JEE Journal of Ecological Engineering

Journal of Ecological Engineering, 2026, 27(10), 33–46
https://doi.org/10.12911/22998993/223955
ISSN 2299–8993, License CC-BY 4.0

Received: 2026.05.12
Accepted: 2026.07.02
Published: 2026.09.01

Integrated risk assessment of heavy metal and microbial exposure in coastal agricultural systems

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ABSTRACT

Environmental contamination in coastal agricultural systems frequently involves the simultaneous occurrence of chemical pollutants and microbiological hazards, creating complex risks for ecosystems, livestock, food safety, and human health. The present study provides an integrated assessment of heavy metal contamination and microbiological pollution across soil, surface water, groundwater, and milk within a coastal agricultural environment. Soil samples exhibited elevated concentrations of copper and mercury, reaching 470,244 mg/kg and 2330 mg/kg, respectively, indicating substantial accumulation of heavy metals within the terrestrial compartment. In contrast, water samples showed relatively low concentrations of heavy metals, with copper ranging from 0.0011 to 0.0016 mg/L. Microbiological contamination exhibited an opposite distribution pattern, river water showing high total coliform concentrations reaching 810 CFU/100 mL, while milk samples reached 590 CFU/100 mL. Multivariate statistical analyses revealed a contamination gradient extending from soil to water and subsequently to milk, supporting the hypothesis of environmental-to-food chain transfer pathways. Principal Component Analysis and hierarchical clustering demonstrated clear differentiation between heavy metal accumulation processes and microbiological contamination patterns. The findings indicate that heavy metals are primarily retained within soil systems, whereas microbiological contaminants display greater environmental mobility through aquatic and food-related compartments. Despite limitations associated with sample size, the study demonstrates the importance of integrated environmental monitoring and supports the application of a One Health framework for assessing environmental and biological risks in coastal agricultural systems.

Keywords: One Health, heavy metals, microbial contamination, coastal agriculture, environmental risk, milk safety.

INTRODUCTION

Coastal agricultural environments represent complex and dynamic systems where natural processes and human activities converge, often leading to the accumulation and interaction of multiple environmental stressors. Among these, heavy metal contamination and microbiological pollution are of particular concern due to their persistence, potential for bioaccumulation, and direct implications for ecosystem integrity, food safety, and public health (Ali et al., 2019; Alloway, 2013).

Heavy metals such as cadmium (Cd), mercury (Hg), and copper (Cu) are widely recognized for their toxicological effects and their capacity to persist in soils and sediments over extended periods, thereby entering the food chain through plant uptake and animal exposure (Ali et al., 2019; Alengebawy et al., 2021).

In parallel, microbial contamination especially by indicator organisms such as total coliforms, *Escherichia coli*, and *Enterobacteriaceae* remains a critical issue in water and dairy systems, reflecting sanitary conditions and the potential presence of pathogenic microorganisms (World Health Organization, 2017; FAO & WHO, 2011). The microbiological quality of water used in dairy farms has also been associated with contamination risks in milk production systems and livestock environments (Terrosu et al., 2012). Similarly, *Escherichia coli* has been recognized as an important microbiological indicator for environmental and public health monitoring in both human and animal systems (Zarić et al., 2023).

Traditionally, environmental assessments have addressed chemical and microbiological contaminants as separate entities, often within distinct disciplinary frameworks. However, increasing evidence suggests that these forms of contamination frequently coexist within agricultural landscapes and may originate from overlapping sources, including agricultural runoff, livestock waste, and inadequate wastewater management (Xu et al., 2024; Li et al., 2009). Such co-occurrence introduces a level of complexity that cannot be adequately captured through single-parameter analysis. Instead, there is a growing need for integrative approaches that consider the interactions between environmental media and biological systems, as well as the pathways through which contaminants are transferred across them (Hou et al., 2020; Rehman et al., 2018).

The lower course of the Vjosa River, particularly within the Vjosa-Nartë Delta, constitutes a representative example of a coastal agro-ecosystem where these challenges are evident. This region is characterized by intensive agricultural activity, livestock farming, and reliance on both surface and groundwater resources for irrigation and animal consumption. Previous investigations in this area have predominantly focused on the hydrochemical characteristics of groundwater and the influence of natural processes such as seawater intrusion on water quality (Dindi & Shehu, 2023).

