ASSESSMENT OF THE ENVIRONMENTAL QUALITY OF SANDY BEACHES ON THE ALBANIAN ADRIATIC COAST

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ABSTRACT

The purpose of this study was to evaluate the quality of six beaches on the Adriatic Coast of Albania, stretching along a 200 km line, to identify the microbiological quality of sand and the preferences and priorities of beachgoers regarding their use. The six beaches considered are the most used areas of the Adriatic coast in the country and are generally perceived as major tourist destinations. Beach quality must be specifically addressed because overcrowding can lead to excessive waste, lower water quality, and ultimately lower socioeconomic value of the area. A significant public health hazard associated with gastrointestinal, dermatological, and other illnesses is microbial contamination of beach sand, especially with faecal characteristics such as *Escherichia coli* and *Intestinal Enterococcus* bacteria, as well as other faecal pathogens. The average levels of both bacteria are slightly higher in 2024 than in 2023, suggesting that while there were more average cases of contamination in 2024, there were not necessarily more severe cases. The lowest results in both years (4 - 5 CFU/g sand) are extremely low, indicating that some samples may have very little or no contamination. Strong outliers are indicated by the extremely high and comparable maximum values in both years, which is also confirmed by boxplot analysis. The large levels of variability in both years support the existence of contamination hotspots, indicating that contamination is not constant but fluctuates widely between samples.

Keywords: *Adriatic, sand beach quality, microbiological pollution, beach user, beach management*

INTRODUCTION

The beaches and waters along the coast offer a variety of activities, including swimming, surfing, sailing, fishing, jet skiing, and bird watching, along with opportunities for sunbathing and relaxation. According to [1], beaches are crucial recreational and leisure destinations for the economies of coastal countries. Coastal areas have become primary tourist destinations due to the growing popularity of beach tourism, and competition between them is growing [2 - 4]. Despite this, it is still challenging to accept the idea of a sandy beach as a system with a distinct identity, and this acceptance is largely influenced by national or local political decisions. The lack of clarity regarding the definition of "beach," the social-ecological category to which it belongs, and the system it symbolizes may be the cause of the lack of emphasis [5 - 7]. Actually, the fact that these transitional systems are important for both terrestrial and marine systems, but are not considered either, may be the cause of this ambiguity. Therefore, neither terrestrial nor marine management frameworks nor programs included sandy beaches.

In recent years, the assessment of sand quality has attracted increasing attention within the framework of public health risk management, mainly due to increased awareness of the presence of microbiological and physicochemical contaminants in these environments [4, 8 - 9]. The Albanian Adriatic coast, which is highly visited during the summer season, is exposed to multiple anthropogenic pressures, including wastewater discharges, urban and agricultural runoff, and coastal erosion. Microbial contamination of beach sand, especially with faecal parameters such as microorganisms *Escherichia coli* and *Intestinal Enterococcus*, as well as other faecal pathogens, has been identified as a major public health risk associated with gastrointestinal, dermatological, and other infections [10, 11]. The purpose of this study is to evaluate the microbiological quality of sand along the Albanian Adriatic coast in the period 2023 - 2024. Through systematic monitoring and statistical analysis, the study aims to identify trends, contamination sources, and high-risk zones, thereby supporting preventive measures and policies for sustainable coastal zone management. This research is in accordance with modern approaches to microbiological risk assessment in coastal recreational environments, referring to international directives such as the EU Bathing Water Directive (2006/7/EC) and USEPA (United States Environmental Protection Agency) recommendations [12 - 14] for monitoring faecal indicators. In case of Albania, for all coastal beach areas, pollution originates from both land-based and water-based sources. Land-based sources include runoff from agriculture, lack of wastewater treatment facilities, urban areas, and processing activities that carry various pollutants and waste. Water-based sources include discharges from ships, sewage overflows, and marine debris.

MATERIALS AND METHODS

Studied areas

This study was conducted along the sandy beaches of Albania, located on the eastern coast of the Adriatic Sea. The coastline stretches for approximately 380 km, from the Drini Bay in the north to the Vlora Bay in the south (Figure 1). The Albanian Adriatic coast consist predominantly of low-lying plains with extensive beaches characterized by fine sand.

