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MONITORING THE MICROBIAL PREVALENCE IN FARMED TROUT SPECIES FROM AN AQUACULTURE FACILITY IN KOSOVO

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ABSTRACT

The primary objective of this research was to evaluate and quantify the presence of mesophilic bacteria on the skin and within the muscle tissue of farmed rainbow trout. Fish specimens were obtained during the summer from a cold-water fish breeding facility in the Istog region of the Republic of Kosovo. A limited number of fish samples were collected under sterile conditions, reflecting the exploratory scope of this study and constraints in sample availability. Most samples were identified as *Oncorhynchus mykiss* (rainbow trout), while a smaller proportion corresponded to *Oncorhynchus mykiss* (golden rainbow trout). The microbiological analysis of the samples was conducted utilizing ISO standard methods for analysing mesophilic bacteria, *Escherichia coli*, *Enterobacteriaceae*, coliforms, and *Enterococcus faecalis*. Results revealed higher contamination on the skin surface compared to muscle tissue, with consistent levels across both trout species. Although differences between tissues were observed, they did not reach statistical significance ($p > 0.05$), likely due to the limited sample size. Variations among samples indicated the influence of handling practices and environmental factors on microbial presence. The analysis showed that coliforms accounted for 37.13% of microbial presence, followed by other mesophilic bacteria at 35.14% and *E. faecalis* at 26.92%, with minimal presence of *E. coli* and *Enterobacteriaceae*. These findings underscore the importance of further research into external factors affecting microbial growth in aquaculture environments and suggest the need for systematic monitoring and control measures to enhance hygiene standards in fish farming operations.

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INTRODUCTION

Rainbow trout and golden rainbow trout are the main species cultivated in fish farms in Kosovo. These fish species were chosen due to the favourable climatic conditions in the region, characterized by a mild, medium continental climate with hot summers and cold winters, and an average water temperature of 11.3°C (Fazliu and Gjinali, 2017). Nevertheless, fish are susceptible to contamination by various microorganisms present in aquatic environments. The microbial flora found in fish is closely linked to the bacterial composition of the water they inhabit (Austin, 2006). While the muscle tissue of healthy live fish is typically considered sterile, significant microbial loads can be found on the skin, gills, and gastrointestinal tract. Improper post-harvest handling can result in the infiltration of muscle tissue by these bacteria, hastening spoilage and presenting potential health hazards (ICMSF, 2005).

At the European Union level, trout production, mainly derived from aquaculture, reached 981,239 tons in 2020, showing a 21% increase from 2011 (811,750 tons), demonstrating a rise in consumption (EUMOFA, 2023). In Kosovo, there are 35 fish farms, 17 of which have their own restaurants for direct fish sales. This situation leads to indirect job creation as fish farming boosts company revenues. Local production of rainbow trout amounts to approximately 1,581 tons per year. The market typically targets live and processed fish weighing around 350-400 grams.

Effective microbiological monitoring involves a systematic check of water, sediment, feed, and fish tissues for potential pathogens. In farmed *O. mykiss*, a study in Turkey reported microbial load ranging between 10^1 and 10^7 CFU/g in fresh muscle under good hygienic conditions, while higher loads are often detected on skin and tool surfaces due to direct environmental exposure (Diler et al., 2000). Early identification of disease outbreaks enables producers to promptly implement preventive measures, such as improved biosecurity, vaccination, and therapeutic interventions. Furthermore, monitoring microbial communities provides valuable insights into the overall health of aquaculture systems, and guides management practices focused on preserving water quality and enhancing fish health. Numerous factors influence fish quality, with the production of histamine associated with histamine decarboxylase, an enzyme produced by various bacterial species (Egerton et al., 2018; Visciano et al., 2014; Giyatmi and Irianto, 2017). Multiple bacteria present in fish, including mesophilic bacteria (*Proteus morganii*, *E. coli*, *Vibrio alginolyticus*, *Salmonella* spp.), play a role in histamine production (Visciano et al., 2014). In addition to microorganisms that cause putrefaction, fish carry pathogens such as *Listeria monocytogenes*, *Clostridium botulinum*, *Vibrio* spp., and *Enterobacteriaceae* (*Yersinia* spp., *E. coli*, and *Salmonella* spp.) (Derome et al., 2016; Novoslavskij et al., 2016; Da Costa et al., 2023; Irshath et al., 2023). The quality and freshness of fish degrade rapidly due to microbial proliferation, internal enzymatic processes, and lipid oxidation, which are further accelerated by the high water activity, neutral pH of fish muscle, and inadequate storage and handling conditions (Olafsdóttir et al., 1997; Pullela et al., 1998; Gram and Dalgaard, 2002; Ghaly et al., 2010). Research conducted in Slovakia demonstrated significant differences in mesophilic bacteria between fresh and frozen rainbow trout during prolonged storage. The study also indicated elevated levels of microbial contamination in samples obtained from the skin and filleted muscles in contrast to sterile muscle samples, highlighting the significance of raw material quality and skin contact as primary sources of both pathogenic and spoilage bacteria in fish fillets (Popelka et al., 2016).