While these studies have provided valuable insights into the geochemical dynamics of the aquifer system, they have largely overlooked the role of microbiological contamination and the potential transfer of pollutants from environmental compartments into the food chain. Coastal environments are also particularly vulnerable to cumulative contamination pressures associated with land use changes and anthropogenic activities (El-Sharkawy et al., 2025; Li et al., 2008). Previous environmental assessments conducted in the wider Vlora coastal area have similarly identified increasing environmental pressures associated with human activity and coastal ecosystem vulnerability (Bakaj et al., 2022).

In this context, the present study adopts a One Health perspective, recognizing the interconnectedness of environmental, animal, and human health (van den Bossche & Devleesschauwer, 2022). By integrating physicochemical and microbiological data from soil, water, and milk samples, this research seeks to advance current understanding of contamination dynamics in coastal agricultural systems. The approach enables the identification of potential exposure pathways linking environmental pollution to livestock and, ultimately, to human consumption. Such transfer processes have been increasingly associated with integrated environmental risk frameworks and soil-to-food contamination pathways (Liu et al., 2022; Rehman et al., 2018).

Contemporary One Health surveillance frameworks have further reinforced the importance of integrating environmental, veterinary, and human health monitoring systems for more effective risk assessment and disease prevention (Singh et al., 2024; Jato-Espino et al., 2023). Through this interdisciplinary framework, the study aims to contribute to a more comprehensive assessment of environmental and biological risks in rural settings, where monitoring and mitigation strategies are often limited.

The significance of this work lies not only in its focus on a geographically sensitive and ecologically important region in southwestern Albania, but also in its effort to bridge existing gaps between environmental chemistry, microbiology, and food safety research. By examining the co-occurrence and distribution of heavy metals and microbial indicators across multiple environmental compartments, the study provides a foundation for more integrated monitoring systems and evidence-based interventions (Xu et al., 2024; Hou et al., 2020). Such approaches are essential for safeguarding ecosystem health and ensuring the safety of agricultural products in regions undergoing rapid environmental and socio-economic change. Furthermore, maintaining microbiological quality and hygienic safety in dairy production systems remains a central requirement for public health protection and agricultural sustainability (European Commission, 2004; FAO & WHO, 2011).

MATERIALS AND METHODS

Study area and sampling design

The study was conducted in a coastal agricultural region located within the Vjosa-Nartë Delta in southwestern Albania. This area represents a transitional environment characterized by the interaction of fluvial, marine, and terrestrial processes, and is subject to intensive agricultural activity and livestock farming. The sampling strategy was designed to capture variability across key environmental compartments, including soil, surface water, groundwater, and dairy products, in order to assess potential contamination pathways within a One Health framework (van den Bossche & Devleesschauwer, 2022). The study area is located within the Vjosa-Nartë Delta in southwestern Albania. The spatial distribution of sampling locations, including soil, water, and milk collection points, is presented in Figure 1.

Sampling locations were selected in the rural zones of Bishan and Patos, as well as along the lower course of the Vjosa River and adjacent groundwater wells used for livestock. The selection criteria were based on land use patterns, proximity to water sources, and relevance to livestock exposure. In addition, milk samples were collected from local dairy farms located in Bishan and Novoselë, representing the final stage of the environmental-to-food chain pathway (Liu et al., 2018).

Sample collection and preservation

All sampling procedures were conducted in accordance with internationally recognized environmental and analytical standards to ensure data reliability, reproducibility, and compliance with regulatory frameworks.

Soil samples were collected from the surface layer (0–20 cm depth) using a composite sampling approach, following the guidelines established by ISO 18400-102:2017 for soil quality sampling. Multiple subsamples were taken within each site using a stainless-steel auger, homogenized to form a representative composite sample, and placed in pre-cleaned polyethylene containers. Samples were transported under controlled conditions and stored at 4 °C prior to laboratory analysis to prevent physicochemical alterations (Alloway, 2013).

Surface water samples from the Vjosa River and groundwater samples from wells were collected in accordance with ISO 5667-6:2014 and ISO 5667-11:2009 standards for water quality sampling. Water samples were collected in acid-washed polyethylene bottles, with in situ rinsing performed prior to sample collection. For heavy metal analysis, samples were acidified to pH < 2 using ultrapure nitric acid, following standard preservation protocols recommended by the American Public Health Association. Microbiological samples were collected in sterile containers, avoiding contamination, and transported in cooled conditions (≤4 °C) to the laboratory for analysis within 24 hours, as required by ISO 19458:2006 for microbiological water sampling (World Health Organization, 2017).