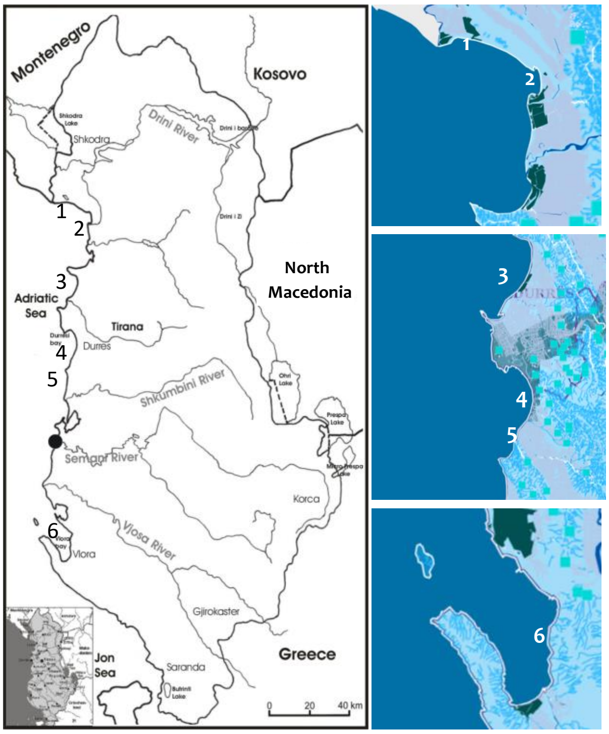

Figure 1. Map and locations of the studied areas (1 - Velipoja, 2 - Shëngjin, 3 - Lalzi, 4 - Durrës, 5 - Kavaja and 6 - Vlora beach)

As shown in Figure 1, the beaches included in this study are:

- Velipoja beach - stretches along the Buna River delta and has fine sand with a high iodine and mineral content, characterized by warm and shallow water.

- Shëngjin beach - located near the town of Lezha, known for its golden sand with a high mineral content.
- Durrës beach - located near the old town, founded by the Illyrians. This beach is characterized by fine sand and warm and shallow water.
- Lalzi Bay beach - The beach stretches between Cape Rodoni and “Bishti i Pallës”. It is characterized by fine sand and clear and shallow water.
- Kavaja beach (including Spille and Qerret Beach) - the beach stretches from Shkëmbi i Kavaja to the mouth of the Leshniqa stream, has fine golden sand. It is characterized by warm and calm water, with gradual depths.
- Vlora beach - stretches from Cape Pllaka in Treport to the Bay of Shën Jani. It consists of fine sand on the old beach and beaches to pebble beaches and small rocks. It is characterized by clean, clear and deep water.

These beaches were selected for their environmental diversity, geographical distribution, and significance in terms of human activity and potential microbiological contamination. The assessment of sand quality along the coastal area was conducted based on 57 sampling stations from May to September, in the period from 2023 to 2024. Sampling was organized in a time sequence to capture variations associated with tourist activity: (i) the pre-season series was conducted in May, before the start of the peak tourism, (ii) in-season series were conducted during the tourist season, in June, July, and August and (iii) the post-season series was conducted in September, after the end of the tourist season. Sampling was carried out at the same geographical coordinates during both years to ensure data consistency and comparability over time. Table 1 shows the number of sampling stations and sampling frequency on the beaches included in this study.

Sample collection: Sand samples were collected approximately 30 m from the shoreline, focusing on the most frequently used areas of beach (usually the supratidal area of the foreshore of the beach). Within each selected location, an area of 1 m² was marked and divided into four equal parts. Samples for microbiological analysis were taken from five points: one on each of the 4 extremities and one in the centre. Using sterile sampling spoons, 50 g of dry sand were collected at each point and placed in sterile, disposable plastic containers (bottles or bags). Each container was marked with the station code, time and date. The samples were stored at 4 °C and transported to the laboratory following standard microbiological procedures to ensure sample integrity and accuracy of results [14].

