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Environmental Detection of Candidozyma (Candida) auris in Surface Waters of the Gediz Delta, a Critical Coastal Wetland in Türkiye: Expanding One Health Surveillance Perspectives

Arzu Gürsoy Ergen
Ankara University
Emre Keskin
Ankara University
Ayşenur Akgün
Ankara University
Hilal Başak Erol
Ankara University
Gulce Edis
Ankara University
İsilay Celik
Ankara University
Banu Kaşkatepe
Ankara University
Sidre Erganiş
Gazi University
Elif Ayça Şahin
Gazi University
Dolunay Gülmez
Hacettepe University
Sevtap Arıkan Akdağlı
Hacettepe University
Çağrı Ergin
Pamukkale University
Oya San Keskin
Ankara Hacı Bayram Veli University
Hakan Yardımcı
Ankara University
Nüket Sivri
Istanbul University - Cerrahpaşa

Gülşen Altuğ
Istanbul University
Ayşe Kalkancı
aysekalkanci@email.com

Gazi University

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Abstract

Background

Candidozyma (Candida) auris is an emerging multidrug-resistant yeast of growing clinical and environmental concern. Despite its increasing detection in healthcare settings worldwide, environmental evidence remains scarce. This study presents the first molecular detection of *C. auris* DNA in surface waters of Türkiye, within the Ramsar-protected Gediz Delta, as part of the national One Health Surveillance Framework.

Methods

A total of 80 surface-water samples were collected from five wetland ecosystems Tuz Lake, Kulu Lake, Göksu Delta (Akgöl and Paradeniz Lagoons), Kızılırmak Delta, and Gediz Delta. Physicochemical parameters; temperature, pH, and salinity were recorded in situ using a multi parameter sensor. Environmental DNA was extracted from 2 L of 0.22 µm Sterivex-filtered water and analyzed via qPCR using *C. auris*-specific (CauF/CauR) and *Candida*-genus (CauRelF/CauRelR) primer sets. Yeast isolation was performed on CHROMagar™ Candida Plus, and identification was achieved by MALDI-TOF MS.

Results

C. auris DNA was detected in one sample (1.25%), specifically from the Gediz Delta (Sample No. 5651, 38.523° N, 26.892° E), with Ct values 33.8–37.2 confirmed by sequencing. Broader *Candida* genus signals were observed in 24% of samples. Culture-based analyses yielded no viable *C. auris*, but 15 yeast isolates were identified, mainly *Pichia kudriavzevii* (*Candida krusei*), *C. albicans*, and *Nakaseomyces glabratus* (*Candida glabrata*).

Conclusion

The culture-negative yet qPCR-positive finding indicates that *C. auris* DNA likely persists in aquatic environments as non-viable or residual material. This finding provides early molecular evidence of environmental dissemination and underscores the need for viability assays, culture-based isolation, and metagenomic monitoring integrated within One Health surveillance programmes.

1. Introduction

Critical coastal wetlands represent highly dynamic ecotonal systems located at the interface between terrestrial, freshwater, and marine environments, characterized by strong physicochemical gradients and elevated ecological productivity. These systems provide essential ecosystem services, including nutrient cycling, carbon sequestration, shoreline stabilization, and habitat provision for diverse biotic communities

[1, 2, 3]. Furthermore, the ability of these wetlands to act as "blue carbon" sinks underscores their global importance in mitigating climate change impacts [4]. Owing to their pronounced environmental heterogeneity, critical coastal wetlands host a wide range of ecological niches shaped by salinity fluctuations, redox conditions, organic matter availability, and hydrodynamic regimes [5, 6]. This heterogeneity supports diverse, functionally specialised microbial communities, thereby facilitating complex biotic interactions, including competition, symbiosis, and microbial succession. Consequently, these habitats are expected to sustain high levels of biodiversity and act as key regulators of ecosystem stability and resilience, particularly through microbially mediated processes [7, 8]. However, the stability of these microbial networks is increasingly threatened by the introduction of non-native and invasive taxa that can alter native community structures [9].

