscle axis, short-chain fatty acids, energy metabolism, immune modulation, avian physiology, microbiota.

Introduction. Despite the fact that the pigeon (*Columba livia*) does not hold as much importance as other farm animals, the literature on this species is abundant in scientific data, both regarding anatomy, morphology, and physiology (Ionescu & Oroian 2019; Ionescu et al 2015; Popescu & Papuc 2026), as well as aspects related to maintaining the health of pigeons (Oroian & Popescu 2026; Popescu & Burduhos 2026), due to its value as a model organism (Zan et al 2023; Zhang et al 2023; Zhang et al 2024b) and the large number of enthusiasts who keep pigeons as a hobby (Popescu & Cîmpean 2026).

The available literature on racing pigeons and other high-endurance birds suggests that gut microbiota are tightly linked to energy metabolism, immunity, and health during prolonged flight, but direct causal links to flight performance in pigeons remain emergent. Evidence comes from pigeon-specific microbiome studies and broader avian and exercise-microbiome research in birds and other animals. Despite increasing interest in the gut microbiome in animal performance, its direct role in flight performance in racing pigeons remains poorly understood.

The aim of this mini-review is to critically evaluate and integrate current knowledge regarding the role of the gut microbiome in influencing flight performance in racing pigeons. Specifically, it seeks to: (i) summarize existing evidence linking gut microbial composition to health and performance outcomes in pigeons; (ii) contextualize these findings through comparative insights from migratory birds and exercise-related microbiome research; and (iii) outline plausible biological mechanisms - particularly those involving energy metabolism, immune regulation, and the gut–muscle axis - that may underpin microbiome-mediated effects on endurance flight. We hypothesize that microbiome-mediated metabolic and immune pathways may contribute to endurance flight performance. Ultimately, the review aims to identify knowledge gaps and highlight directions for future experimental research.

Microbiome Features in Racing Pigeons and Performance-Related Health. Racing pigeons host diverse intestinal *Enterococcus* communities, dominated by *E. columbae* and including at least eight additional species, many carrying virulence genes and high levels of antibiotic resistance (Dolka et al 2020). During a racing season, health disturbances (coccidiosis, trichomonosis, respiratory disease) and rising stress are associated with increased coliforms and opportunistic pathogens (e.g. *E. coli*, *Enterococcus faecium*, *Enterococcus gallinarum*, staphylococci), while birds with the lowest prevalence of these pathogens and *Eimeria spp*. maintain the most stable and best race results (Kalinaj et al 2024).

Long-distance trained pigeons (≈2669 km in 9 weeks) develop a gut microbiota taxonomically distinct from non-flying conspecifics; despite large taxonomic variation among individuals, the inferred metabolic potential is relatively stable, and flying birds show enrichment of biosynthetic metabolic pathways among the pathways most associated with flight status (Ferrari et al 2023). This suggests functional convergence toward enhanced biosynthetic capacity in actively flying pigeons (Table 1).

Table 1

Links between pigeon gut microbiota, health and race outcomes

Aspect	*Main finding*	*Performance relevance*	*References*
Enterococcus community	9 species, many with virulence genes, frequent antibiotic resistance	Potential chronic inflammation, pathogen reservoir	(Dolka et al 2020)
Seasonal health and pathogens	Higher coliforms, *E. coli, E. faecium, E. gallinarum*, staphylococci with stress/disease; low levels linked to best race points	Lower pathogen load aligns with more consistent performance	(Kalinaj et al 2024)
Flight training vs. non-flying	Distinct microbiota; enriched biosynthetic pathways in flyers	Indicates metabolic adaptation of gut microbiome to endurance	(Ferrari et al 2023).

