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Spatio-Temporal Dynamics of Fecal Bacterial Contamination in Groundwater and Associated Health Risks in the Feija Plain, Zagora, Morocco

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Abstract

Groundwater resources in arid agricultural regions face severe vulnerability to anthropogenic contamination, posing significant public health and environmental risks. This study evaluates the spatio-temporal dynamics of microbiological groundwater quality in the highly exploited Feija plain, Zagora province, Morocco. Over a 24-month period (2022–2024), eight strategic monitoring wells (P1–P8) were systematically analyzed for fecal indicators, general environmental flora, and strict pathogens. The results revealed a pronounced and recurrent seasonal cyclicity, with microbial loads systematically peaking during summer campaigns. For instance, *Escherichia coli* concentrations averaged 12.55 ± 2.91 CFU/100 mL in summer compared to 5.46 ± 2.39 CFU/100 mL in winter. Spatial profiling identified wells in the northern agricultural sector (P1–P3) as critical vulnerability hotspots, exhibiting maximum total coliforms reaching 1940 CFU/100 mL, whereas the hydrochemical reference site (P8) maintained baseline microbial signatures. Moreover, the consistent appearance of both recent (*E. coli*) and hardy (*Clostridium perfringens*) indicators from fecal pollution points to constant pollution in the area. Even though the average concentration of *E. coli* still lies within the acceptable level of irrigation according to the FAO (< 1000 CFU/100 mL), constant exceedances of strict WHO standards for zero tolerance in drinking water, together with occasional appearances of *Salmonella* spp., show deteriorated sanitary conditions in general. Highly correlated spatial variation of these indicators indicates that pollution of the aquifers is caused by diffuse agricultural pollution rather than any point source pollutants.

Introduction

Groundwater represents the cornerstone of socio-economic development and domestic water security in arid and semi-arid regions, particularly in southeastern Morocco, where surface water resources are critically scarce [1, 2]. Within the Zagora province, the Feija plain serves as a vital agricultural hub that relies entirely on its underlying Plio-Quaternary alluvial aquifer [3]. However, this indispensable resource is currently facing unprecedented quantitative and qualitative degradation. Escalating climate variability, coupled with a rapid regional transition toward water-intensive agricultural practices most notably, cash-crop watermelon cultivation has triggered severe aquifer overexploitation and an alarming depletion of piezometric levels [4, 5].

While the progressive salinization and broad hydrochemical deterioration of the Feija aquifer are well-documented [1], the structural hydrogeology of the plain renders it acutely susceptible to microbial pollution. The aquifer is characterized by a highly permeable sandy matrix that offers negligible natural attenuation or filtration capacity against the rapid infiltration of surface runoff. This vulnerability is heavily exacerbated by extensive agricultural return flows and shifting, extreme precipitation patterns [3]. Consequently, diffuse anthropogenic pollutants ranging from agricultural leachates laden with organic fertilizers [6] to untreated domestic wastewater originating from decentralized rural settlements [7, 8] percolate rapidly into the water table. This unmitigated infiltration introduces a severe, yet frequently under-evaluated, bacteriological threat to the groundwater matrix [9]. Although prior environmental investigations in the Zagora region have predominantly emphasized physicochemical deterioration,

biological contamination constitutes an immediate and critical public health crisis. The direct intrusion of fecal matter introduces pathogenic microbial indicators—such as total coliforms, *Escherichia coli*, and fecal streptococci into the primary drinking water supply of local communities. The chronic consumption of this untreated groundwater exposes the rural population to a heightened risk of acute waterborne gastrointestinal diseases [10, 11].

Fecal indicator bacteria such as total coliforms, *Escherichia coli*, fecal streptococci and the spores of *Clostridium perfringens* are widely used to detect fecal pollution of water, each with its own persistence and specificity [12, 13]. Among them, *E. coli* can travel long distances underground, which makes it a useful marker of fecal contamination in aquifers [14]. Groundwater is often presumed to be microbiologically safe, yet reviews show that enteric pathogens occur in a considerable proportion of groundwater samples and that consumers of untreated groundwater remain exposed to enteric disease [15, 16]. Fecal contamination is also frequent in rural and unprotected water sources of low- and middle-income countries [17], and several waterborne bacterial pathogens, including *Salmonella*, *Shigella* and *Pseudomonas aeruginosa*, are of recognized public health concern [18].

In view of filling this significant gap in knowledge, it is essential that a comprehensive bacteriological analysis be conducted in order to fully assess the level of sanitation in the Feija aquifer. Thus, this study will seek to conduct a comprehensive analysis of the biological characteristics of the region's groundwater. These include (i) assessment of microbial biological loads in the aquifer; (ii) identification of vectors of fecal contamination in space and time; and (iii) evaluation of direct sanitary risks for the region's inhabitants. By moving the scientific discourse away from conventional physical parameters and towards biological characteristics of water, this study provides an important basis for implementing sanitation interventions in arid regions.