Over recent decades, cumulative anthropogenic pressures acting across multiple spatial scales have not only reduced the spatial extent of coastal wetlands but also degraded their ecological quality, thereby reshaping the physical-biological controls that underpin system resilience [10]. However, increasing evidence suggests that such wetlands may function not only as biodiversity hotspots but also as environmental reservoirs and transmission interfaces for opportunistic and potentially pathogenic microorganisms [6, 11]. Their role as environmental convergence zones promotes the accumulation, persistence, and potential adaptation of anthropogenically influenced microbial populations. In particular, the detection of emerging fungal pathogens in these systems raises concerns regarding their ecological plasticity, environmental persistence, and potential dissemination across interconnected aquatic networks [12]. The transition of fungi from environmental saprobes to human pathogens is often facilitated by their inherent thermotolerance and ability to withstand high osmotic pressure [13]. In this context, understanding the occurrence and environmental behavior of such organisms, especially in critical coastal wetlands, has become a key research priority. This concern is particularly pronounced for *Candidozyma (formerly Candida) auris*, a globally emerging, potentially multidrug-resistant fungal pathogen. The demonstrated environmental resilience and niche plasticity of *C. auris* position it as a plausible occupant of critical coastal wetland systems, with significant implications for environmental persistence and cross-ecosystem transmission within the One Health approach.

C. auris is a globally emerging multidrug-resistant yeast with significant implications for public health due to its ability to cause high-mortality infections, frequent misidentification in clinical laboratories, and established environmental persistence. Fungal pathogens like *C. auris* are profoundly influenced by environmental factors, a key principle of One Health analyses [14]. Climate change, ecosystem disruption, and cross-domain transmission dynamics increasingly shape these fungi, connecting environmental, animal, and human health sectors. It has been hypothesized that the emergence of *C. auris* may be a direct consequence of global warming, as the fungus adapts to survive at mammalian body temperatures [15]. Environmental reservoirs are crucial for their emergence and spread; *C. auris* notably persists for up to 30 days in water [16]. Türkiye’s position on migratory bird routes and the Gediz Delta’s Ramsar status amplify concerns, suggesting wildlife, wastewater, salinity gradients, and anthropogenic pressures collectively facilitate fungal dispersion.

In the absence of prior reports documenting *C. auris* in Türkiye's surface waters, this study focused on the Gediz Delta as a representative critical coastal wetland to (**i**) identify *C. auris* DNA via targeted molecular approaches and (**ii**) evaluate its environmental relevance within a One Health perspective. The detection reported here constitutes the first evidence of *C. auris* in this ecologically sensitive system, thereby filling a key knowledge gap and underscoring the need to incorporate coastal wetlands into emerging pathogen surveillance frameworks.

2. Materials & Methods

2.1 Study Area

The selection of sampling sites was strategically informed by the unique physiological attributes of *C. auris*, notably its enhanced thermotolerance and superior osmotolerance in hypersaline environments compared to closely related *Candida* species [17]. Representative wetlands were selected from each geographical region based on specific criteria: ambient temperatures consistently exceeding 20°C during summer and autumn (July-September), elevated soil salinity levels typical of the Turkish landscape, extensive reed beds, significant avian populations, and minimal anthropogenic disturbance. Sampling was concentrated within the halophytic reed beds and dune formations of the Kızılırmak, Gediz, Kocaçay, and Göksu Deltas, where coastal wetlands interface with marine ecosystems. In Central Anatolia, efforts focused on the highly saline environments of Tuz Gölü (Salt Lake) and Kulu Gölü. Wetlands in Thrace (Meriç Delta), Eastern Anatolia (Dönemeç Delta), and Southeastern Anatolia (Nehil Plain) have been spared for future study, and data collection for these sites remains pending. The Gediz Delta (38°31'02"N 26°51'29"E), a Ramsar site in Türkiye, is a critical wetland on the northeastern Gulf of İzmir coast. Characterized by a heterogeneous landscape of lagoons, hypersaline marshes, and expansive reed beds formed by the Gediz River, this ecosystem functions as a critical sanctuary for avian biodiversity, providing essential habitats for over 300 bird species of international significance. This area serves as a crucial stopover and breeding ground for migratory birds, despite facing threats from pollution and habitat alteration.