Milk samples were obtained directly from dairy cows under hygienic conditions, following standard procedures for food sampling in accordance with ISO 707:2008 for milk and dairy products. Samples were collected in sterile containers immediately after milking, ensuring minimal external contamination, and were transported under refrigeration (4 °C) to the

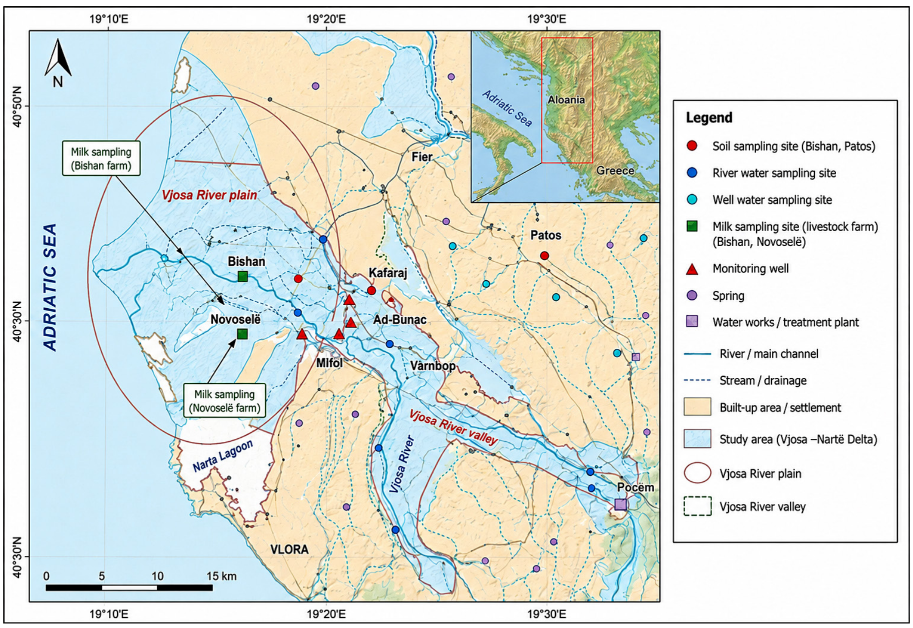

Figure 1. Study area and sampling locations within the Vjosa–Nartë Delta

laboratory for microbiological and chemical analysis within 24 hours (FAO & WHO, 2011; European Commission, 2004).

Chemical analysis

The determination of heavy metals (Cu, Cd, Hg, Ni) in soil and water samples was performed using Atomic Absorption Spectroscopy (AAS), following standard digestion and analytical procedures. Soil samples were digested using acid digestion methods in accordance with ISO 11466:1995, while water samples were prepared following APHA Standard Methods (3030E). Mercury analysis was conducted using cold vapor AAS techniques due to its specific analytical requirements (Ali et al., 2019).

Nitrate (NO_3^-) and nitrite (NO_2^-) concentrations were determined using UV-Vis spectrophotometry, following standard colorimetric methods as described in APHA (2017) Standard Methods for the Examination of Water and Wastewater. Calibration curves were prepared using certified reference standards to ensure analytical accuracy.

All analytical procedures were performed under strict quality control conditions, including the use of blanks, duplicates, and certified reference materials, to ensure data validity and minimize analytical error.

Microbiological analysis

Microbiological analyses were conducted to quantify total coliforms, Escherichia coli, and *Enterobacteriaceae* in water and milk samples. These analyses were performed in accordance with internationally recognized ISO standards. Total coliforms and E. coli were determined using ISO 9308-1:2014, based on membrane filtration techniques and selective culture media. *Enterobacteriaceae* were quantified following ISO 21528-2:2017 using colony count methods (World Health Organization, 2017).

All microbiological analyses were carried out under aseptic laboratory conditions to prevent contamination. Results were expressed in colony-forming units (CFU) per milliliter or gram, depending on the sample type. The obtained values were compared against established regulatory thresholds, including guidelines provided by the World Health Organization and relevant European Union food safety standards (European Commission, 2004).

Statistical and multivariate analysis

Statistical analysis was performed to explore relationships among physicochemical and microbiological parameters and to identify potential contamination patterns. Descriptive statistics were used to summarize the data, while correlation analysis (Pearson and Spearman coefficients) was applied to evaluate associations between variables.

Multivariate statistical techniques, including Principal Component Analysis (PCA) and hierarchical clustering, were employed to investigate the structure of the dataset and to identify underlying gradients in contamination across environmental compartments. These methods allowed for the visualization of relationships between soil, water, and milk samples, supporting the identification of potential environmental-to-food chain pathways (Qi et al., 2020; Ullah et al., 2018). Similar multivariate approaches have also been widely applied for contamination pattern recognition, ecological risk assessment, and interpretation of land-use impacts on environmental quality (Li et al., 2008; Panqing et al., 2023). Recent environmental risk assessment studies have further demonstrated the value of integrated statistical and multivariate analyses for identifying contamination gradients and pollution sources in agricultural ecosystems (Su et al., 2023).