Materials and Methods

Study Area

Feija plain, found in Zagora province, eastern Morocco, is found within the arid pre-Saharan zone, which has a desert type of climate, very little rainfall, and a lot of evaporation (Fig. 1). It is because of the climate that the water found underground becomes necessary for irrigation and domestic use in this zone. This area falls within the watershed of Drâa and is made up of alluvium containing sand, silt, and gravel; it makes the underground water easy to circulate. This zone covers Feija plain with a total area of 1,000 km². It lies on the right side of the Drâa river, Oued Drâa, south of Zagora town.

It is considered a synclinal depression whose substrate is schist, covering a distance of about 80 kilometers eastward from west to east and is confined by mountainous reliefs on both sides. The upper part of the plain is a region which covers an average length of 8 to 12 kilometers and ends up moving eastward to meet the Drâa Valley which acts as the main drainage system for this huge plain. In general, the direction taken by the Feija is slightly shifted to the south because of the deposition of sediments.

The Feija's terrain is described as having a slight slope towards the south averaging at about 0.7 percent and another towards the east measuring 0.3 percent through the RN12 national route that connects Zagora to Foum Zguid.

Sampling and Sampling Sites

Groundwater samples were taken from eight wells (P1 to P8), which are situated in the Feija plain in the Zagora province. Well P8 served as a reference point because of its less impacted hydrochemistry owing to its distance from human activities. The sampling was carried out periodically during the period of December 2022 to December 2024. Each sample was collected after purging the wells to ensure the representativeness of water taken from the aquifer. The samples were collected in sterile bottles and kept refrigerated at 4 °C, after which they were delivered to the laboratory. Bacteriological tests were done in the Public Laboratory for Testing and Studies (Laboratoire Public d'Essais et d'Études).

Bacteriological Evaluation of Groundwater

The determination of the bacteriological water quality of groundwater was carried out according to the prevailing standards of Morocco; in particular, the standards NM ISO 9308-1 (2007) to determine the total coliforms and *Escherichia coli* bacteria, and the standard NM ISO 7899-2 (2007) to determine fecal streptococci. Membrane filtration technique, using filters with 0.45 microns pores, was used to determine the concentrations of the bacterial indices of fecal pollution. After the filtration step, the membranes were inoculated on specific selective culture media at the specified temperature and period, permitting the appearance of colonies with distinctive characteristics. The measurements were provided in CFU/100mL units as per international guidelines for the microbiological water analysis. These procedures are comparable to those described in Standard Methods for the Examination of Water and Wastewater [19].

The water samples were collected in 500 mL polyethylene bottles that were sterilized, using methods recommended by the World Health Organization (WHO) for the microbial examination of water meant for human consumption. The collected samples were kept in a refrigerator at 4 °C and delivered to the laboratory for testing in a maximum period of 24 hours.

The microbiological analyses targeted several indicators of fecal and environmental contamination, including *Escherichia coli* (*E. coli*), total coliforms, fecal streptococci, cultivable microorganisms (heterotrophic plate counts) at 22 °C and 37 °C, *Clostridium perfringens*, sulfite-reducing clostridia, *Pseudomonas aeruginosa*, *Pseudomonas* spp., *Aeromonas hydrophila*, *Legionella* spp., *Salmonella* spp., *Shigella* spp., *Vibrio cholerae*, as well as yeasts and molds.

Statistical Analysis

The analysis of the microbiological data was done using R Studio (4.4.0). Descriptive statistics of the data, such as average value, minimum, maximum, and standard deviation, were used to measure data spread and the level of contamination from each microbiological parameter examined. In order to analyze the level of compliance of the samples with WHO drinking water standards, frequency was conducted. Moreover, a correlation matrix using Pearson correlation was computed to explore possible relations among different microbiological parameters and identify the potential source of contamination. Finally, comparative analysis was done to assess the variability in space and time of the groundwater bacterial contamination within the Feija Plain area.

Results

Baseline Microbiological Quality and Seasonal Variations

Descriptive statistics representing the baseline quality of microbiological components of the Feija plain groundwater are shown in Table 1. It can be noticed that there was a significant seasonality for each of the taxonomic groups under investigation, as indicated by consistent increases in the loads of microbes during the warm season. General environmental bacteria and total coliforms are represented by the highest number of microorganisms, with average summer numbers of 1652.20 ± 275.50 CFU/100 ml (at 22°C) and 1428.21 ± 319.58 CFU/100 ml, respectively. These high levels of baselines are followed by the presence of strict indicators of faeces contamination. Thus, E.coli and fecal streptococci have higher numbers in summer than in winter, which were observed at an absolute maximum of 18 and 481 CFU/100 ml, respectively.