Gut Microbiome, Endurance Flight, and Energetics in Birds. Across long-distance migratory birds, active migration is often associated with reduced microbiome diversity and expansion of specific taxa; some microbial traits correlate with body condition and fat stores (Capilla-Lasheras & Risely 2025; Trevelline et al 2023). In Blackpoll Warblers, fall migration is accompanied by convergent microbiome remodeling: marked increase of Proteobacteria (Enterobacteriaceae) and enrichment of pathways for vitamin, amino acid, fatty acid biosynthesis and carbohydrate metabolism, which correlate positively with body mass and subcutaneous fat (Trevelline et al 2023). Similar functional shifts are reported in shorebirds, where *Corynebacterium* and other taxa are enriched and may support energy requirements during migration (Zhang et al 2021).

Stopover passerines immediately after long flights show Firmicutes- and Proteobacteria-dominated communities; seasonal differences in microbiota are clearer than relationships with momentary energetic condition, highlighting strong environmental and dietary influences (Lewis et al 2016).

In black-necked cranes, late overwintering (pre-migration) gut microbiota are enriched in Proteobacteria species capable of degrading chitin, cellulose and lipids, and producing acetate, glutamate, essential amino acids, and vitamins; functional pathways for fatty acid degradation are also enriched, suggesting microbiota-aided energy accumulation prior to migration (Li et al 2023) (Table 2). These findings may not be directly transferable to pigeons due to species-specific metabolic adaptations.

Table 2

Functional remodeling of avian gut microbiomes around migration and energy needs

Bird system	*Key microbial/functional change*	*Energetic implication*	*References*
Blackpoll Warbler	↑ Proteobacteria; ↑ vitamin, AA, FA biosynthesis, carb metabolism	Supports fat and energy stores during migration	(Trevelline et al 2023)
Migratory shorebirds	Enriched *Corynebacterium*, other taxa; diet-associated shifts	Potential support for energy requirement	(Zhang et al 2021)
Black-necked crane	Proteobacteria with complex polysaccharide degradation; ↑ FA degradation pathways	Enhanced digestion, energy harvest, feeding stimulation	(Li et al 2023)
Migratory birds overall	Reduced diversity, expansion of select taxa during active migration	Possible adaptive remodeling for migration demands	(Capilla-Lasheras & Risely 2025).

Mechanistic Links: Gut-Muscle Axis, SCFAs, and Immune Modulation. Although not studied mechanistically in pigeons, broader animal and poultry data outline plausible gut–flight performance pathways. The gut–muscle axis literature indicates that optimal microbiota can improve muscle protein synthesis, mitochondrial biogenesis, glycogen storage, and reduce oxidative stress and inflammation; dysbiosis from overtraining or poor diet may impair adaptation and performance (Mach & Fuster-Botella 2016; Xie & Huang 2024; Przewłócka et al 2020; Zhang et al 2024a).

Endurance exercise in mammals is tightly connected to microbiota-mediated control of oxidative stress, inflammation, and energy expenditure, and microbiome profiling may reflect exercise-induced stress and metabolic disorders (Mach & Fuster-Botella 2016; Zhang et al 2024a). Probiotic modulation can, in some contexts, improve general health, energy availability, and performance (Mach & Fuster-Botella 2016; Przewłócka et al 2020; Zhang et al 2024a; Wang et al 2025).

Short-chain fatty acids (SCFAs), particularly butyrate, propionate, and acetate, are central metabolites linking microbiota to host physiology. In poultry, SCFAs are major energy substrates for enterocytes, lower gut pH to suppress pathogens, modulate cytokines (TNF-α, IL-2, IL-6, IL-10), promote regulatory T cells, repair mucosa, and strengthen tight junctions, thereby improving barrier function and reducing inflammation (Liu et al 2021; Mátis et al 2022). Butyrate supplementation in broilers improves performance, tight junction protein expression, and endogenous SCFA production (Mátis et al 2022). In chickens, gut-derived butyrate regulates antiviral responses in lung epithelium, shaping gut–lung axis immunity (Saint-Martin et al 2024), while broader immunology work shows that SCFAs regulate mucosal and systemic immunity via G protein–coupled receptors and histone deacetylase inhibition (Mann et al 2024). These mechanisms are inferred from other models and remain hypothetical in pigeons.