Given the limited number of sample types included in the study, statistical interpretations were treated as exploratory, with emphasis placed on identifying trends rather than establishing definitive causal relationships.

RESULTS

Descriptive statistics and distribution of contaminants

The measured physicochemical and microbiological parameters exhibited substantial variability across environmental compartments, reflecting distinct contamination processes. A summary of the measured physicochemical and microbiological parameters across environmental compartments is presented in Table 1.

The dataset demonstrates a differentiated distribution of contaminants among environmental compartments. Heavy metals were predominantly associated with soil samples, whereas

Table 1. Physicochemical and microbiological parameters measured across environmental compartments

Environmental compartment	Parameter	Value	Unit
Soil	Copper	470.244	mg/kg
Soil	Mercury	2.33	mg/kg
River water	Copper	0.0016	mg/L
Well water	Copper	0.0011	mg/L
River water	Nickel	0.007154	mg/L
Well water	Nickel	0.005157	mg/L
River water	Total coliforms	810	CFU/100 mL
River water	*Escherichia coli*	30	CFU/100 mL
River water	*Enterobacteriaceae*	200	CFU/100 mL
Milk	Total coliforms	590	CFU/mL
Milk	*Enterobacteriaceae*	140	CFU/mL
Well water	Total coliforms	<1	CFU/100 mL

microbiological contamination was more pronounced in river water and milk samples.

Heavy metal concentrations were predominantly elevated in soil samples, with copper reaching 470.244 mg/kg and mercury 2.330 mg/kg, indicating significant accumulation within the terrestrial compartment. Such accumulation patterns are commonly associated with the low mobility and persistence of trace metals in soils (Alloway, 2013; Hou et al., 2020). In contrast, aqueous matrices showed markedly lower concentrations, with copper ranging from 0.0011 to 0.0016 mg/L and nickel between 0.005157 and 0.007154 mg/L. Cadmium and mercury in water samples remained below detection thresholds.

Microbiological indicators displayed an inverse distribution pattern. River water exhibited the highest contamination levels, with total coliform counts reaching 810 CFU/100 mL, while *Escherichia coli* and *Enterobacteriaceae* were measured at 30 CFU/100 mL and 200 CFU/100 mL, respectively. Milk samples also showed elevated microbial loads (590 CFU/mL coliforms and 140 CFU/mL *Enterobacteriaceae*), whereas well water remained largely uncontaminated (<1 CFU/100 mL). These values indicate potential fecal contamination and reflect environmental hygiene conditions relevant to water and food safety monitoring (World Health Organization, 2017; FAO & WHO, 2011).

These findings indicate a compartmentalized distribution of contaminants, with heavy metals concentrated in soil and microbiological contamination predominating in water and milk. The observed distribution pattern is consistent with previous studies describing contaminant retention in soil matrices and microbial transport through aquatic systems (Kabata-Pendias, 2011; Li et al., 2009).

Correlation analysis of physicochemical and microbiological parameters

To evaluate relationships among variables, Pearson correlation coefficients were calculated according to Equation (1):

$$r_{xy} = \frac{\sum(x_i-\bar{x})(y_i-\bar{y})}{\sqrt{\sum(x_i-\bar{x})^2\sum(y_i-\bar{y})^2}} \tag{1}$$

where: r_{xy} represents the Pearson correlation coefficient between variables x and y, $\bar{x}$ and $\bar{y}$ denote the mean values of the variables, and n represents the total number of observations.

The resulting correlation matrix (Fig. 2) reveals distinct association patterns among heavy metals and between chemical and biological parameters. Strong positive correlations ($r \approx 1.00$) were observed among copper (Cu), cadmium (Cd), and mercury (Hg), suggesting a common source or similar geochemical behavior. Such associations are frequently linked to agricultural and anthropogenic contamination sources and to the persistent environmental behavior of heavy metals (Ali et al., 2019). Conversely, nickel (Ni) exhibited negative correlations with Cu and Cd ($r \approx -0.56$), indicating potential differences in mobility, solubility, or source origin.