The coexistence of *Clostridium perfringens*, with an average abundance of 83.93 ± 14.53 CFU/100 mL in summer, further strengthens the evidence of persistent and longstanding contamination of the aquifer with fecal matter. In addition to this, even though strict enteric pathogens, such as *Salmonella* spp. and *Shigella* spp., had been found in negligible amounts and were commonly undetectable in the winter season, their occasional occurrence along with opportunistic pathogens such as *Pseudomonas aeruginosa* (with an average abundance of 7.73 ± 1.00 CFU/100 mL in summer) poses a potential threat from a hygiene point of view.

Table 1 Spatio-temporal descriptive statistics of the primary microbiological parameters in the Feija plain groundwater during summer and winter campaigns (2022–2024)

Microbiological parameter (CFU/100 mL)	Summer (mean ± SD)	Winter (mean ± SD)	Overall maximum
Fecal indicators			
Escherichia coli	12.55 ± 2.91	5.46 ± 2.39	18
Total coliforms	1428.21 ± 319.58	746.94 ± 186.36	1940
Fecal streptococci	353.87 ± 81.66	177.78 ± 42.20	481
Clostridium perfringens	83.93 ± 14.53	52.67 ± 9.80	104
General environmental flora			
Cultivable microorganisms (22 °C)	1652.20 ± 275.50	1026.17 ± 204.90	1980
Cultivable microorganisms (37 °C)	1082.53 ± 184.03	680.60 ± 152.60	1295
Opportunistic and strict pathogens			
Pseudomonas aeruginosa	7.73 ± 1.00	5.40 ± 0.80	10
Salmonella spp.	0.15 ± 0.07	0.01 ± 0.01	0.33
Shigella spp.	0.02 ± 0.01	0.00 ± 0.00	0.08

CFU colony-forming units; SD standard deviation

Spatio-temporal Dynamics of Fecal Indicator Bacteria

As can be observed from Fig. 2, the main markers of faecal pollution, *Escherichia coli*, faecal streptococci, and *Clostridium perfringens* showed a definite seasonal trend in 2022 to 2024. In each of the three years studied, bacterial concentrations reached a peak during the summer sampling periods and dramatically decreased in the winter months. It is noteworthy that such a repeated seasonal trend implies that high summer temperatures, perhaps in combination with particular agricultural activities or seasonal changes in groundwater recharge processes, create an environment highly conducive to bacteria thriving.

Of all the indicators studied, fecal streptococci exhibited the highest levels, with this bacterium being predominant within the microbial fecal indicator group. Its average presence attained a peak level of 376.75 CFU/100 ml during summer 2022, following which its numbers fell by about half, reaching 188.40 CFU/100 ml during the winter season that followed. Another microorganism whose levels followed the same trend was *Clostridium perfringens*, a strong indicator of fecal contamination owing to its ability to form spores. The bacterium showed fluctuations between levels of 88.40 CFU/100 ml (summer 2022) and 49.60 CFU/100 ml (winter 2024). Though *Escherichia coli* recorded the lowest relative abundance of the three, it maintained strict seasonality in that its average summertime levels (between 11.88 CFU/100 ml and 13.38 CFU/100 ml) were consistently more than double those found in winter (5.00 CFU/100 ml

to 6.00 CFU/100 ml). The large deviation bars in summer suggest significant variation in space, implying areas of particular vulnerability on the Feija plain during the summer season. In addition to the striking seasonal variability, the results depicted in Fig. 2 also illustrate a slight interannual decline in the mean concentration levels for all three fecal contaminants from 2022 to 2024. In spite of this mild temporal decline in the mean levels of fecal indicators, the constant presence of recent contaminant (*E. coli*) as well as resistant contaminant (*C. perfringens*) indicates that the Feija plain aquifer remains susceptible to anthropogenic/agricultural pollution. The constant violation of the WHO zero tolerance standards by these fecal indicators is indicative of a serious water degradation problem necessitating effective water management interventions.

Spatial Distribution of Microbial Contamination Across Wells

Spatial profiling of the selected wells (P1-P8) demonstrates the presence of contamination clusters in the north part of the agricultural sector (wells P1, P2, and P3), registering maximal values for all environmental markers, as well as fecal bacteria like *E. coli* and *C. perfringens*. In contrast, the control well (P8) showed microbial baseline values (Fig. 3). The high degree of synchronization in spatial variations for all microorganisms, starting with abundant total coliforms and ending with rare opportunistic pathogens, allows assuming that the major threat to groundwater quality in the Feija plain is non-point pollution, which may include agricultural leaching.