In racing pigeons, bile acid supplementation in drinking water reduces *Trichomonas gallinae* burden, improves intestinal morphology and immunity (higher soluble CD8), and increases beneficial *Lactobacillus* dominance, thereby enhancing intestinal health, reducing mortality, and supporting better tissue integrity under infection pressure (Ma et al 2023). Alongside observations that low burdens of opportunistic pathogens and protozoa are associated with better race consistency (Kalinaj et al 2024), this positions gut health as a key mediator of performance.

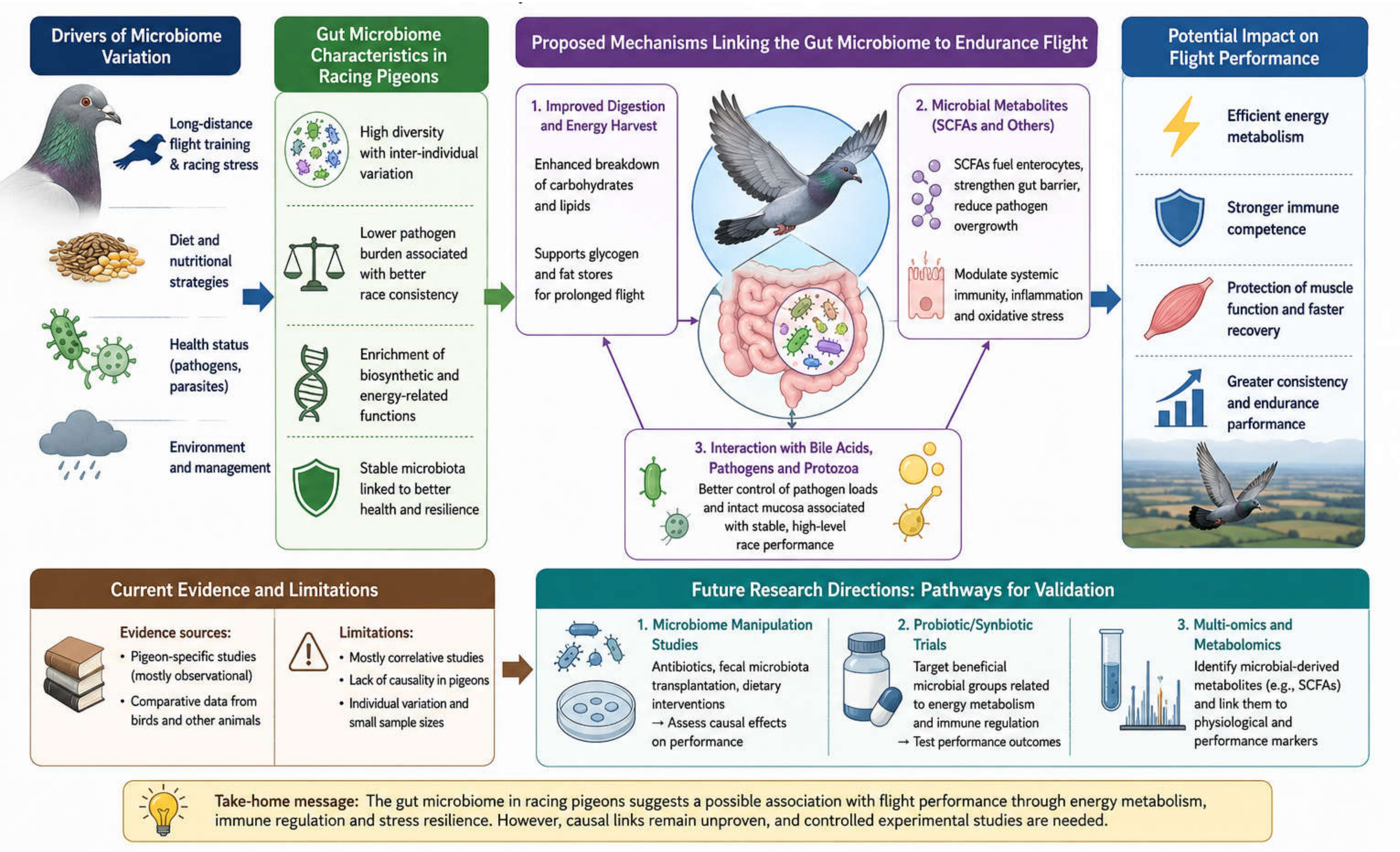

Figure 1. The gut microbiome and flight performance in racing pigeons: evidence, mechanisms anf future directions.