Table 1. Number of sampling stations and sampling frequency on beaches (VE - Velipoja, SH - Shëngjin, DR - Durrës, LA - Lalzi, KA - Kavaja, VL - Vlora)

Code/Beach name		No/stations		Sampling frequency	Type of beaches
		2023	2024		
VE	Velipoja	7	7	5	sandy
SH	Shëngjini	5	5	5	sandy
DR	Durrës	21	21	5	sandy
LA	Lalzi	5	5	5	sandy
KA	Kavaja	15	15	5	sandy
VL	Vlora	4	4	5	sandy

Microbiological parameters: Sand samples were tested for *Escherichia coli (E. coli)* and *Intestinal Enterococci (IE)* microorganisms using the membrane filtration method. Microbiological concentrations were estimated in terms of Colony-Forming Units (CFU) using selective media: ECD (Escherichia coli direct) agar for *E. coli* and TTC (Triphenyltetrazolium chloride) agar for *IE*.

Quantification of E. coli microorganisms: The analysis of *E. coli* was performed in accordance with the standard method ISO 9308-1:2014 for the detection and enumeration of *Escherichia coli*. A 100 mL of the sample was filtered through a membrane filter with a pore size of 0.45 µm. The filter was then transferred to a Petri dish containing ECD-MUG (4-methylumbelliferyl-β-D-glucuronidae) agar and incubated at 37 °C for 48 h. After incubation, all lactose-positive colonies, which differ in size and exhibit green fluorescence under ultraviolet light, were counted as presumptive *E. coli*. Suspected coliform colonies were further subjected to confirmatory tests, including the oxidase test and an indole production, to verify the presence of *E. coli*.

Quantification of Intestinal Enterococci microorganisms: The analysis of *Intestinal Enterococci (IE)* was performed in accordance with the ISO 7899-2:2000 standard for the determination of *Enterococci*. A 100 mL of the sample was filtered through a membrane filter with a pore size of 0.45 µm. The filter was then placed on Slanetz and Bartley Agar supplemented with TTC and incubated at 44 °C for 72 h. After the incubation period, the membranes were examined, and all colonies showing the characteristics of *IE*, especially red to brown colonies were counted. Membranes with colonies suspected to be *IE* were subsequently transferred to Bile Esculin Agar. After an additional 2 h of incubation, colonies surrounded by a black or dark brown colour were confirmed as positive for *IE* microorganisms.

Sample analysis: The sand samples were homogenized in the laboratory. The sample was diluted with sterile distilled water (autoclaved at 121 °C for approximately 20 min) in a ratio of 1:10. A 10 g of sand was separated from the sample and transferred to an Erlenmeyer flask containing 90 mL of water. The container was shaken for 2 min, and then allowed to settle for 30 s. The sample was filtered using the membrane filtration method and aseptically transferred to a Petri dish containing selective ECD or TTC agar. After incubation, the results were observed at the macroscopic level. Colonies were counted and expressed as Colony Forming Units (CFU)/g of sand [15, 16].

Data analysis: For data processing and tabular and/or graphical presentation, the statistical software SPSS (IBM Statistics 27) and Microsoft Excel were used. The following tests was applied: (i) the data were subjected to descriptive analysis (descriptive statistics, frequencies). The Kolmogorov-Smirnov non-parametric test was used to assess their distribution (if the p-value is > 0.05, the data does not follow a normal distribution); (ii) non-parametric tests Kruskal-Wallis, Frideman test and Wilcoxon Signed-Rank test were used for analysis of variance when the data did not follow a normal distribution (if the p-value is less than the significance level (α = 0.05), the null hypothesis (H0) is rejected, and it is accepted that there are significant differences between the groups); (iii) a cluster analysis was performed to group the beaches based on their microbiological contamination and sampling stations; (iv) hierarchical clustering was performed using Ward`s method, creating a Euclidean distance matrix. The matrix was organized in Euclidean space and visualized using the Principal Components Analysis (PCA) method; (v) all statistical analyses were conducted with an α value of 0.05; (vi) scree plot, scatter plot, boxplot, bar graph, etc., were used to visualize the data distribution.

RESULTS AND DISCUSSION

570 collected sand samples were evaluated for the microbiological presence of *E. coli* and *IE* microorganisms. For *E. coli* microorganisms, the minimum value in 2023 was 5 CFU/g of sand, and the maximum value was $2.2×10^3$ CFU/g of sand (Table 2). The mean value was $1.7×10^2$ CFU/g, with a standard deviation of $3.1×10^2$ CFU/g. In 2024, the minimum value was 4 CFU/g, and the maximum was $1.9×10^3$ CFU/g. The mean value was $1.7×10^2$ CFU/g, with a standard deviation of $3.1×10^2$ CFU/g. For *IE* microorganisms, the minimum value in 2023 was 1 CFU/g of sand, and the maximum value was $2.4×10^3$ CFU/g. The mean was $1.6×10^2$ CFU/g, with a standard deviation of $2.9×10^2$ CFU/g. In 2024, the minimum value was 4 CFU/g, and the maximum was $2.4×10^3$ CFU/g. The mean was $1.8×10^2$ CFU/g, with a standard deviation of $3.1×10^2$ CFU/g.