Generally speaking, wells P7 and P8 demonstrate low values for a wide spectrum of microorganisms. The probable reasons for such an effect may include more significant distance between those wells and primary sources of pollution, better protection of the boreholes, and more adverse local hydrogeological conditions, which do not favor contamination of the water body. Thus, obtained data provide evident evidence that microbiological contamination in the Feija plain groundwaters is heterogeneously distributed. Spatial discrepancies noted for the tested wells are caused by multiple factors, including environment, anthropogenic pressure, and local hydrogeological conditions of the studied area.

Spatio-temporal Dynamics of Microbial Contamination

In regard to the temporal analysis of the quality of water in terms of the degree of microbial contamination, as seen in Fig. 4a, it can be identified that a highly organized recurrent seasonal pattern exists concerning the fecal contamination. Based on the assessment of *Escherichia coli*, which constitutes one of the main indicators of intestinal contamination, it should be stated that it reaches its maximum values during summer field samplings (between 11.88 and 13.38 CFU/100 ml), whereas it considerably decreases during winter sampling (in the range of 5.00-6.00 CFU/100 ml). The notable value of the standard deviation during the summer season indicates the high susceptibility of the aquifer under the conditions of increased temperature. It should be pointed out that the peak values of microbial

concentrations might be associated with elevated temperatures facilitating bacteria survival, increased irrigations, and consequently the migration of runoff contaminated with anthropogenic pollutants to the vadose zone.

In addition to the temporal variation, it is also interesting to examine the spatial variability in Fig. 4b that illustrates the spatial variability of the microbial contamination in the Feija plain monitoring network. The simultaneous presence of Total Coliforms and *E. coli* on the dual axis provides an insight into the high level of synchronization of their spatial distribution. It was found that wells located in the northern or agriculturally developed regions (P1, P2, and P3) were particularly vulnerable and exhibited the highest levels of microbial contamination (for instance, Total Coliforms above 1200 CFU/100 mL). In contrast to this, the further movement from north towards south resulted in a gradual decrease in the microbial concentration. As seen from Fig. 4b, the shaded area represents well P8, which was constantly characterized by the lowest levels of the microbial baseline, thus confirming its selection as a hydrochemical reference point. Importantly, the presence of such spatial correlation implies that the contamination is associated with non-point sources of pollution rather than point sources.

Comparison of Microbiological Parameters with International Water Quality Standards

An examination of the parameters related to the groundwater microbiological analysis (Table 2) shows that there is no uniformity in contamination, especially when considered based on the FAO/WHO criteria and the WHO guidelines for irrigation.

Table 2 Assessment of the microbiological quality of the Feija plain groundwater according to FAO/WHO guidelines for irrigation

Microbiological parameter	Observed mean	Irrigation standards (FAO/WHO)	Evaluation
Escherichia coli (CFU/100 mL)	8.73	< 1000 CFU/100 mL	Compliant
Total coliforms (CFU/100 mL)	1074.99	Variable depending on use	Acceptable with monitoring
Fecal streptococci (CFU/100 mL)	265.4	Monitoring recommended	Moderate risk
Salmonella spp.	Occasional presence	Absence recommended	Health risk
Total microbial load	High	Not specified	Monitoring required

FAO Food and Agriculture Organization; WHO World Health Organization; CFU colony-forming units

The WHO standards can therefore act as a key reference, especially in regards to the microbial quality of water. This applies especially to faecal indicator bacteria, such as *Escherichia coli*, which should not be present in any number in 100 ml of water used for drinking purposes, but need to be strictly controlled in case the water is recycled for irrigation.

The average level of *E. coli* is 8.73 CFU/100 ml, far lower than the limit of 1000 CFU/100 ml defined by WHO for irrigation water, but exceeding the very strict WHO standards for water used for drinking purposes. The total coliforms have a significant mean content of 1074.99 CFU/100 mL. Even though there is no established critical point for such a parameter in terms of irrigation by the WHO, this demonstrates the significant bacterial contamination of the sample and implies a deterioration of the microbiological quality of water, hence, necessitating constant monitoring. Fecal streptococci demonstrate a mean content of 265.4 CFU/100 mL. Since there is no established limit value of the parameter under consideration according to WHO directives, this result indicates moderate fecal contamination of the sample. Moreover, the detection of *Salmonella* spp. on some occasions should raise serious health concerns, as WHO mandates that there should be no traces of this microorganism in the sample of water designated for human or irrigation purposes.

Lastly, there is an elevated presence of the total number of microbes even without the availability of the critical value of this parameter as stipulated by WHO. This implies that there is much microbial activity and this may be associated with the abundance of organic matter and conditions that favor bacterial growth. From these findings, it is apparent that there is poor microbiological water quality owing to the prevalence of microbial presence, especially the presence of bacteria. This makes it necessary for appropriate control measures to be implemented, in adherence to WHO guidelines.