A strong positive association was identified between Ni and Zn ($r \approx 0.91$), suggesting co-occurrence or shared transport mechanisms in

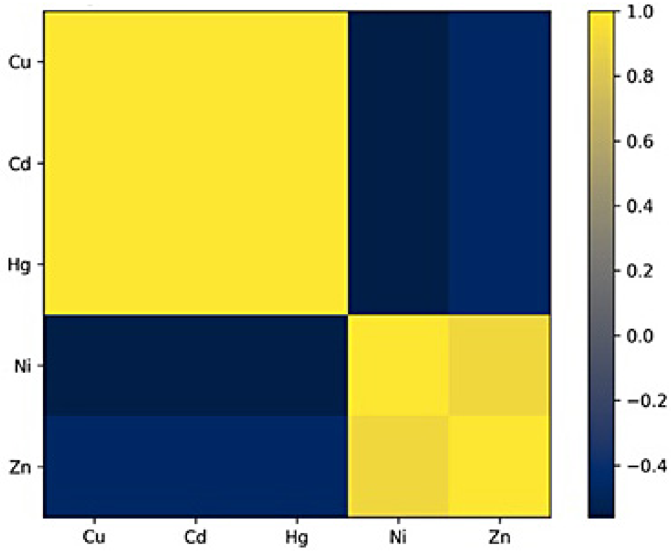

Figure 2. Integrated eco-health correlation matrix of physicochemical and microbiological parameters. Heatmap showing Pearson correlation coefficients between heavy metals and microbiological indicators across environmental samples

the aqueous phase. Microbiological indicators showed moderate to strong associations with selected chemical parameters, supporting the hypothesis of co-contamination processes linked to anthropogenic inputs such as agricultural runoff or livestock waste. Similar relationships between heavy metals and coliform bacteria have been previously reported in integrated environmental monitoring and environmental risk assessment studies (Qi et al., 2020; Ullah et al., 2018), while microbiological contamination associated with water and dairy environments has also been documented in agricultural systems (Ribeiro et al., 2019; Terrosu et al., 2012).

However, given the limited sample size (n = 4), the statistical significance of these correlations remains constrained. Therefore, these results should be interpreted as indicative trends rather than definitive relationships.

Multivariate analysis: Principal component analysis

Principal component analysis (PCA) was applied to reduce dimensionality and identify dominant patterns within the dataset. The transformation follows Equation (2):

$$Z = X \cdot W \tag{2}$$

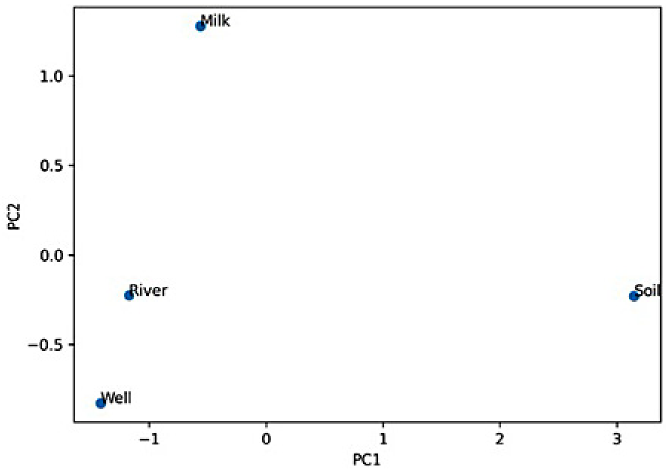

Figure 3. Principal component analysis of environmental samples. Projection of soil, river water, well water, and milk samples onto the first two principal components (PC1 and PC2), illustrating the distribution and separation of contamination patterns across environmental compartments

where: X represents the standardized data matrix and W represents the eigenvector matrix used for dimensionality reduction and component transformation.

The first two principal components accounted for the majority of the dataset variance. The PCA biplot (Fig. 3) reveals a clear separation between environmental compartments. Similar approaches have been widely applied in integrated environmental risk assessment and river basin studies (Li et al., 2008; Ullah et al., 2018; Qi et al., 2020).

The PCA results reveal a clear separation between environmental compartments. Soil samples are positioned distinctly along the first principal component (PC1), reflecting high heavy metal concentrations. In contrast, river and well water samples occupy intermediate positions, while milk samples are separated along the second component (PC2), indicating differences in contamination profiles.

The distribution suggests a gradient from soil to water and subsequently to milk, supporting the hypothesis of environmental-to-food chain transfer. The proximity between well water and milk samples indicates a potential linkage between groundwater quality and dairy contamination. Similar transfer pathways between contaminated soils, water systems, and agricultural products have been documented in previous eco-health studies (Rehman et al., 2018; Liu et al., 2022).