Several studies have examined the microbiological quality of farmed trout in various European countries, but there is a lack of specific data for Kosovo. The existing literature primarily focuses on large-scale aquaculture systems or regions with established monitoring frameworks, which may not fully represent the production practices, environmental conditions, and hygiene management in Kosovo's trout farms. Notably, there have been no published studies that systematically assess and compare the microbial levels on the skin and muscle tissues of farmed rainbow and golden rainbow trout raised under local conditions in river-fed artificial ponds. This absence of country-specific and tissue-based microbiological data presents a significant knowledge gap, hindering evidence-based risk assessment and the formulation of targeted control measures. It is imperative to address this gap to enhance food safety management, support national surveillance efforts, and bring Kosovo's aquaculture sector in line with international and EU food safety standards.

The primary objective of this research was to evaluate and quantify the presence of mesophilic microorganisms on the skin and within the muscle tissue of farmed rainbow trout raised in a cold-water fish breeding facility supplied with water from the streams of the Istog River. Monitoring microbiological activity is essential for the sustainability of aquaculture. Through the implementation of comprehensive surveillance programs and the use of advanced diagnostic techniques, the aquaculture sector can effectively manage disease risks, improve the well-being of fish, and ensure the production of safe, high-quality products for consumers.

MATERIALS AND METHODS

Sampling

In this research, fish specimens were obtained during the summer season from a cold-water fish breeding facility situated in the Istog region of the Republic of Kosovo (Figure 1).

Fig 1. Map of sampling site: Istog City – ponds located along the Istog River

A total of 10 samples (Figure 2a, b) were gathered under sterile conditions to assess hygienic quality. For each fish, samples were taken from the external skin surface (lateral side, above the lateral line) as well as from the underlying muscle tissue. Prior to muscle sampling, the skin was aseptically removed to avoid cross-contamination. From each specimen, multiple subsamples (skin and muscle) were collected and processed individually for microbiological analysis. Out of the total samples collected, eight (n = 8) were identified as *O. mykiss*, while the remaining two (n = 2) belonged to *O. mykiss*.

Fig 2. Morphological appearance of a) rainbow trout (*Oncorhynchus mykiss*) and b) golden rainbow trout (*Oncorhynchus mykiss*) sampled from a pond along the Istog River

Following capture, the fish were immediately rendered unconscious using a 42 W electric current and then transported to the laboratory in chilled containers lined with polyester and filled with crushed ice at a temperature of +5 °C (Fig. 3).

Fig 3. Sample processing flow chart: 1. Sampling point - the place where the study was conducted; 2. Sampling at the base - removing the fish from the water with clean tools; 3. Packaging the sample in the field - placing the fish in sterile bags, closing and labelling; 4. Transporting the sample - placing in a thermo-insulating box, storing in cold conditions; 5. Receiving the sample in the laboratory - recording the bulk and preparing for analysis; 6. Dissection and obtaining biological material - opening the fish under sterile conditions, obtaining tissues for testing and starting laboratory analyses

Each fish was measured for length and weight before testing. From each sample, approximately 10 g (±1 g) of muscle tissue (skin and underlying muscle) was collected aseptically, along with a defined skin area of 10 cm² for assessment of external contamination. The samples were subjected to microbiological testing at the Food Microbiology Laboratory, a division of the Food and Veterinary Laboratory of Kosovo, which is accredited in accordance with the standard EN ISO/IEC 17025:2017. Microbiological analysis of the collected samples was conducted utilizing ISO standards.