2.2 Sample Collection

Field coordinates of environmental sampling sites were mapped, sampling plans finalized, and field teams mobilized for surface water collection. Sampling covered five major wetland ecosystems, including Kulu Lake, Göksu Delta (Akgöl and Paradeniz Lagoons), Tuz Lake basin, Kızılırmak Delta, and the Gediz Delta. In Fig. 1, the sampling locations across the map of Türkiye are shown. Environmental sampling was conducted across 80 sites nationwide, including 10 locations within the Gediz Delta, as part of the national One Health surveillance network. Sampling took place during summer-fall 2025. Seawater samples were collected 0–30 cm deep under aseptic conditions in sterile 1 L polypropylene bottles and were transported to the laboratory using a cold chain [18]. Surface water samples were collected using 100 mL sterile polypropylene Falcon tubes. Each tube was horizontally immersed to a depth of 0–30 cm below the water surface to collect representative samples, and the sampling was conducted at 10–15 m intervals along the designated transects. At each sampling site, in situ physicochemical parameters,

including temperature, pH, salinity, and electrical conductivity, were measured and recorded using a portable multiparameter probe. Parameters measured included water temperature (°C), atmospheric pressure (mmHg), specific conductance (SPC, µS/cm), conductivity (C, µS/cm), salinity (ppt), and pH.

Figure 1: **The environmental sampling locations across the map of Türkiye**

2.3 Microbiological Analysis

To prevent exposure to direct sunlight, bottles designed for metagenomic processing were wrapped in aluminium foil, and all collected samples were stored in a portable field cooler until transported to the laboratory for further analysis. For metagenomic analysis, 2 L of water per site were filtered through 0.22 µm Sterivex cartridges, immediately preserved in fixRNA solution, and stored at -80°C until processing. The sampling network encompassed five major wetland ecosystems representing diverse salinity and ecological gradients across Türkiye. Subsequently, aliquots of each sample were transferred to the Evolutionary Genetics Laboratory (Ankara) for molecular detection, quantitative PCR (qPCR), and sequencing analyses. In addition to molecular analysis, water samples were subjected to microbiological culture. A total of 80 surface water samples collected from multiple wetland ecosystems across Türkiye were delivered to the Department of Pharmaceutical Microbiology, Faculty of Pharmacy, Ankara University, for microbiological analysis.

Each water sample was subdivided into 10 mL aliquots in sterile glass vials, and 5 mL of Sabouraud Dextrose Broth (SDB) and 5 mL of Tryptic Soy Broth (TSB) were added to promote the growth of fungal and bacterial communities, respectively. The samples were incubated under controlled laboratory conditions at 37°C for 24 hours for bacterial growth and 30°C for 48 hours for yeast isolation. Following incubation, all tubes showing visible turbidity were streaked onto CHROMagar™ Candida Plus medium for the detection of *C. auris*. Colonies possibly exhibiting light blue coloration with blue halos were selected for presumptive identification and subsequently analyzed by matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) at the Department of Medical Microbiology, Gazi University Faculty of Medicine Hospital. Although soil and faecal (avian droppings) samples were also collected during the same field missions for comparative ecological assessment, these datasets are not included in the present article and will be analyzed and reported separately.