PC1 was primarily associated with heavy metal loadings (Cu, Cd, Hg), reflecting soil contamination, while PC2 was dominated by microbiological variables (coliforms, *E. coli*, *Enterobacteriaceae*), representing biological contamination in water and milk.

A spatial gradient was observed along PC1, progressing from soil to water and subsequently to milk, indicating a dilution and transfer process across environmental compartments. Milk samples were positioned closer to well water samples, suggesting a strong linkage between groundwater quality and dairy contamination. This interpretation aligns with integrated eco-health frameworks emphasizing environmental exposure pathways between ecosystems, livestock, and human health (van den Bossche & Devleesschauwer, 2022).

Hierarchical clustering analysis

Hierarchical clustering was performed using Euclidean distance as in Equation (3):

$$d(x, y) = \sqrt{\sum_{i=1}^{n} (x_i - y_i)^2} \quad (3)$$

where: $d(x, y)$ represents the Euclidean distance between observations x and y, calculated across all measured variables.

The resulting dendrogram (Fig. 4) reveals three primary clusters. Cluster analysis based on Euclidean distance and average linkage method, illustrating similarity relationships among soil, river water, well water, and milk samples according to their physicochemical and microbiological characteristics.

The first cluster groups river water samples, characterized by high microbiological contamination. The second cluster includes well water and milk samples, indicating a closer relationship between groundwater and dairy contamination pathways. The third cluster consists of soil samples, which remain distinct due to elevated heavy metal concentrations.

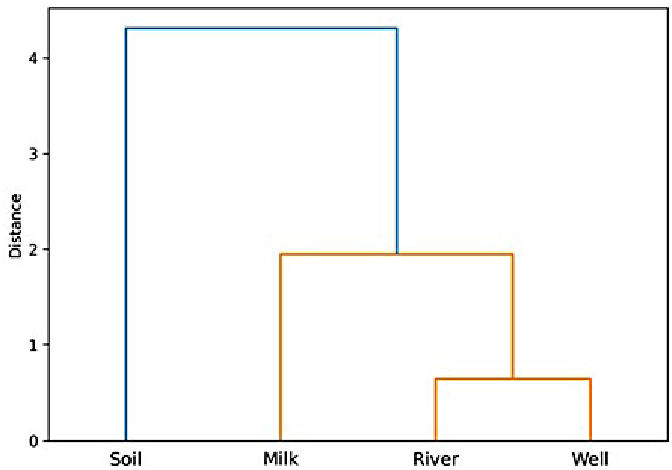

Figure 4. Hierarchical clustering dendrogram of environmental samples.

This clustering structure supports the hypothesis of differentiated contamination pathways, with soil acting as a reservoir of chemical pollutants and water serving as the primary vector for biological contamination. Comparable environmental compartmentalization has been described in hydro chemical investigations of the Vjosa River aquifer system (Dindi & Shehu, 2023; Li et al., 2008).

Integrated eco-health interpretation

The combined analysis of physicochemical and microbiological data suggests a multi-pathway contamination system. The distribution patterns indicate that heavy metals are largely retained within the soil matrix, while microbiological contaminants are more mobile and are transferred through water systems into the food chain. This behavior is consistent with the environmental persistence and mobility patterns described for agricultural pollutants (Ali et al., 2019; Hou et al., 2020).

The observed proximity between well water and milk samples in both PCA and clustering analyses highlights groundwater as a critical exposure pathway. This finding is consistent with the conceptual framework of environmental-to-food chain transfer and underscores the importance of water quality in livestock production systems (Oliver et al., 2005; FAO & WHO, 2011).

Despite the robustness of the multivariate approach, the limited dataset restricts the statistical generalization of the results. Future studies should incorporate larger sample sizes and temporal monitoring to validate these patterns and strengthen predictive modeling. Such integrated monitoring approaches are increasingly recommended for environmental and public health surveillance within One Health frameworks (van den Bossche & Devleesschauwer, 2022).

DISCUSSION

The integrated assessment performed in the present study demonstrates that contamination dynamics within coastal agricultural systems are governed by distinct but interconnected physicochemical and biological processes. The simultaneous evaluation of soil, surface water, groundwater, and milk samples revealed a compartmentalized distribution of pollutants, highlighting the complexity of environmental exposure pathways in agro-ecosystems influenced by agricultural and livestock activities.