Table 2. Descriptive data of *E. coli* and *IE* microorganisms in sand

Descriptive statistics				
Year of monitoring	2023		2024	
	E. coli	*IE*	*E. coli*	*IE*
N	285	285	285	285
Minimum	5	1	4	4
Maximum	2.2×10^3	2.4×10^3	1.9×10^3	2.4×10^3
Mean	1.7×10^2	1.6×10^2	1.7×10^2	1.8×10^2
Std. Deviation	3.1×10^2	2.9×10^2	3.1×10^2	3.1×10^2
Variance	101.352×10^3	88.970×10^3	100.449×10^3	98.500×10^3
Skewness	3.73	3.93	3.504	3.559
Kurtosis	16.532	19.185	13.602	15.521

The classification of beach sand under the "Blue Flag" award criteria (section 7.2.1-WHO guidelines 2003) is based on the following: for *IE* microorganisms, a guideline of 60 CFU/g or MPN (Most probable number)/g of sand is used as a compliance criterion for all sampling events; *E. coli* microorganisms are used as an additional faecal indicator for compliance with the parametric standard of the European directive on bathing waters, using a reference compliance limit of 25 CFU/g [17]. According to the above, for *E. coli* microorganisms, 80.7 % of the analysed samples were above the limit value in 2024, and 79.3 % in 2023. For *IE* microorganisms, 52.6 % of the analysed samples were above the limit value in 2024, and 51.2 % in 2023. Based on the comparative box plot for *E. coli* concentrations during the monitoring months (2023 and 2024), it is possible to conclude the following (Figure 2): in May the values are lower for both years; however, in 2024 the distribution is narrower and there are fewer outliers compared to 2023. In June and July, the values are higher and more widely distributed. In August and September, the distribution of values shows a downward trend and becomes more stable, with fewer outliers, especially in 2024. Comparing the two years of research, it is evident that 2024 generally shows a narrower distribution and fewer extreme values. In contrast, 2023 shows higher microbiological contamination in certain months, particularly in June and July.

The comparative boxplot (Figure 3) of *Intestinal Enterococci* concentrations over months and monitoring years shows the following: in May, contamination levels are low for both years, but in 2023 there is a slightly higher prevalence, without significant number of outliers.

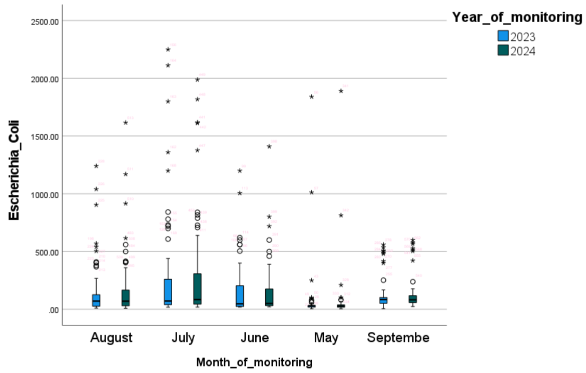

Figure 2. Boxplot of *E. coli* microbiological contamination data by months and year of monitoring

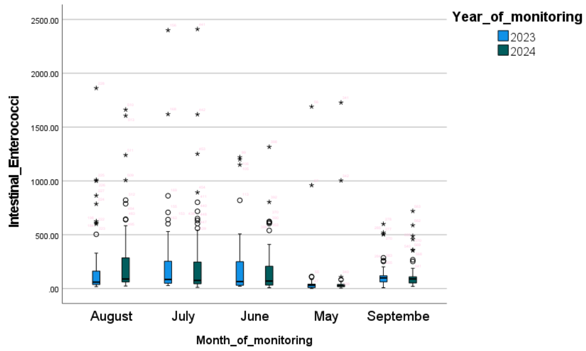

Figure 3. Boxplot of *IE* microbiological contamination data by months and year of monitoring

During June, July, and August, there was a noticeable increase in microbiological contamination in both years, but in 2023, more outliers were observed. July shows the highest level of contamination, marked by increased concentrations of *IE*. In September, contamination levels decrease significantly, and the concentration values are more tightly clustered, with fewer extreme values.