Discussion

Temporal Dynamics and Thermal Proliferation of Enteric Bacteria

The systematic temporal fluctuations observed throughout the 2022–2024 monitoring period highlight an acute seasonal vulnerability within the Feija plain aquifer. The recurrent summer peaks in primary fecal indicators (*E. coli*, fecal streptococci, and *C. perfringens*) demonstrate that elevated ambient and soil temperatures actively stimulate the survival and proliferation rates of enteric bacteria within the vadose zone [20]. In arid agricultural regions, intensified summer irrigation acts as the primary hydrodynamic transport vector, mobilizing surface contaminants downward into the water table [21]. The fact that *Clostridium perfringens*, which is a spore-forming microorganism resistant to severe environmental conditions, exhibits the same pattern in its seasonal variation similar to more vulnerable microbes such as *Escherichia coli* proves that this phenomenon occurs due to continuous pollution rather than mere re-suspending of past microorganisms [22]. Such cyclical nature in seasonal variations is completely different from what occurs in temperate climates, where biological contamination is linked to rainfall in autumn or winter months.

Spatial Heterogeneity and Signatures of Diffuse Pollution

The microbial loading pattern shows a high degree of heterogeneity, emphasizing the extreme sensitivity of the aquifer to localized human influences. In particular, the contamination levels detected in the northern region (wells P1, P2, and P3) correspond to areas with high levels of agricultural activity and the use of organic soil amendments. The swift movement of agricultural waste, which is rich in fecal bacteria from organic fertilizers, has long been identified as the major cause of groundwater pollution in aquifers with high filtration rates [23]. The clean microbial signature detected in the control well (P8) clearly confirms that the degradation process has nothing to do with the natural hydrogeological nature of the aquifer. It is, rather, a reaction to the pressure exerted by the human environment on it [24]. Manure-enriched composts are being evaluated as agricultural inputs in Morocco [25], which underlines the importance of ensuring the sanitary quality of organic amendments applied above vulnerable aquifers.

Regulatory Compliance and Public Health Implications

In assessing the suitability of Feija plain groundwater quality within the context of international legislation, one can observe an interesting sanitary contradiction. According to the FAO standards that allow for using water for irrigation without restrictions provided the level of *E. coli* does not exceed 1000 CFU/100 mL [26], the concentration of bacteria within the studied samples is far from the critical value of 8.73 CFU/100 mL. Hence, there is no problem with applying this water source to regional irrigation practices. Irrigation guidance for fecal indicators is also provided in the WHO guidelines for the safe use of wastewater, excreta and greywater in agriculture [27]; because groundwater used for irrigation is not wastewater, this comparison should be read as indicative.

In comparison with WHO's requirements for potable water standards, the above data becomes highly concerning. As per WHO, there should be zero content of *E. coli* and total coliforms in water supplied to people [28].

The intermittent presence of bacteria such as *Salmonella* spp., alongside the persistent presence of pathogens such as *Pseudomonas aeruginosa*, directly threatens the health of residents of these rural communities who rely on these wells as sources of water without any preliminary treatment measures. This deterioration of the microbial quality of water, which is typical of multi-factorial situations of vulnerability in areas where drought is common [29], requires immediate action regarding water usage separation and proper sanitary supervision.

Evidence from other regions indicates that fecal contamination of groundwater-based supplies is common in rural settings [17] and that untreated groundwater is repeatedly associated with enteric illness [15, 16]. For the Feija plain, the priority measures are therefore the disinfection of water before drinking, the sanitary protection of wells, the sound management of manure and other organic amendments in the northern agricultural sector, and a routine microbiological monitoring programme with reinforced sampling during the summer season.

Indicator–Pathogen Relationships and Study Limitations

Indicator bacteria provide a practical and cost-effective measure of fecal pollution, but their quantitative relationship with pathogens is inconsistent across studies and settings [13, 30]. In this study, pathogenic bacteria were detected only occasionally and at low levels, so the health risk is inferred from the exceedance of guideline values and not quantified.

Several limitations should be acknowledged. Sampling was organized in seasonal (summer and winter) campaigns, which may not capture short-term events such as irrigation pulses or rainfall. Microbial source tracking was not performed, so the attribution of contamination to agricultural inputs rather than to domestic wastewater rests on spatial patterns and on the synchrony among parameters, not on source-specific markers. Well construction, sanitary protection and the hydrochemical characterization of the plain reported previously [3] were not integrated into the present analysis, and no epidemiological data on waterborne disease in the local population were available. Future work combining microbial source tracking, well-protection surveys and quantitative microbial risk assessment would strengthen the evaluation of health risks.