One of the most significant findings of the investigation was the pronounced accumulation of heavy metals within the soil compartment. Copper concentrations reached 470.244 mg/kg, while mercury concentrations reached 2.330 mg/kg, indicating substantial metal retention within agricultural soils. Such accumulation patterns are consistent with the persistent nature of trace metals and their strong adsorption to soil mineral and organic fractions (Alloway, 2013; Kabata-Pendias, 2011). Similar contamination profiles have been associated with long-term agricultural inputs, fertilizer application, and diffuse anthropogenic activities (Ali et al., 2019; Briffa et al., 2020). In contrast, water samples exhibited very low heavy metal concentrations, with copper values ranging between 0.0011 and 0.0016 mg/L, suggesting limited metal mobility under the environmental conditions of the investigated area. The relatively low concentrations observed in milk samples further indicate that heavy metal transfer through the food chain remained restricted compared to soil accumulation (Zwierzchowski & Ametaj, 2018).

Microbiological contamination exhibited an opposite distribution pattern characterized by greater environmental mobility. River water samples showed the highest contamination levels, with total coliform concentrations reaching 810 CFU/100 mL, accompanied by detectable levels of *Escherichia coli* and *Enterobacteriaceae*. These values strongly suggest fecal contamination associated with agricultural runoff, livestock activity, and environmental exposure processes. In contrast, groundwater samples remained largely uncontaminated, indicating partial natural filtration within subsurface systems. Nevertheless, milk samples exhibited elevated microbial loads, with total coliform concentrations reaching 590 CFU/100 mL and *Enterobacteriaceae* reaching 140 CFU/100 mL. The presence of microbiological contamination in dairy products suggests indirect transfer mechanisms involving contaminated water sources, livestock exposure, or hygienic conditions during milk collection and handling (Oliver et al., 2005; FAO & WHO, 2011).

The multivariate analyses provided additional insight into contamination dynamics. Principal Component Analysis revealed a clear separation between heavy metal variables and microbiological indicators, with the first two principal components accounting for more than seventy percent of total dataset variance. Soil samples were strongly associated with copper, cadmium, and mercury loadings, whereas river water and milk samples were positioned closer to microbiological indicators. The proximity observed between groundwater and milk samples suggests a potential functional relationship between water quality and dairy contamination pathways. Such environmental-to-food transfer mechanisms have previously been reported in terrestrial food-web and eco-health investigations (Rehman et al., 2018; Liu et al., 2022).

Correlation analysis further supported the existence of differentiated contamination processes. Strong positive correlations were identified among copper, cadmium, and mercury, indicating common environmental behavior or similar contamination sources. In contrast, nickel displayed negative correlations with several heavy metals, suggesting differences in geochemical mobility and transport mechanisms. A particularly strong association was observed between nickel and zinc, with correlation values approaching 0.91, indicating potential co-transport within aquatic environments. Similar relationships between microbiological contamination and heavy metal occurrence have been described in integrated environmental monitoring and environmental risk assessment studies (Qi et al., 2020; Ullah et al., 2018), while microbiological contamination associated with water and dairy environments has also been documented in agricultural systems (Ribeiro et al., 2019; Terrosu et al., 2012).

The hierarchical clustering analysis reinforced these observations by separating samples into distinct environmental groups. Soil samples formed an independent cluster associated with heavy metal accumulation, while river water samples were differentiated primarily by microbiological contamination. The clustering of well water and milk samples further supports the hypothesis that groundwater quality may represent an important intermediary pathway connecting environmental contamination to livestock products.

These findings extend previous hydrochemical studies conducted within the Vjosa River basin. Earlier investigations mainly emphasized the role of natural hydrogeological processes such as seawater intrusion in shaping groundwater chemistry (Dindi & Shehu, 2023). However, the present results demonstrate that environmental risk assessment in coastal agricultural systems should also incorporate microbiological indicators and food-chain transfer mechanisms. Even when heavy metal concentrations in water remain relatively low, biological contamination may still represent a substantial environmental and public health concern (Prüss-Ustün et al., 2016).

Although a quantitative source apportionment analysis was beyond the scope of the present investigation, several plausible anthropogenic contamination sources may contribute to the observed environmental patterns within the study area. The investigated coastal agricultural region is characterized by intensive agricultural practices, livestock production systems, fertilizer application, manure management, groundwater abstraction, and localized human activities. Elevated soil copper concentrations may plausibly be associated with long-term agricultural inputs, including fertilizers, agrochemicals, and diffuse agricultural runoff, whereas microbiological contamination observed in river water and milk may reflect livestock-associated fecal inputs, inadequate sanitary management, or contamination linked to irrigation and water handling practices. Previous investigations conducted within the wider Vjosa basin and coastal Albanian environments have similarly reported increasing environmental pressures associated with agricultural land use, hydrochemical alteration, and anthropogenic disturbance. Nevertheless, definitive identification of contamination sources would require dedicated source-tracing approaches, expanded geospatial sampling, and isotopic or chemical fingerprinting analyses in future studies.