Methods

The determination of mesophilic bacteria in fish muscle tissue was conducted following the protocol outlined in EN ISO 4833-1:2013. The Maximum Recovery Diluent was utilized for decimal dilution at a ratio of 1:10, with 10 grams of the sample being mixed with 90 ml of MRD. A volume of 1 ml from each dilution series was spread onto two 90 mm plates and incubated on Plate Count Agar under aerobic conditions at 30 °C ±1 °C for 72 ± 3 hours. Quantification of the results was performed in accordance with EN ISO 7218:2024.

Enumeration of mesophilic bacteria from swabs

As per the guidelines outlined in the standard EN ISO 18593:2018, the procedure involved wiping off biofilms with a swab soaked in peptone water broth, and applying it in two perpendicular directions while ensuring full coverage of the entire surface. The swabs were then placed in a microtube containing 2.5 mL of sterile saline solution. Following this, the microtube containing the swabs was vortexed for 20 seconds to facilitate mixing. The resulting supernatants were utilized for subsequent enumeration analyses. Enumeration was conducted using PCA as a solid nutrient medium, and the incubation took place under aerobic conditions at 30 °C. Colony counting was performed after 48 and 72 hours of incubation. The logarithmic calculation (log CFU/cm^2) of the skin surface area results is calculated from the lowest countable value (1 CFU) compared to the sample surface area (10 cm^2) and the dilution scheme applied. This corresponds to the minimum level at which microorganisms can be reliably detected using the applied method. The average of two plates from one dilution was considered for calculation purposes. The detection limit for this analysis was set at 0.5 log CFU/cm^2 of the sampled area. To validate the results, reference strains for method quality control, *E. faecalis* ATCC 29212 and *E. coli* ATCC 8739, were used.

Enumeration, isolation and identification of bacteria

Five pure bacterial colonies grown for 72 hours were transferred to a non-selective nutrient medium, Nutrient Agar. They were then spread onto selective chromogenic media such as Tryptone Bile X-glucuronide for *E. coli* growth at 44 ± 2 °C for 24 ± 2 hours (EN ISO 16649-2:2001), Violet Red Bile Glucose Agar (VRBGA) for *Enterobacteriaceae* growth at 36 ± 2 °C for 24 ± 3 hours (EN ISO 21528-2:2017), Violet Red Bile Lactose Agar (VRBLA) for coliform growth at 36 ± 2 °C for 24 ± 2 hours (ISO 4832:2006), and Slanetz and Bartley medium for *E. faecalis* identification at 36 ± 2 °C for 44 ± 4 hours (EN ISO 7899-1:1998/Cor.1:2000). Biochemical confirmation tests, including the peroxidase test, oxidase test, sugar fermentation, motility test, methyl red test, Voges-Proskauer test, indole test, urease test, and citrate test were conducted. Following biochemical confirmation, the microbial isolates were categorized, and any unidentified groups were noted. All reagents were obtained from Liofilchem® S.r.l., Roseto degli Abruzzi, TE, Italy.

RESULTS

The findings of this study present data on rainbow trout species reared in a cold-water fish breeding facility in the Istog region of the Republic of Kosovo. The first specimens, known as *O. mykiss* (rainbow trout), consisted of samples labelled as F2, F3, F4, F5, F6, F7, F8, and F9. The average length of this species was approximately 29.6 cm, with an average weight of around 371.58 g. The other specimens, *O. mykiss* (golden rainbow trout), included samples F1 and F10, with an average length of approximately 30.35 cm and an average weight of around 316.63 g.