Proposed Conceptual Framework for Racing Pigeons. Integrating pigeon-specific and comparative data supports a conceptual framework in which long-distance flight training and race stress select for a microbiome with enhanced biosynthetic and energy-related functions (Ferrari et al 2023; Mach & Fuster-Botella 2016; Capilla-Lasheras & Risely 2025; Trevelline et al 2023; Li et al 2023).

Evidence-based components. Available data indicate that such a microbiome may:
i) Improve digestion and energy harvest (including complex carbohydrates and lipids), supporting glycogen and fat stores critical for prolonged flight (Ferrari et al 2023; Mach & Fuster-Botella 2016; Trevelline et al 2023; Li et al 2023);
ii) Produce SCFAs and other metabolites that fuel enterocytes, stabilize barrier integrity, reduce pathogen overgrowth, and modulate systemic inflammation and oxidative stress, thereby protecting muscle function and recovery (Liu et al 2021; Saint-Martin et al 2024; Mann et al 2024; Mátis et al 2022);
iii) Interact with bile acids, protozoal infections, and opportunistic bacteria, where better-controlled pathogen loads and intact mucosa correlate with more stable, high-level race performance (Kalinaj et al 2024; Ma et al 2023).

Hypothetical components. Based on indirect and comparative evidence, it is proposed that microbiome remodeling during repeated endurance effort may enhance host metabolic efficiency and immune resilience in a manner that translates into improved flight consistency and recovery (Figure 1). However, these relationships remain inferential, as current pigeon data are largely correlative, with no direct manipulative trials linking defined microbiome changes to measurable improvements in speed or homing.

Experimental validation pathways. Future research should prioritize controlled experimental approaches to test this framework, including:
i) Microbiome manipulation studies (e.g., antibiotics, fecal microbiota transplantation, or controlled dietary interventions) to assess causal effects on performance metrics;
ii) Targeted probiotic or synbiotic trials designed to enhance specific functional microbial groups associated with energy metabolism and immune regulation;
iii) Integrated metabolomics and multi-omics approaches to quantify microbiome-derived metabolites (e.g., SCFAs) and link them to physiological parameters relevant to endurance flight.

Together with strong mechanistic evidence from poultry and exercise studies in other species, these approaches would allow a more rigorous evaluation of the pigeon gut microbiome as a modifiable factor potentially influencing flight performance through energy metabolism, immune competence, and resilience to race-season stress (Ferrari et al 2023; Mach & Fuster-Botella 2016; Liu et al 2021; Kalinaj et al 2024; Saint-Martin et al 2024; Przewłócka et al 2020; Ma et al 2023; Zhang et al 2024a; Mátis et al 2022; Li et al 2023).

Conclusions. Current evidence suggests a possible association between gut microbiome composition and factors relevant to flight performance in racing pigeons, including metabolic efficiency, immune competence, and resilience to stress and disease. Birds with more stable microbiota and lower levels of opportunistic pathogens tend to exhibit more consistent racing outcomes; however, these observations remain primarily correlational and do not establish direct causative relationships.

Comparative data from migratory birds and other animal models further indicate that sustained physical activity may induce functional remodeling of the gut microbiome, favoring enhanced biosynthetic and energy-harvesting capabilities. Proposed mechanistic pathways involve the gut–muscle axis, microbial production of short-chain fatty acids (SCFAs), and modulation of host immune responses. Nevertheless, the extent to which these mechanisms operate in racing pigeons specifically remains insufficiently validated.