A quantitative human health risk assessment (HHRA) was considered conceptually within the One Health framework adopted by the study. However, the available dataset was not sufficient to support a robust quantitative exposure assessment according to internationally recognized HHRA methodologies. Such approaches generally require expanded sampling density, exposure frequency parameters, population-specific exposure assumptions, toxicological reference doses, and detailed contaminant concentration datasets across multiple environmental media and food products. Nevertheless, the observed occurrence of elevated heavy metal concentrations in soil and microbiological contamination in water and milk indicates the potential relevance of future quantitative health risk assessments addressing environmental, livestock, and human exposure scenarios in coastal agricultural systems.

From a broader scientific perspective, the study strongly supports the relevance of the One Health framework. The simultaneous occurrence of chemical and biological contaminants across soil, water, livestock, and food products demonstrates the interconnected nature of environmental quality, animal exposure, and human health (Destoumieux-Garzón et al., 2018). In particular, the detection of elevated microbiological contamination in milk highlights a direct exposure pathway with implications for food safety and rural public health protection.

Despite the scientific relevance of the integrated analytical framework, several limitations should be acknowledged. First, the relatively limited number of samples constrains statistical robustness and reduces the generalizability of the findings. Consequently, correlation analysis, PCA, and hierarchical clustering should be interpreted as exploratory analytical tools aimed at identifying environmental trends rather than establishing predictive or causal relationships. Second, the investigation was based on a single sampling campaign and therefore does not capture seasonal variability in hydrological conditions, agricultural practices, livestock activity, or contaminant dynamics. Coastal agricultural environments are characterized by pronounced temporal fluctuations that may significantly influence contaminant mobility, dilution, microbial persistence, and environmental exposure pathways. Future investigations should incorporate larger sample populations, repeated seasonal monitoring campaigns, and longitudinal datasets to strengthen statistical confidence and improve characterization of environmental transfer mechanisms.

Nevertheless, the study provides important evidence supporting integrated environmental monitoring strategies in coastal agricultural ecosystems. By combining chemical, microbiological, and multivariate analytical approaches within a unified eco-health framework, the research contributes to a more comprehensive understanding of contamination dynamics and environmental exposure pathways in environmentally sensitive agricultural regions.

CONCLUSIONS

The present study demonstrated that contamination processes within coastal agricultural systems are characterized by differentiated but interconnected chemical and biological pathways. Soil samples exhibited pronounced accumulation of heavy metals, with copper concentrations reaching 470,244 mg/kg and mercury concentrations reaching 2330 mg/kg, confirming the role of soil as the principal reservoir of persistent chemical contaminants.

In contrast, microbiological contamination was more strongly associated with aquatic and food-related compartments. River water samples showed elevated total coliform concentrations of 810 CFU/100 mL, while milk samples reached 590 CFU/100 mL, indicating significant biological contamination and potential environmental-to-food chain transfer. The close relationship observed between groundwater and milk samples through multivariate analyses suggests that groundwater quality may represent an important exposure pathway in livestock production systems.

Principal Component Analysis and hierarchical clustering confirmed the existence of distinct contamination regimes, separating heavy metal accumulation processes from microbiological contamination pathways. These findings demonstrate the value of combining physicochemical and microbiological indicators within integrated environmental assessment frameworks.

The study highlights the importance of adopting One Health approaches for environmental monitoring in coastal agricultural environments, where interactions among soil, water, livestock, and human exposure pathways are closely interconnected. Although the limited dataset constrains broader statistical generalization, the research provides an important baseline for future investigations and emphasizes the necessity of continuous environmental surveillance, improved groundwater protection, and enhanced hygienic management practices in dairy production systems.

Overall, the findings demonstrate that integrated eco-health methodologies are essential for identifying contamination pathways and for supporting food safety and environmental protection strategies in environmentally vulnerable agricultural regions.

Acknowledgements

The authors would like to express their gratitude to the Faculty of Technical and Natural Sciences, University "Ismail Qemali" of Vlorë, for providing institutional support during the development of this study. Special appreciation is extended to TENUIS Laboratories for conducting the certified laboratory analyses and for their technical contribution to sample processing and data generation. The authors also acknowledge the cooperation of local agricultural and dairy producers who facilitated field sampling activities within the study area.

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