Regarding the microbiological aspect, enumeration and reporting of results followed the guidelines outlined in ISO 7218, with a calculated measurement uncertainty of ±0.1. The concentration of mesophilic bacteria in the muscle tissue of rainbow trout species ranged from 10^1 to 10^4 CFU/g, while in golden rainbow trout species, it was 10^1 CFU/g. Additionally, swab samples taken from the skin surface revealed a log count of approximately 3.28 CFU/cm^2 for rainbow trout, and around 3.56 CFU/cm^2 for golden rainbow trout (Table 1).

In the assessment of the total microbial count of mesophilic microorganisms (TVC), the comparison between muscle tissue and skin surface swabs revealed that the swabs from the skin surface exhibited higher microbial loads. Analysis of the data (Table 1 and Figure 4) indicated that the samples with the highest microbial loads in the swab samples were F1, F7, F2, F3, F8, F9, F5, F4, F10, and F6. Conversely, in the muscle tissue, samples with the highest microbial counts were F5, F2, F9, F8, F4, and F6. Notably, samples F3, F6, and F10 exhibited microbial counts below 10 colonies (CFU), while sample F1 showed no detectable colonies. These findings clearly illustrate that skin surface swabs harbour a greater microbial load in comparison to fish flesh.

Variations in microbial colony levels among different samples and the absence of colonies in some samples suggest significant diversity in microbial loads, possibly influenced by factors such as sample collection methods, storage conditions, or environmental contamination.

The samples were analysed for various hygienic parameters, such as *E. coli*, *Enterobacteriaceae*, *E. faecalis*, coliforms, and other mesophilic bacteria. Sample F5, which was identified as rainbow trout, exhibited the highest bacterial colony counts, including coliforms (37.13%), other mesophilic bacteria (35.20%), *E. faecalis* (26.92%), and lower levels of *E. coli* (EC) (0.34 %) and *Enterobacteriaceae* (EB) (0.41%) (Table 2).

Significant variations in the presence of bacterial species were noted in samples F2, F3, F4, F6, F7, F8, and F9 of the same species, indicating a diverse microbial composition among the samples. In contrast to these findings, sample F5 of rainbow trout and sample F1 of golden rainbow trout did not exhibit any bacterial colonies, distinguishing them from the other samples. Conversely, sample F10 of golden rainbow trout displayed the presence of *E. faecalis*, coliforms, and other mesophilic bacteria at levels of 33.3% (Table 2 and Figure 5).

Table 1. The values of the fish body sizes and the presentation of the results for each sample

Sample code	Body dimensions		Results	
	Weight (g)	Length (cm)	Muscle tissue cfu/g	Swabs form the fish surface log CFU/cm²
F1	407.10	33.10	Absent	4.69
F2	299.30	29.40	4.66×10^2	4.06
F3	288.78	30.10	$< 1.0 \times 10^1$	4.04
F4	610.70	34.50	2.22×10^2	2.73
F5	557.20	33.60	1.60×10^4	2.81
F6	565.90	33.80	$< 1.0 \times 10^1$	2.27
F7	162.53	24.20	6.2×10^1	4.38
F8	229.60	26.20	2.24×10^2	2.99
F9	258.63	25.00	4.57×10^2	2.92
F10	226.15	27.60	$< 1.0 \times 10^1$	2.43