Comparing the two years, in 2023 microbiological contamination is more fluctuating (unstable), with a wider distribution and a larger number of outliers. In contrast, 2024 shows a narrower distribution of microbiological contamination levels and less extreme values. *IE* are strong indicators of faecal contamination. These data suggest that faecal contamination increases significantly in the months with high temperatures as a result of influx of tourists, elevated temperatures that favour bacterial growth, etc. Based on the result of the Kolmogorov-Smirnov test of data distribution, the P-value (Sig.) for both variables is 0.001, indicating that the data does not follow a normal distribution, which suggests that contamination levels vary considerably. The non-parametric Wilcoxon Signed-Rank test was applied to assess whether there is a statistically significant difference between the presence of the microorganism *E. coli* and *IE* between 2023 and 2024. The test result supports the alternative hypothesis, indicating that there is a significant difference between the two years. Referring to the boxplots for the distribution of microbiological contamination by years, it is observed that the highest levels of contamination were recorded in 2024. To enable a clear comparison of the microbiological contamination with *E. coli* and *IE* microorganism across the months of monitoring, but from the same sampling points each month, the Friedman test was used (Table 3).

The following findings are reported based on the mean rank from Friedman test. For *E. coli*, July and September were identified as the most contaminated months, while May was the cleanest month in 2024. Although no statistically significant differences were found between the two years, August and June 2024 showed significantly higher levels of contamination. For *IE*, August 2024 showed a significant increase in contamination, which may be related to the increased tourist flow. In contrast, an improvement is observed in May and July compared to 2023. Contamination levels during the other months appeared relatively stable. Both microorganisms show seasonal patterns, with higher contamination in July and August. *E. coli* contamination is relatively consistent between 2023 and 2024, with some localized improvements and some minor deteriorations. In contrast, *IE* shows an improvement in July, but a significant increase in August 2024, suggesting a potential environmental or anthropogenic impact during that period. By evaluating the p-value = 0 (less than 0.05), from the Friedman test, it can be conducted that the changes in the levels of contamination by *E. coli* and *IE* microorganisms between the months of 2023 and 2024 are statistically highly significant.

Table 3. The result of the Friedman test for *E. coli* and *IE*

Friedman test for E. coli				
Month	Mean rank (2023)	Mean rank (2024)	Difference	Comment
May	1.93	1.74	-0.19	Slightly less polluted in 2024
June	2.86	2.98	+0.12	Slight increase in 2024
July	3.90	3.68	-0.22	Still the most polluted, but on the decline
August	2.73	2.95	+0.22	Increase in contamination in 2024
September	3.58	3.66	+0.08	Similar trend
Friedman test for Intestinal Enterococci				
May	1.74	1.52	- 0.22	Slight improvement (cleaner in 2024)
June	3.03	2.99	- 0.04	Stable levels
July	3.84	3.46	- 0.38	Lower contamination in 2024
August	3.03	3.88	+ 0.85	Significant increase in 2024
September	3.37	3.16	- 0.21	A little cleaner in 2024

Cluster analyses were used to group microbiological contamination of sand by *E. coli* and *IE* into homogeneous groups (clusters) based on internal similarities between them. The elbow method is used to determine the optimal number of clusters. Using K-means clustering to group stations into similar clusters and visualizing the results with PCA, an analysis of cluster distribution across sampling stations was performed. The line chart shows the within-cluster sum of squares (WCSS) versus the different number of clusters (K). The 'elbow' point, where the rate of reduction changes abruptly, indicates the optimal number of clusters (Figures 4 and 5). The scatter plot shows the levels of microbiological contamination categorized by the number of clusters. Each dot represents a case, grouped according to a specific cluster based on *E. coli* and *IE* contamination. The contamination is unevenly distributed, and the elbow method suggests that k = 6 is the best number of clusters (Table 4).