A major limitation of the current body of research is the lack of experimental and causal evidence in pigeons, with most available studies relying on observational or crosssectional designs. Consequently, the functional significance of specific microbiome configurations for flight performance remains uncertain.

Future research should prioritize controlled intervention trials, including microbiome manipulation and probiotic supplementation, to directly test performance outcomes. In addition, longitudinal studies tracking microbiome dynamics across training and racing seasons, as well as functional assays such as metabolomics and transcriptomics, are essential to clarify mechanistic pathways and establish causality.

Acknowledgements. OpenAI ChatGPT-5.3 - https://openai.com - was used for plate editing. An AI-powered search engine for research - https://consensus.app - Consensus NLP, Inc – was used to summarize data in tables.

Authors Contributions. IVPM wrote the manuscript; KEK read and revised the manuscript.

Conflicts of Interest. The authors declare that there is no conflict of interest.

Data Availability. The data supporting the findings of this study are available from the corresponding author upon reasonable request.

Funding. This research received no external funding.

References

Capilla-Lasheras P., Risely A., 2025 Migratory microbiomes: the role of the gut microbiome in bird migration eco-physiology. Journal of Avian Biology 2025: e03406.

Dolka B., Czopowicz M., Chrobak-Chmiel D., Ledwoń A., Szeleszczuk P., 2020 Prevalence, antibiotic susceptibility and virulence factors of Enterococcus species in racing pigeons (*Columba livia* f. domestica). BMC Veterinary Research 16:7.

Ferrari E., Oliveira B., Creasey H., Da Silva D., Nakamura A., Bresciani K., Widmer G., 2023 The impact of physical effort on the gut microbiota of long-distance fliers. Microorganisms 11(7): 1766.

Ionescu H., Oroian T. E., 2019 Hematological aspects of the Galati players pigeon breed. ABAH Bioflux 11(1):21-25.

Ionescu H., Oroian T. E., Botha M., 2015 Phenotypic characterization of a population of Galati players pigeon breed blue flecked white and white unicolor variety. ABAH Bioflux 7(2):183-187.

Kalinaj B., Zigo F., Farkašová Z., Lacková Z., Récky A., Arvaiová J., Rehan I., 2024 The influence of health status on the changes of gut microbiota and performance of racing pigeons. International Journal of Avian & Wildlife Biology 8(2):49-53.

Lewis W., Moore F., Wang S., 2016 Characterization of the gut microbiota of migratory passerines during stopover along the northern coast of the Gulf of Mexico. Journal of Avian Biology 47: 659-668.

Li W., Zhao J., Tian H., Shen Y., Wang Y., Shao M., Xiong T., Yao Y., Zhang L., Chen X., Xiao H., Xiong Y., Yang S., Tan C., Xu H., 2023 Gut microbiota enhance energy accumulation of black-necked crane to cope with impending migration. Applied Microbiology and Biotechnology 107: 4635-4646.

Liu L., Li Q., Yang Y., Guo A., 2021 Biological function of short-chain fatty acids and its regulation on intestinal health of poultry. Frontiers in Veterinary Science 8:736739.

Ma H., Bian S., Han P., Li Y., Ni A., Zhang R., Ge P., Wang Y., Zhao J., Zong Y., Yuan J., Sun Y., Chen, J., 2023 Supplementation of exogenous bile acids improve antitrichomonal activity and enhance intestinal health in pigeon (Columba livia). Poultry Science 102(7): 102722.

Mach N., Fuster-Botella D., 2016 Endurance exercise and gut microbiota: A review. Journal of Sport and Health Science 6:179-197.