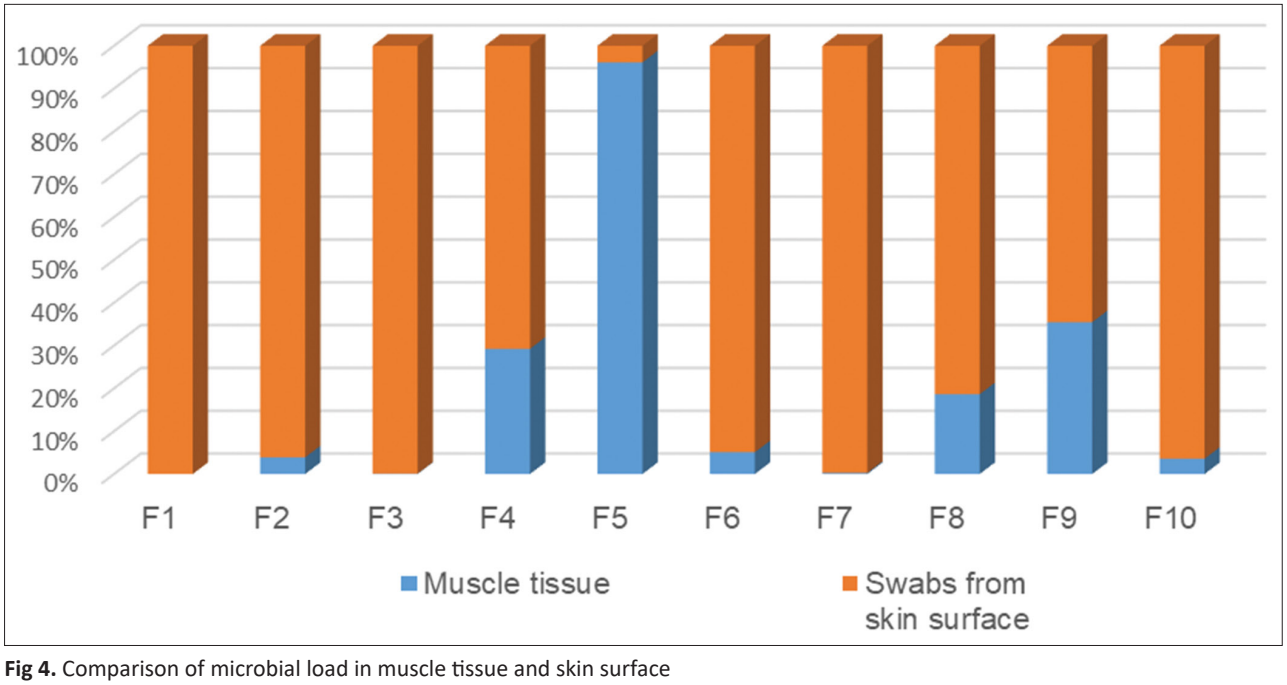

Fig 4. Comparison of microbial load in muscle tissue and skin surface

Table 2. Microbial count of mesophilic bacteria among the samples examined

Samples	Total CFU/g	*E. coli*	No. of CFU / Percentage (%)			
			Entero-bacteriaceae	*E. faecalis*	Coliforms	Others
F1	0	0 / 0.00%	0 / 0.00%	0 / 0.00%	0 / 0.00%	0 / 0.00%
F2	466	1 / 0.21%	2 / 0.43%	98 / 21.00%	96 / 20.60%	269 / 57.72%
F3	9	0 / 0.00%	0 / 0.00%	1 / 11.10%	3 / 33.30%	5 / 55.60%
F4	222	1 / 0.45%	1 / 0.45%	49 / 22.10%	50 / 22.50%	121 / 54.50%
F5	16000	48 / 0.3%	58 / 0.36%	4398 / 27.50%	6148 / 38.40%	5348 / 33.43%
F6	8	0 / 0.00%	0 / 0.00%	2 / 25.00%	2 / 25.00%	4 / 50.00%
F7	62	1 / 0.02%	1 / 0.02%	10 / 16.20%	20 / 32.3%	30 / 48.4%
F8	224	4 / 1.78%	3 / 1.34%	47 / 21.00%	60 / 26.80%	110 / 49.10%
F9	457	5 / 1.09%	7 / 1.53%	91 / 19.90%	100 / 21.90%	254 / 55.60%
F10	6	0 / 0.00%	0 / 0.00%	2 / 33.30%	2 / 33.30%	2 / 33.30%
Total	17454	60 /0.34%	72 / 0.41%	4698 / 26.92%	6481 / 37.13%	6143 / 35.20%