2.4 DNA Extraction from Surface Water Samples

To obtain DNA for downstream metagenomic analyses, DNA extraction was carefully performed under sterile conditions from the filtered surface water samples collected in the field. During the field phase, water from each site had been filtered through 0.22 µm pore-size Sterivex cartridges. Upon arrival at the laboratory, filters were equilibrated to room temperature for a short period before processing. Each Sterivex unit was opened aseptically to prevent contamination, and the internal filter membranes were cut into smaller fragments according to the manufacturer's specifications. These filter fragments were directly transferred into the isolation tubes of the MN NucleoSpin eDNA Water Kit (Macherey-Nagel, Germany), and DNA extraction was performed strictly following the manufacturer's protocol. After extraction, DNA concentration and purity were assessed using a SPECTROstar Nano spectrophotometer

(BMG Labtech, Germany). These measurements were used to evaluate isolation efficiency and to verify the suitability of the extracted DNA for subsequent metagenomic sequencing and molecular analyses.

2.5 Quantitative PCR (qPCR) Amplification and Detection

Analysis. Genomic DNA extracted from the filtered surface water samples was analyzed by quantitative polymerase chain reaction (qPCR) to identify *Candida* species at both the genus and species levels. The assays employed two primer pairs that had been previously optimized through preliminary testing. The CauF (5'-CGCACATTGCGCCTTGGGGTA-3') and CauR (5'-GTAGTCCTACCTGATTTGAGGCGAC-3') primers were used for specific detection of *Candida auris*, while the CauRelF (5'-GCGATACGTAGTATGACTTGCAGACG-3') and CauRelR (5'-CAGCGGGTAGTCCTACCTGA-3') primers targeted multiple *Candida* species, including *C. auris, Candidozyma* (formerly *Candida) duobushaemulonii, Candidozyma haemuli* (formerly *Candida haemulonii*), and *Clavispora* (formerly *Candida*) *lusitaniae*, as described by [19]. All qPCR reactions were performed using the SsoAdvanced™ Universal Inhibitor-Tolerant SYBR® Green Supermix (Bio-Rad, USA) on a CFX Connect Real-Time PCR Detection System (Bio-Rad, USA). Each reaction included positive controls, negative controls, and no-template controls (NTC) to ensure assay reliability and exclude contamination. The inhibitor-tolerant formulation of the SYBR Green Supermix was specifically selected to minimize the effects of potential PCR inhibitors derived from environmental matrices. Amplification conditions were optimized for efficiency and specificity, and the resulting amplification curves were examined to confirm the accurate amplification of the target sequences. All qPCR data were evaluated to validate the detection of *C. auris* DNA in surface water samples, ensuring analytical precision and environmental relevance within the scope of this One Health surveillance study.

3. Results

Table 1 summarises the environmental characteristics of the studied wetlands, including Tuz Lake, Kulu Lake, Göksu Delta (Akgöl and Paradeniz Lagoons), Gediz Delta, Kızılırmak Delta (Cernek and Balık Lakes), and Kocaçay Delta(Dalyan Lake). Water temperature ranged between 17.3°C and 35.3°C, while pH values were generally neutral to slightly alkaline (6.53–8.84). Salinity varied markedly among sampling sites, from 2.35 ppt in the Kızılırmak Delta to 83.17 ppt in Tuz Lake, reflecting diverse hydrological and ecological conditions. Conductivity and SPC values followed a similar trend, being highest in Tuz Lake and lowest in Kızılırmak Balık Lake, consistent with observed salinity gradients across the study regions. A total of 80 surface water samples were collected across Türkiye during the first phase of national One Health surveillance, including 10 samples from the Gediz Delta wetland system. The sampling locations across the map of Gediz Delta are shown in Fig. 2. Environmental DNA was extracted from Sterivex-filtered units, and aliquots were transferred to the Evolutionary Genetics Laboratory (Ankara) for molecular screening. Of these, one sample tested positive for *C. auris* DNA, with Ct values ranging between 33.8 and 37.2, confirming low-level amplification signals consistent with trace environmental DNA (Fig. 3). Amplicons verified the *C. auris*-specific signature in one Gediz Delta sample, designated Sample No. 5651, corresponding to a surface water site located within the central lagoon of the delta (38°31'02"N 26°51'29"E). The remaining samples were negative for *C. auris*, but several exhibited broad *Candida* genus-

level positivity. Spatially, detections were localized to brackish, anthropogenically influenced sites near wastewater discharge points and bird aggregation zones, indicating that *C. auris* DNA may transiently persist in surface waters impacted by human activity. Representing the first environmental detection of *C. auris* DNA in Türkiye, these findings confirm the molecular presence and potential spread of the pathogen within the Ramsar-protected Gediz Delta.