Principal component analysis (PCA) was applied to reduce the dimensionality of the dataset and identify underlying patterns in the concentrations of *E. coli* and *IE* across different monitoring stations and time periods. Kaiser-Meyer-Olkin (KMO) values for *E. coli* (KMO = 0.700) and *IE* (KMO = 0.631) indicate that correlations between variables are adequate for factor analysis. Additionally, a p-value of 0 ($p < 0.05$) for both microorganisms confirms that the correlation matrix is significantly different from the identity matrix, suggesting the presence of significant correlations among the variables. Dendrograms were constructed based on the three principal components (from PCA) for the 57 sampling stations, using the Ward`s linkage method. As a result, the samples were grouped into four clusters based on their similarity within the PCA component space for *E. coli* microorganism (Figure 4) and *IE* microorganism (Figure 5).

Table 4. Summary of clusters based on levels of microbiological contamination with *E. coli* and *IE*

Cluster	N (Samples)	Mean *E. coli*	Mean *IE*	Description
1	10	1409.4	1556.2	Very high contamination
2	2	1934.0	2405.0	Extreme contamination, isolated hotspot
3	67	343.3	326.9	Medium/moderate contamination
4	34	663.6	780.9	High contamination, but not extreme
5	6	1742.5	450.2	Asymmetry - E. coli very high, but Enterococci are lower
6	451	56.3	63.2	Very clean area (largest cluster)

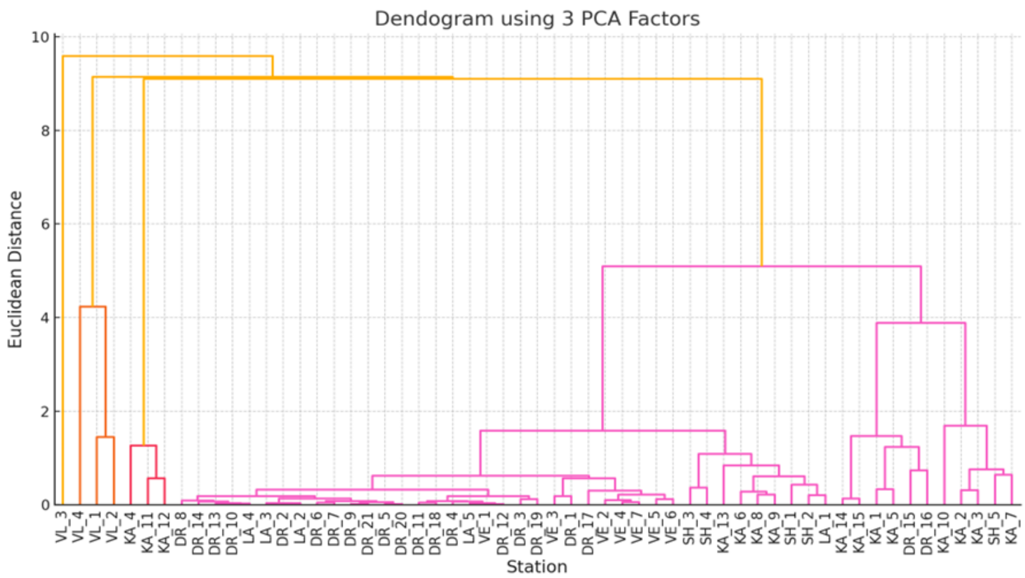

Figure 4. Dendrogram of monitoring stations based on three PCA components for *E. coli* microorganism