Mann E., Lam Y., Uhlig H., 2024 Short-chain fatty acids: linking diet, the microbiome and immunity. Nature Reviews Immunology 24: 577-595.
Mátis G., Mackei M., Boomsma B., Fébel H., Nadolna K., Szymański Ł., Edwards J., Neogrády Z., Kozłowski K., 2022 Dietary protected butyrate supplementation of broilers modulates intestinal tight junction proteins and stimulates endogenous production of short chain fatty acids in the Caecum. Animals: an Open Access Journal from MDPI 12(15): 1940.
Oroian I., Popescu A., 2026 Paramyxovirus-1 infection in pigeons: epidemiology, vaccination, and control. HVM Bioflux 18(1):35-39.
Popescu A., Burduhos P., 2026 Trichomoniasis in domestic pigeons: pathogenesis, diagnosis, and resistance patterns. HVM Bioflux 18(1):30-34.
Popescu A., Cimpean A., 2026 Aerodynamic efficiency and wing morphology in high-performance racing pigeons (Columba livia). ABAH Bioflux 18(1):62-68.
Popescu A., Păpuc T., 2026 Environmental pollutants and their effects on pigeon health and flight performance. AES Bioflux 18(1):12-16.
Przewłócka K., Folwarski M., Kaźmierczak-Siedlecka K., Skonieczna-Żydecka K., Kaczor J., 2020 Gut-muscle axis exists and may affect skeletal muscle adaptation to training. Nutrients 12(5): 1451.
Saint-Martin V., Guillory V., Chollot M., Fleurot I., Kut E., Roesch F., Caballero I., Helloin E., Chambellon E., Ferguson B., Velge P., Kempf F., Trapp S., Guabiraba R., 2024 The gut microbiota and its metabolite butyrate shape metabolism and antiviral immunity along the gut-lung axis in the chicken. Communications Biology 7:1185.
Trevelline B., Sprockett D., DeLuca W., Andreadis C., Moeller A., Tonra C., 2023 Convergent remodelling of the gut microbiome is associated with host energetic condition over long-distance migration. Functional Ecology 37(11): 2840-2854.
Wang C., Liu H., Zhang S., Ren C., Xu J., Chen J., Chen H., Wu W., 2025 Spirulina supplementation alleviates intense exercise-induced damage and modulates gut microbiota in mice. Nutrients 17(2): 355.
Xie X., Huang C., 2024 Role of the gut–muscle axis in mitochondrial function of ageing muscle under different exercise modes. Ageing Research Reviews 98: 102316.
Zan Y., Song X., Gong L., Hou Q., Tang J., 2023 Bionic variable structure UAV design and flight control. International Journal of Applied Mathematics in Control Engineering 6(2023):37-43.
Zhang, L., Li, H., Song, Z., Liu, Y., & Zhang, X. (2024a). Dietary strategies to improve exercise performance by modulating the gut microbiota. Foods 13(11): 1680.
Zhang S., Shen Y., Huang W., Shang C., Chen W., Shi Q., 2023 Modeling and design of a pigeon-inspired robot with passively bending wings. IEEE Robotics and Automation Letters 8(8):5251-5258.
Zhang S., Shen Y., Huang W., Wang W., Shi Q., 2024b Design and optimization of a pigeoninspired flapping-wing robot. In 2024 International Conference on Advanced Robotics and Mechatronics (ICARM). Pp. 364-369.
Zhang Z., Yang Z., Zhu L., 2021 Gut microbiome of migratory shorebirds: Current status and future perspectives. Ecology and Evolution 11: 3737-3745.

Received: 07 April 2026. Accepted: 17 May 2026. Published online: 18 May 2026.
Authors:
Kouassi Elisee Kporou (KEK), Department of Biochemistry and Microbiology, Excellence Group of Research on products of Traditional Pharmacopoeia (GeRProPhaT), Jean Lorougnon Guédé University, Ivory Coast, e-mail: elykoua@yahoo.fr , elykoua@gmail.com
Ioan Valentin Petrescu-Mag (IVPM), Department of Environmental Engineering and Protection, Faculty of Agriculture, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Calea Mănăștur street, 400372 Cluj-Napoca, Romania, e-mail: ioan.mag@usamvcluj.ro

How to cite this article:
Kporou K. E., Petrescu-Mag I. V., 2026 Gut microbiome and flight performance in racing pigeons: emerging evidence and mechanistic links. ABAH Bioflux 18(1):89-95.