Table 1: **Environmental characteristics of the studied wetlands, Saturation, SPC (uS/-cm): Specific Conductance, C (uS/-cm): Conductivity]**

Figure 2: **Sampling locations across the map of Gediz Delta**

Yeast colonies isolated from surface water samples collected at Kulu Lake, Göksu Delta (Akgöl and Paradeniz Lagoon), Gediz Delta, Kızılırmak and Tuz Lake were identified using MALDI-TOF MS. The results of species-level identification are presented in Table 2. A total of 15 yeast isolates were successfully identified from surface water samples. The predominant species was *Pichia kudriavzevii* (formerly *Candida krusei*), followed by *Nakaseomyces glabratus* (formerly *Candida glabrata*), *Candida albicans*, and *Geotrichum candidum*. Importantly, *C. auris* was not isolated from any of the surface water samples. Although *C. auris* DNA was previously detected by qPCR analysis in certain Gediz Delta samples, no viable colonies corresponding to this species were recovered through culture-based methods. This finding suggests that the environmental presence of *C. auris* in surface waters may be limited to non-viable or residual DNA fragments, rather than living propagules capable of growth under laboratory conditions. The dominance of *Pichia kudriavzevii* across multiple sites indicates a broad environmental tolerance and possible anthropogenic contribution, consistent with previous reports describing its persistence in wastewater, sediment, and surface water systems. Although bacterial growth was observed in some enrichment broths, bacterial isolates were excluded from the scope of this study and were not analyzed further.

Table 2: **The results of species-level identification of environmental yeasts isolated from surface waters**

Table 1
Environmental characteristics of the studied wetlands SPC (uS/-cm): Specific Conductance, C (uS/-cm): Conductivity]

Location	Coordinates	Altitude (m)	Water Temp (°C)	Pressure (mmHg)	SPC (uS/-cm)	C (uS/-cm)	Salinity (ppt)	pH
Tuz Lake (Aksaray)	39°04'20"N 33°24'34"E	905	35.3	680.2	112,532	134,753	83.17	6.53
Kulu Lake (Konya)	39°04'52"N 33°08'12"E	965	-	-	-	-	-	-
Göksu Delta/Akgöl (Mersin)	36°17'04"N 33°57'33"E	1	31.8	755.2	28,073	31,716	17.13	7.87
Göksu Delta/ Paradeniz (Mersin)	36°17'10"N 33°57'50"E	-1	32.3	765.5	55,628	63,352	36.67	8.13
Gediz Delta (İzmir)	38°31'02"N 26°51'29"E	-41 cm	27.8	755.4	49,820	61,788	28.9	8.2
Kızılırmak Delta/ Cernek Lake (Samsun)	41°38'49"N 36°04'44"E	10 cm	22.9	760.2	4,406	4,229	2.35	8.84
Kızılırmak Delta/ Balık Lake (Samsun)	41°33'10"N 36°04'52"E	2 m	22.6	761.1	2,269	2,163	1.16	8.95
Kocaçay Delta/ Dalyan Lake (Bursa)	40°23'35"N 28°29'45"E	1 m	17.3	760.5	10,477	8,937	5.95	7.91

Table 2
The results of species-level identification of environmental yeasts isolated from surface waters.