Conclusions

This 24-month survey of eight wells in the Feija plain shows that groundwater is persistently affected by fecal bacterial contamination, with a marked summer peak for all fecal indicators; for example, *E. coli* averaged 12.55 ± 2.91 CFU/100 mL in summer against 5.46 ± 2.39 CFU/100 mL in winter. The wells of the northern agricultural sector (P1–P3) were the most affected, whereas the reference well P8 showed the lowest loads, and the synchronous spatial variation of the indicators points to diffuse, mainly agricultural, pollution rather than point sources.

Mean *E. coli* levels meet the FAO irrigation threshold (< 1000 CFU/100 mL) but consistently exceed the zero-tolerance WHO value for drinking water, and *Salmonella* spp. occurred occasionally. Groundwater from the Feija plain should therefore not be consumed without treatment. Disinfection at the point of use, sanitary protection of wells, better management of manure and organic amendments in the northern sector, and routine summer-focused monitoring are recommended, and future studies should add microbial source tracking and quantitative microbial risk assessment.

Declarations

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Ethics approval and consent to participate

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Author contributions

Hamid Nadi: Conceptualization, Investigation, Writing – original draft. Fathalah Elwahab: Methodology, Formal analysis, Visualization, Writing – review & editing, Supervision, Corresponding author. Hicham Ouhakki, Mehdi Boudraine: Investigation, Data curation. Siham Belkacemi, Hanae Marjaa: Investigation, Resources. Safouane El Ghouddany, Nabila Auajjar: Investigation, Validation. Naima Dohou, Khalid Yamni: Writing – review & editing. Moulay Laarbi Ouahidi: Supervision, Project administration. All authors read and approved the final manuscript.

Competing interests

The authors declare that they have no competing financial or non-financial interests.

Data availability

The datasets generated and analysed during the current study are available from the corresponding author on reasonable request.