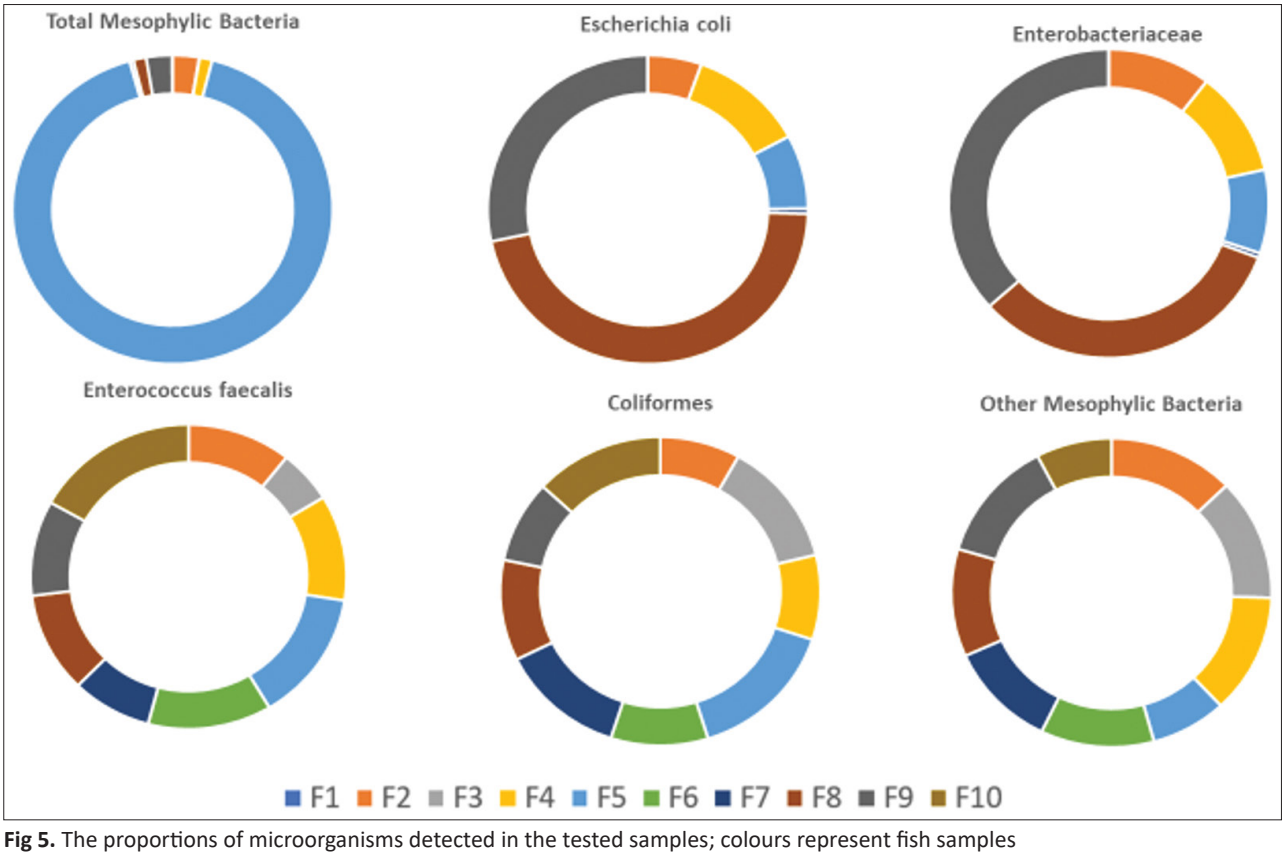

Fig 5. The proportions of microorganisms detected in the tested samples; colours represent fish samples

DISCUSSION

This research assessed the microbiological aspect of rainbow trout species farmed in a cold-water fish breeding facility in Istog, Kosovo. However, the results are interpreted with caution, considering several limitations of the study. In particular, the relatively small sample size and unequal representation of rainbow trout may have affected the statistical power of the analyses and the comparability between species. These factors may also limit the generalizability of the findings. Therefore, future studies with larger sample sizes and a more balanced distribution between species are necessary to confirm and extend these results.

The average length and weight of trout in our study ranged from 24.2 to 34.5 cm in length and from 162.5 to 610.7 g in weight. In the research conducted during May – August 2023-2024 at the same location in Kosovo, average values of length and weight were identified as 22.6–27.3 cm and 126–227.6 g, respectively (Iseni et al., 2025).