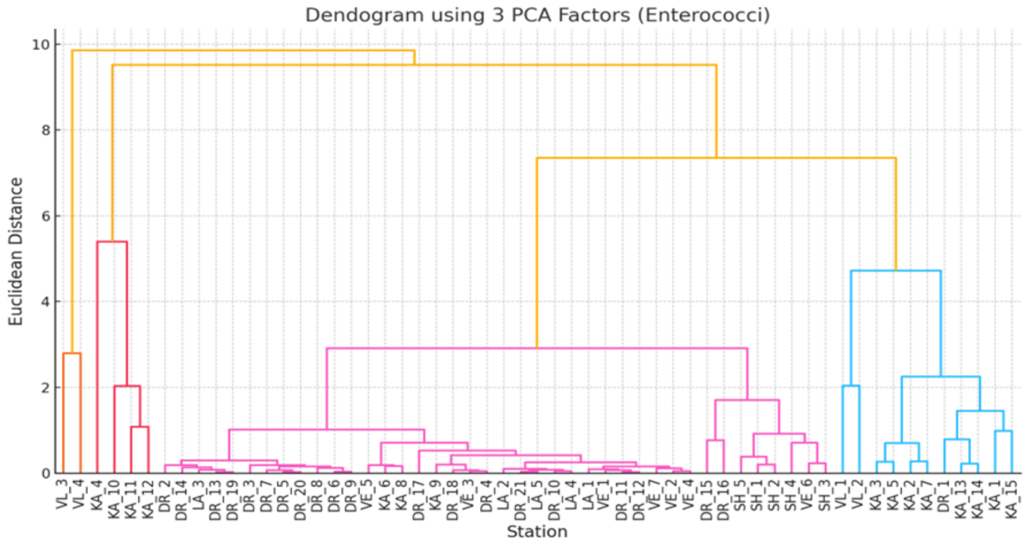

Figure 5. Dendrogram of monitoring stations based on three PCA components for IE microorganism

Table 5 presents a detailed summary of the cluster analysis results for *E. coli* and *Intestinal Enterococci (IE)* microorganisms, based on principal component analysis (PCA). Each cluster is characterized by the mean values of the three principal components (FCA (Factorial Component Analyses)1, FCA2, FCA3), reflecting different contamination patterns and environmental impacts at the monitoring stations. The interpretation of these clusters provides insight into the spatial distribution and potential sources of microbiological contamination in the study area (Table 5).

The average values are slightly higher in 2024 compared to 2023 for both microorganisms, indicating that there were more average cases of contamination in 2024, but not necessarily more extreme cases. The minimum values are very low in both years (4 - 5 CFU/g sand), suggesting very low or no contamination in some samples. The maximum values are very high and similar in both years, indicating strong outliers, which is also confirmed by the boxplot analysis [18]. Both years show high levels of variability, suggesting that contamination is not uniform but varies significantly between samples, reinforcing the presence of contamination hotspots. The comparative boxplots for *E. coli* and *Intestinal Enterococci (IE)* concentrations in 2023 and 2024 reveal several trends. For *E. coli*, May 2024 showed lower and more stable values with fewer outliers compared to 2023. In June and July, higher values were recorded with a wider distribution, while in August and September, a decrease in contamination was recorded, particularly in 2024, which had fewer extreme values. In comparison, 2023 exhibited more variability and higher contamination in June and July. For *IE*, low contamination levels were recorded during May in both years, but 2023 had slightly higher values. June, July, and August showed increased contamination in both years, with more outliers in 2023, especially in July. September showed decreased contamination, with more tightly clustered values in 2024. Overall, 2024 showed a narrower distribution with fewer extreme values compared to the more fluctuating and unstable levels in 2023. These patterns indicate that higher temperatures and increased tourism in summer months contribute to greater faecal contamination. Deviation from a normal distribution indicates that the microbiological contamination by the presence of *E. coli* or *IE* is not uniformly distributed between stations or periods. This suggests that the contamination is not stable, but varies significantly, perhaps as a result of local factors (sources of contamination, rainfalls, and human-induced (anthropogenic) contamination etc.). Cluster 6 accounts for 79 % of all samples and represents the least microbiologically contaminated monitoring stations. This cluster reflects areas with consistently low levels of *E. coli* and *IE* microorganisms. Clusters 1, 2, 4, and 5 together make up approximately 9 % of the samples and correspond to the most contaminated areas. Among them, the cluster 5 is particularly notable due to the very high concentration of *E. coli* but relatively low levels of *IE,* potentially indicating different sources of contamination or recent contamination events. Cluster 2 contains samples with extreme contamination values, indicating the presence of a localized contamination hotspot. Cluster 3 includes 12 % of the samples and represents areas with moderate or intermediate contamination, making it the second most common contamination profile. From the principal component analyses (PCA), the first principal component (FCA1) explains most of the variance for *E. coli* (52.7 %) and *IE* (48.7 %) microorganisms, followed by FCA2 and FCA3. Together, the three components account for 86 % of the variance for both microorganisms, indicating that the PCA model effectively captures key patterns of microbial contamination at the monitoring stations.