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Figures

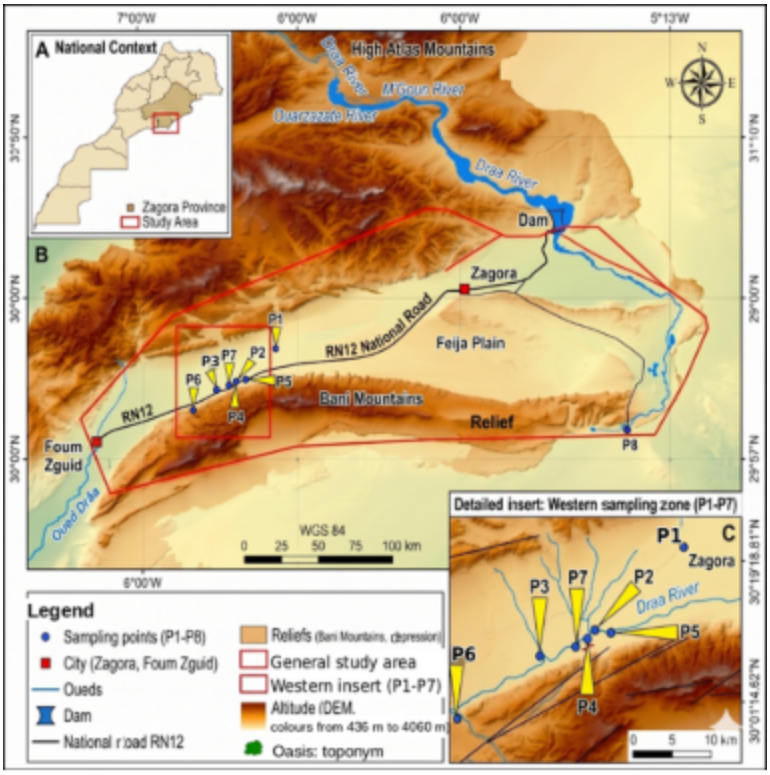


Figure 1

Geological map of the Feija plain

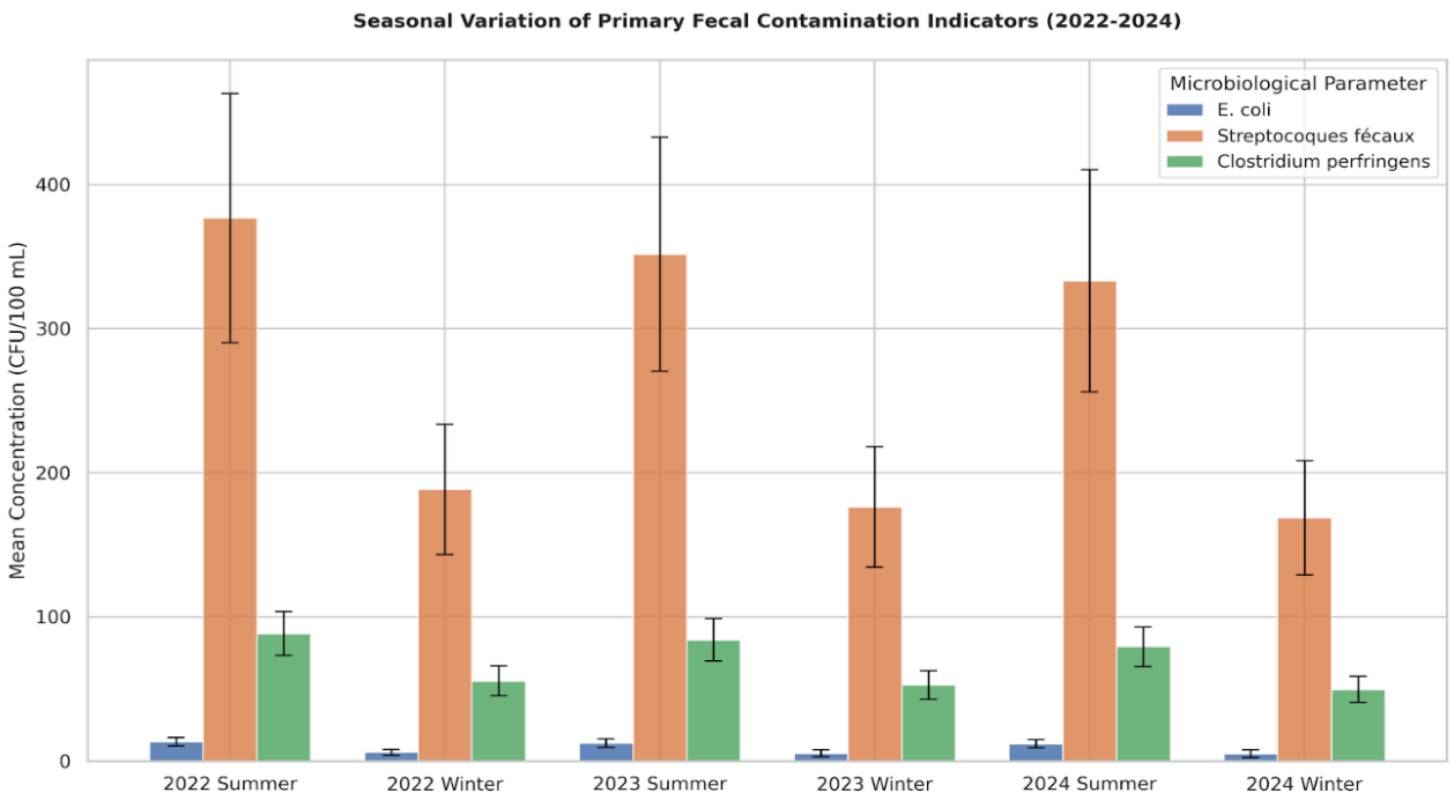


Figure 2

Spatio-temporal dynamics of primary fecal indicator bacteria concentrations (CFU/100 mL) during summer and winter sampling campaigns from 2022 to 2024