The study compared the total count of mesophilic microorganisms and other hygiene indicators in both muscle tissue and skin surface. The findings revealed that muscle tissue had the lowest microbial load, whereas the skin surface had a higher presence of microorganisms. This discrepancy indicates the microbiological ecology of trout, as external surfaces are in constant contact with the aquatic environment and thus harbour a greater diversity of hygiene indicator microorganisms, including potentially pathogenic species, compared to muscle tissue.

Muscle tissues of rainbow trout and golden rainbow trout were compared across different samples, and no significant differences were found in the presence of mesophilic microorganisms. The levels ranged from approximately 10^1 to 10^4 colony-forming units per gram. These results were notably lower than those reported in previous studies on raw fish fillets sold in retail settings, where the average presence of mesophilic microorganisms was around 5.7 log CFU/g (Poa et al., 2008). Another research investigation, focusing on rainbow trout preservation under refrigerated conditions, found that the mean microbial count of total mesophilic bacteria ranged between 2.6 and 4.5 log CFU/g. This count exhibited a gradual increase over the storage period (Duarte et al., 2020).

Compared with the provided data, the findings of this study indicate that the analysed muscle samples fell within the expected range for fresh or slightly contaminated fish, and in some instances, even registered levels lower than the standard baseline levels documented in existing literature. The relatively low microbial presence in fish muscle can be attributed to the inherent biological characteristics of fish. Typically, the muscle tissue of live, healthy fish is considered almost devoid of microorganisms, with contamination occurring mainly post-capture or during subsequent handling and processing stages. Available research suggests that fresh fish muscle generally harbours approximately 2-3 log CFU/g of microbes, a figure that varies depending on fish species, environmental conditions, and the methods employed during post-harvest processing (Duarte et al., 2020).

All microbial counts are presented in logarithmic form (log CFU/g for muscle tissue and log CFU/cm² for skin swabs) to facilitate comparison, standardization, and clarity of interpretation. In contrast, microbial counts on the skin surface were higher, with average values of approximately 3.28 log CFU/cm² for rainbow trout and 3.56 log CFU/cm² for golden rainbow trout. These findings are in line with previous research indicating that fish skin harbours significantly higher levels of mesophilic bacteria due to their aquatic habitat and environmental factors such as water and organic material. The data reveals that in freshly caught fish, the microbial load on the skin ranged from 3 to 5 log CFU/g, whereas the muscle tissue predominantly exhibited lower levels (Lowore et al., 2022). Studies on farmed fish have also shown higher bacterial counts on the skin compared to internal tissues, highlighting the external source of most microbial contamination (Afolabi et al., 2022).

The greater quantities detected in skin swabs as opposed to muscle samples in this study align with well-established microbiological principles. Comparisons between researched subjects reveal that some samples exhibit a limited or absent presence of microorganisms on their skin, a phenomenon attributed to various factors within the aquaculture environment. Key ecological conditions such as water quality, temperature, and organic matter directly influence the population of microbial communities on fish skin. Furthermore, factors such as handling practices, feeding schedules, stress levels, and physiological disparities among samples can impact the colonization of microorganisms. Existing literature also suggests that the diversity and quantity of the skin microbiome can vary based on the sampling location, health condition, and environmental variables in aquaculture systems (Pavić et al., 2024).

Such variability may account for the significant differences in bacterial counts observed among samples of the same species in the study. There was also notable variation in the presence of other types of microorganisms indicative of hygiene within the samples examined. The high prevalence of visible coliforms at 37.13% served as a hygiene marker for the environment, while the presence of mesophilic bacteria and *E. faecalis* at 26.92% in some samples indicated treatment-related factors. In most samples, lower levels of *E. coli* and *Enterobacteriaceae* were detected, aligning with previous research showing *E. coli* is typically present in only a small percentage of trout samples and generally at minimal concentrations. These findings suggest limited faecal contamination in the aquaculture environment under investigation (Pao et al., 2008).

The study found that sample F5 had high levels of mesophilic bacteria, suggesting that environmental conditions or handling methods may contribute to sporadic contamination incidents. It was expected that fish skin, as a key ecological component, would harbor a greater abundance of microorganisms compared to trout muscle tissues, which exhibited relatively low microbial levels (Silviu et al., 2025).