No.	Sample Code	Identified Yeast Species
	M4	***Pichia kudriavzevii* (*Candida krusei*)**
	M5	*Pichia kudriavzevii* (*Candida krusei*)
	M6	*Pichia kudriavzevii* (*Candida krusei*)
	M7	*Pichia kudriavzevii* (*Candida krusei*)
	M8	*Nakaseomyces glabratus* (*Candida glabrata*)
	M9	*Pichia kudriavzevii* (*Candida krusei*)
	M13	*Pichia kudriavzevii* (*Candida krusei*)
	M14	*Pichia kudriavzevii* (*Candida krusei*)
	M16	*Candida albicans*
	M17	*Pichia kudriavzevii* (*Candida krusei*)
	M18	*Nakaseomyces glabratus* (*Candida glabrata*)
	M19	*Candida albicans*
	M20	*Geotrichum candidum*
	M22	*Pichia kudriavzevii* (*Candida krusei*)
	M23	*Pichia kudriavzevii* (*Candida krusei*)

Figure 3: **Amplification curves obtained using the CauF and CauR primer pair in qPCR analysis. The graph displays amplification curves for the positive control, negative control, no-template control (NTC), and the surface water sample No. 5651 collected from the Gediz Delta. Amplification of the 5651 sample confirms the presence of Candida auris-specific DNA detected using the CauF-CauR primer pair.**

4. Discussion

This investigation reports the initial environmental detection of *C. auris* DNA in surface water bodies within Türkiye, thereby providing substantial evidence supporting the existence of non-clinical reservoirs. Prior scientific literature indicates that various fungal species, including *C. auris*, exhibit viability in aquatic environments for periods extending up to one month, a factor that significantly increases their environmental persistence and potential for transmission. The Gediz Delta, characterised by its dynamic interplay of resident and migratory avian life cycles including breeding and wintering populations, agricultural drainage, and urban effluent inputs, constitutes a plausible interface that facilitates the nexus of environmental, wildlife, and human exposure pathways.

Climate-driven ecological shifts are increasingly recognized as drivers of fungal emergence and antifungal resistance. Findings from Europe indicate warming, hydrological instability, and increased flooding events reshape fungal pathogenic niches. In the context of Türkiye, salinity gradients, wastewater leakage, wild bird carriage, and algal/floc matrices may facilitate organism stability or DNA persistence. Detection of *C. auris* DNA in environmental samples, in the absence of any culture-based isolation of viable organisms, underscores the distinction between molecular detection and microbial viability. The culture negativity observed across all surface water samples suggests that *C. auris* may persist only transiently in aquatic environments as non-viable or degraded DNA fragments. Detection of DNA rather than living cells highlights the need for future studies employing enrichment cultures, viability assays, and metagenomic surveillance to better understand the environmental fate and persistence of this emerging pathogen. Nonetheless, the detection of *C. auris* environmental DNA represents a critical early warning signal, reinforcing the importance of integrated One Health surveillance linking clinical, environmental, and wastewater monitoring frameworks. Globally, multiple studies have highlighted the capacity of *C. auris* to persist outside clinical environments. A systematic review by Silva et al. [20] documented its detection in wastewater, seawater, soil, salt marshes, and even on fruits and animals, underscoring its ecological adaptability. Similarly, viable isolates were recovered from the coastal wetlands of the Andaman Islands, confirming *C. auris*'s ability to survive under saline and marine conditions [21]. These findings strongly support the environmental origin hypothesis, suggesting that wetlands and estuarine zones such as the Gediz Delta may provide natural niches conducive to fungal persistence.

This study provides qPCR-based evidence that *C. auris* was found in lake waters, suggesting notable environmental adaptability and ecological resilience of these yeasts. This initial detection highlights the organism's capacity to persist beyond clinical settings, necessitating critical inquiry into its environmental reservoirs and transmission dynamics. Despite these challenges, the detection of *C. auris* DNA confirms that this genus can persist for extended periods in aquatic and benthic environments, consistent with previous studies reporting adaptation to temperature, pH, and salinity variability [22, 23]. Signal detection in the Gediz Delta sample suggests that *C. auris* DNA may be present transiently in environmental waters. However, the generally low amplification intensity indicates that the detected material likely represents degraded or transported DNA fragments rather than viable cells [20]. Considering the known resistance of *C. auris* to high temperature, salinity, and disinfectants, it appears plausible that residual DNA could persist for limited periods within wastewater systems [24, 25].