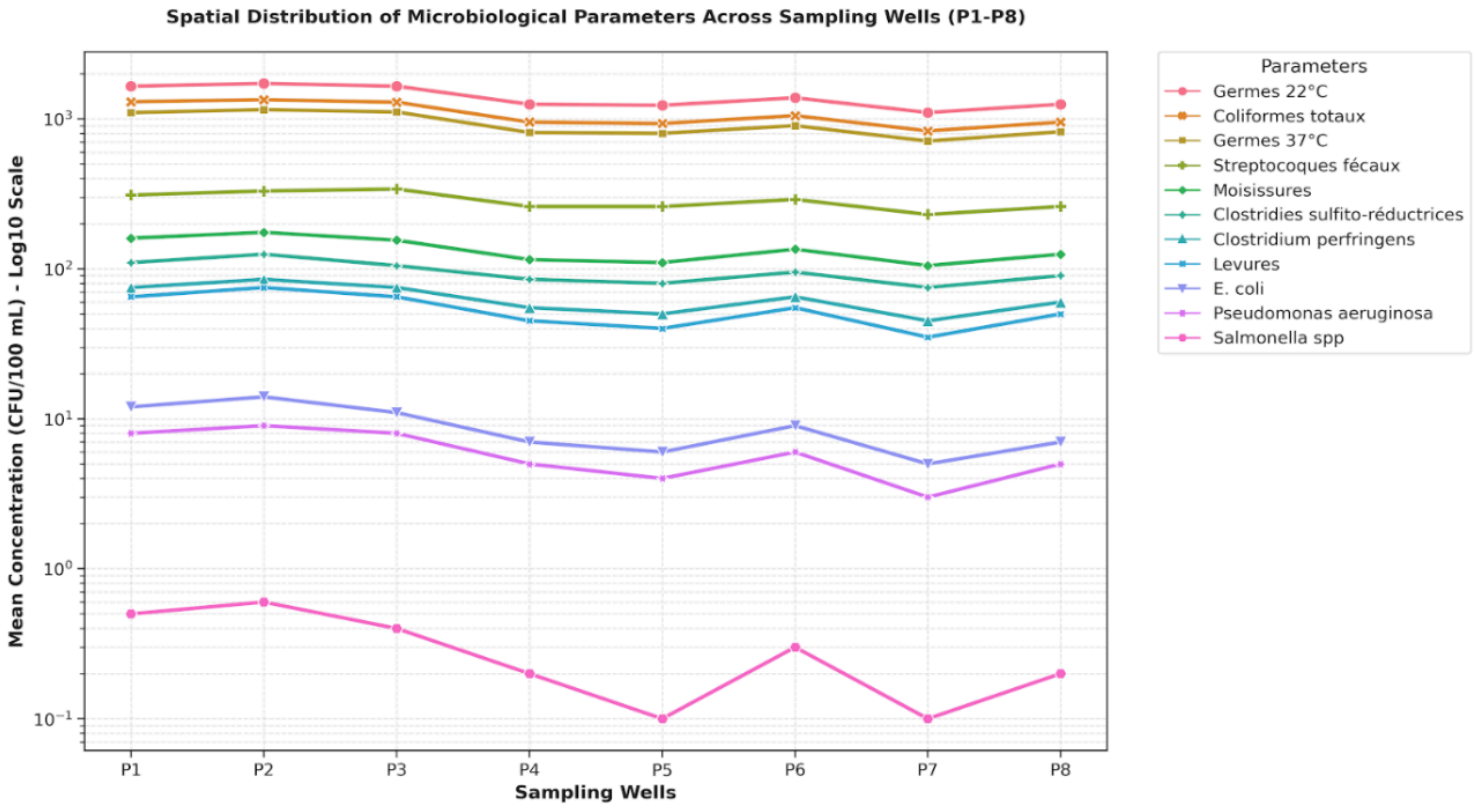


Figure 3

Spatial distribution and mean concentrations of microbiological parameters across the monitored groundwater wells (P1–P8)

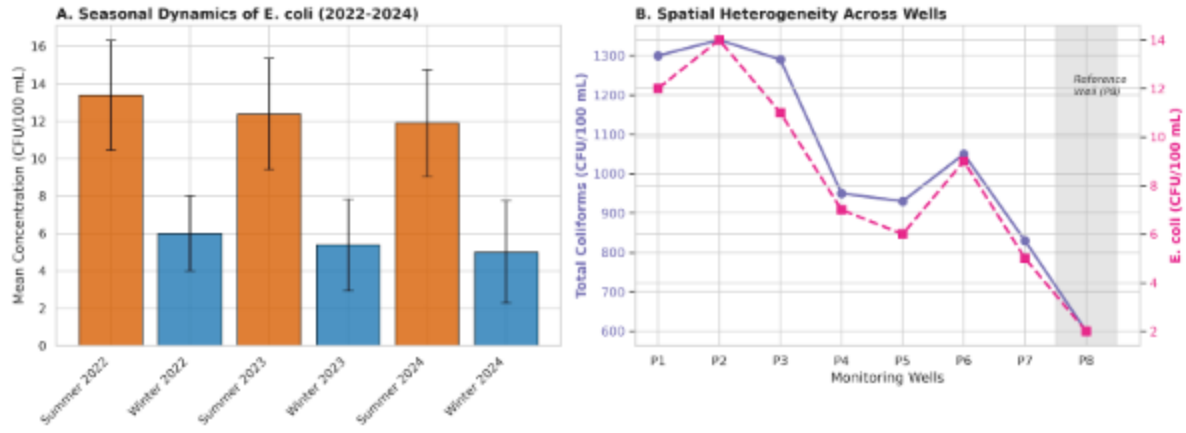


Figure 4

Comprehensive spatio-temporal dynamics of primary fecal contamination indicators. (a) Seasonality of *Escherichia coli* population in the three-year monitoring period from 2022 to 2024. The error bars represent the standard deviation and point out the consistent summer spikes. (b) Geographical

representation of the concentration of total coliforms (left y-axis) and *Escherichia coli* (right y-axis). The grey zone points out well P8, which is used for hydrochemical referencing and has the lowest number of microorganisms