Based on the study findings, it is evident that microbial loads in the muscles of trout were relatively low, while higher numbers were observed on the skin surface. This emphasizes the importance of implementing improved handling procedures and continuous monitoring of hygiene parameters in aquaculture systems to maintain the microbiological safety and quality of fish products.

CONCLUSION

This study is of initial importance, and future studies with a wider range of samples and additional conditions may confirm and expand the understanding of the microbiological status of trout. The study provides crucial insights into the microbial contamination of rainbow trout and golden rainbow trout raised in a cold-water aquaculture facility fed by water from the Istog River in Kosovo. These fish species, particularly the “Istog trout”, are commonly consumed in Kosovar cuisine and are highly regarded for their nutritional value.

The results indicated noticeable discrepancies in microbial levels between the skin and muscle tissue of trout. There was a higher presence of mesophilic bacteria on the skin, suggesting that factors such as environmental exposure, handling, and storage conditions have a significant impact on contamination levels. While muscle tissue generally had lower levels of contamination, it still poses a potential risk to food safety. Both rainbow trout and golden rainbow trout exhibited similar levels of skin contamination, with golden rainbow trout showing slightly higher average microbial counts. However, there was considerable variability among sample fish, indicating the influence of environmental factors, handling techniques, and the overall health of the fish. These findings underscore the importance of ongoing microbiological surveillance and enhanced hygiene practices to ensure the safety and quality of aquaculture products.

PRAĆENJE MIKROBNE PREVALENCIJE U UZGOJENIM VRSTAMA PASTRVI IZ RIBOGOILIŠTA NA KOSOVU

SAŽETAK

Primarni cilj ovog istraživanja bio je procijeniti i kvantificirati prisutnost mezofilnih bakterija na koži i unutar mišićnog tkiva uzgojene kalifornijske pastrve. Uzorci ribe dobiveni su tijekom ljetne sezone iz uzgoja ribe u hladnoj vodi smještenog u regiji Istog u Republici Kosovo. Ograničen broj uzoraka ribe prikupljen je u sterilnim uvjetima, što odražava istraživački opseg ove studije i ograničenja u dostupnosti uzoraka. Većina njih identificirana je kao *Oncorhynchus mykiss* (kalifornijska pastrva), dok je manji udio odgovarao *Oncorhynchus mykiss* (zlatna kalifornijska pastrva). Mikrobiološka analiza prikupljenih uzoraka provedena je korištenjem ISO standardnih metoda za analizu mezofilnih bakterija, *Escherichia coli*, *Enterobacteriaceae*, koliformnih bakterija i *Enterococcus faecalis*. Rezultati su pokazali veću kontaminaciju na površini kože u usporedbi s mišićnim tkivom, s konzistentnim razinama kod obje vrste pastrve. Iako su uočene razlike između tkiva, one nisu dosegle statističku značajnost ($p > 0,05$), vjerojatno zbog ograničene veličine uzorka. Varijacije među uzorcima ukazivale su na utjecaj praksi rukovanja i čimbenika okoliša na prisutnost mikroba. Analiza je pokazala da su koliformne bakterije činile 37,13% prisutnosti mikroba, zatim druge mezofilne bakterije s 35,14% i *E. faecalis* s 26,92%, uz minimalnu prisutnost *E. coli* i *Enterobacteriaceae*. Nalazi naglašavaju važnost daljnjih istraživanja vanjskih čimbenika koji utječu na rast mikroba u akvakulturnim okruženjima i sugeriraju potrebu za sustavnim praćenjem i kontrolnim mjerama za poboljšanje higijenskih standarda u uzgoju ribe.

Ključne riječi: higijena hrane, kalifornijska pastrva, akvakultura, mikrobiologija riba, mezofilne bakterije, kvaliteta hrane

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CONFLICT OF INTEREST

The author has declared no conflict of interest.

DATA AVAILABILITY STATEMENT

The datasets generated and/or analysed during the current study are not publicly available but are available from the corresponding author upon reasonable request.

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