Analyses performed using the CauRelF-CauRelR primer pair, targeting the *Candida* (*Candidozyma*) genus, yielded positivity across lake water samples. Positive signals obtained from lake water samples further indicate that *C. auris* is not limited to human-associated pollution but is also present in natural aquatic ecosystems. The detection of *Candida* genus-specific amplification in samples from Paradeniz, Akgöl, Kulu, and Tuz Lake suggests that these yeasts can adapt to stress conditions such as high osmotic pressure, fluctuating pH, and salinity. Among these, the Paradeniz Lake sample (No. 5673) exhibited the strongest amplification signal, implying that lake systems may function as environmental reservoirs for *Candida*. This finding likely reflects the combined influence of agricultural runoff, domestic wastewater discharge, and surface flow, contributing to the transport of organic and microbial loads.

Although *C. auris* is well recognised for its remarkable tolerance to heat, salinity, desiccation, and disinfectants, no viable colonies were recovered in culture [26, 27]. This finding does not contradict its environmental resistance. Rather, it likely reflects the difference between the persistence of DNA and the persistence of viable, culturable cells. In aquatic environments, especially open wetland systems, *C. auris* may remain detectable at the molecular level even after losing culturability due to UV exposure, intermittent dilution, predation by protozoa, or transition into viable-but-non-culturable (VBNC) states. In contrast, other *Candida* species with faster growth kinetics (e.g., *P. kudriavzevii*, *N. glabratus*) readily outcompete stressed or low-abundance *C. auris* cells during enrichment. Thus, the absence of *C. auris* growth in culture, despite its known environmental resilience, likely reflects extremely low viable cell numbers or VBNC physiology rather than true environmental vulnerability. The presence of *C. auris* in the Gediz Delta, rather than in other areas, could be due to several factors. This significant wetland ecosystem may present unique physicochemical parameters such as elevated salinity, fluctuating thermal profiles, or distinct organic matter composition that selectively favor *C. auris*'s extremophilic adaptation and persistence. Furthermore, its introduction could be facilitated by migratory avifauna acting as vectors or by anthropogenic factors, including agricultural runoff containing antifungals or discharge from healthcare-associated facilities, potentially exerting selective pressures that promote *C. auris* dominance in this specific region.

A limitation of the present study is the lack of clade-level characterization and whole genome sequencing (WGS) data for the detected *Candidozyma (Candida) auris* DNA. While the qPCR-based approach provided sensitive and specific detection, it does not allow further phylogenetic or genomic interpretation. Therefore, the relationship of the detected environmental signal to known clinical lineages could not be assessed. However, considering the low concentration and likely fragmented nature of environmental DNA in the positive samples (Ct 33.8–37.2), such analyses would require deep sequencing approaches and optimized enrichment strategies. These investigations are planned as part of the ongoing project.

Future studies should aim to sequence to confirm positive samples and explore possible links between environmental isolates and antifungal resistance or virulence genes, contributing to a more comprehensive understanding of *Candida* and/or *Candidozyma* ecology. Based on the qPCR results, DNA from selected positive samples, both *C. auris-specific* and genus-level *Candida* detections, will be subjected to advanced molecular analyses. Representative samples from hospital wastewater, lake water, and sediments will undergo shotgun metagenomic (metabarcoding) sequencing to resolve the fungal community structure at high resolution. This approach will allow identification of *Candida* species alongside other yeasts and filamentous fungi, offering an integrated view of microbial diversity and ecological interactions.