Table 5. Cluster characteristics based on PCA components

Cluster	FCA mean value	Interpretation	Monitoring stations
E. coli microorganism			
1	FCA1_mean = 1.9347 FCA2_mean = -0.3897 FCA3_mean = 3.0532	This cluster includes stations with high positive values, particularly in the third component (FCA3), which may indicate a significant presence of E. coli.	VL_1, VL_2, VL_4
2	FCA1_mean = 1.8673 FCA2_mean = 2.8596 FCA3_mean = -1.1938	Very high values of FCA1 and FCA2 suggest a strong influence from specific pollution sources affecting these stations.	KA_4, KA_11, KA_12
3	FCA1_mean = -0.3102 FCA2_mean = -0.0675 FCA3_mean = -0.0421	This is the most stable and largest cluster, characterized by moderate mean values, likely representing homogeneous environments with low to moderate E. coli presence.	VE_1–VE_7, SH_1–SH_5, DR_1–DR_21, LA_1–LA_5, KA_1–KA_3, KA_5–KA_10, KA_13–KA_15
4	FCA1_mean = 4.1020 FCA2_mean = -4.0351 FCA3_mean = -3.4748	This cluster represents a strong outlier, significantly different from all the others. It may reflect an instance of extraordinary contamination or an unusual local factor.	VL_3
IE microorganism			
1	FCA1_mean = 3.7000 FCA2_mean = -3.0924 FCA3_mean = 0.4250	This cluster is characterized by very high values of FCA1 and very low values of FCA2, indicating a distinct profile. It includes outlier stations, possibly reflecting unique contamination events.	VL_3, VL_4
2	FCA1_mean = 1.7226 FCA2_mean = 1.9428 FCA3_mean = -1.9409	Stations in this cluster show strong positive values of FCA1 and FCA2, but pronounced negative values of FCA3, indicating the influence from specific pollution sources with a distinct microbial or environmental signature.	KA_4, KA_10, KA_11, KA_12
3	FCA1_mean = -0.4299 FCA2_mean = -0.1672 FCA3_mean = -0.1880	Statistically the most stable and largest cluster, with most stations showing moderate negative or near-zero values for all components. It likely reflects low to moderate and consistent levels of contamination.	VE_1–VE_7, SH_1–SH_5, DR_2–DR_21, LA_1–LA_5
4	FCA1_mean = 0.2643 FCA2_mean = 0.4638 FCA3_mean = 1.3123	This cluster shows a notable increase of FCA3, potentially related to environmental conditions or anthropogenic influences affecting these stations.	DR_1, KA_1, KA_2, KA_3, KA_5, KA_7, KA_13, KA_14, KA_15, VL_1, VL_2

The clustering results reveal different patterns of microbiological contamination at the monitoring stations. For *E. coli* microorganism, cluster 3 represents the largest and the most stable group, characterized by moderate contamination, while clusters 1 and 2 highlight areas with elevated levels likely influenced by specific sources of contamination. Cluster 4 stands out as a significant outlier, indicating localized and potentially extraordinary contamination. Similarly, for *Intestinal Enterococci (IE)*, cluster 3 includes most stations with low to moderate contamination, whereas clusters 1 and 2 encompass stations with strong deviations in component values, indicating potential hotspots or targeted pollution. Cluster 4 shows increased values for the third component (FCA3), possibly reflecting environmental or anthropogenic influences. These findings support the identification of spatially distinct microbiological contamination zones and can serve as a basis for targeted monitoring and remediation activities.

CONCLUSION

Analysis of microbiological contamination of beach sand with *E. coli* and *Intestinal Enterococci (IE)* microorganisms revealed several key findings regarding contamination levels and distribution across monitoring stations in 2023 and 2024. While both years exhibited variability in contamination, 2024 generally showed slightly higher average contamination levels for both microorganisms, although not necessarily more extreme cases. The presence of high maximum values and significant outliers, along with a high level of variability, suggests that contamination is not uniform and tends to concentrate in specific hotspots. In conclusion, the findings highlight the spatially varying and episodic nature of beach sand contamination, suggesting that targeted monitoring and mitigation strategies are needed for areas with high contamination levels, especially during peak tourist seasons. Understanding the seasonal and spatial variability of contamination is crucial for ensuring the safety and quality of beach environments.

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