5. Conclusion

Collectively, these findings suggest that the Gediz Delta’s hydrological variability, salinity gradients, migratory bird activity, and anthropogenic pressures provide a realistic ecological setting for *C. auris* persistence or DNA accumulation. While the current study identifies DNA rather than viable isolates, this molecular evidence provides an early indication of environmental dissemination and supports expanding

surveillance through culture-based and metagenomic methods. The detection of *C. auris* DNA in the surface waters of the Gediz Delta extends the emerging global footprint of this multidrug-resistant pathogen into critical coastal wetland systems, highlighting its capacity to persist beyond clinical and engineered environments. These findings position coastal wetlands not merely as passive recipients of contamination but as active environmental interfaces where pathogen persistence, ecological adaptation, and potential transmission pathways may converge [28]. In this context, our results reinforce the urgent need for integrated One Health surveillance frameworks that explicitly incorporate environmental matrices alongside human and animal health domains. By providing initial evidence from a critical wetland system, this study establishes a foundation for systematic environmental monitoring, targeted wetland screening, wildlife-associated surveillance, and improved wastewater management strategies aimed at anticipating and mitigating the environmental dimension of fungal pathogen emergence.

Declarations

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Figures



Figure 1

The environmental sampling locations across the map of Türkiye



Figure 2

Sampling locations across the map of Gediz Delta

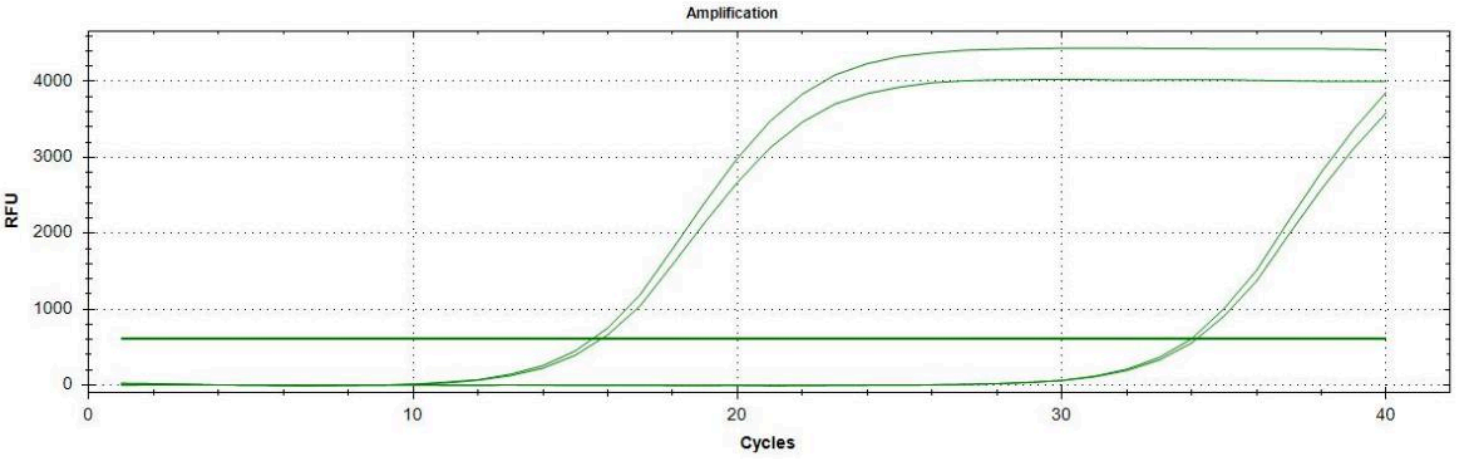

Figure 3

Amplification curves obtained using the CauF and CauR primer pair in qPCR analysis. The graph displays amplification curves for the positive control, negative control, no-template control (NTC), and the

surface water sample No. 5651 collected from the Gediz Delta. Amplification of the 5651 sample confirms the presence of *Candida auris*-specific DNA detected using the CauF-CauR primer pair.