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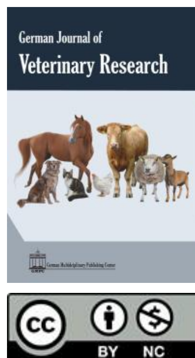
Research article

Yeast diversity in chicken meat products: Occurrence, hazards, and quality implications

Sónia Saraiva[1*], Cristina Saraiva[1], Tomai Lazou[2], Serafeim Chaintoutis[3], João R. Mesquita[4], Ana C. Coelho[1], and Patrícia Poeta[1,5,6]

[1] Animal and Veterinary Research Centre (CECAV), Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), 5000-801 Vila Real, Portugal
[2] Department of Hygiene and Technology of Food of Animal Origin, School of Veterinary Medicine, Faculty of Health Sciences, Aristotle University of Thessaloniki, 54124 Thessaloniki, Greece
[3] School of Veterinary Medicine, Faculty of Health Sciences, Aristotle University of Thessaloniki, 54627 Thessaloniki, Greece
[4] School of Medicine and Biomedical Sciences (ICBAS), Porto University, 4050-313 Porto, Portugal
[5] Microbiology and Antibiotic Resistance Team (MicroART), Department of Veterinary Sciences, UTAD, Vila Real, Portugal
[6] LAQV-REQUIMTE, Department of Chemistry, NOVA School of Science and Technology, University Nova de Lisboa, Caparica, Portugal



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***Corresponding author:**
Sónia Saraiva
soniasaraiva@utad.pt;
soniasarai@gmail.com

Abstract

Food spoilage poses a significant challenge for both the food industry and consumers, rendering products unfit for consumption and leading to substantial food waste and economic losses. This study aimed to assess the occurrence of yeasts in five distinct types of raw meat poultry products (feet, gizzard, heart, liver, and neck) under two packaging conditions, providing insights into potential spoilage agents. For this purpose, one hundred poultry samples were collected from retail markets and supermarkets in Portugal to evaluate the total yeast count and assess the profiles and diversity of mycological species. Species identification was based on culture morphology, microscopic examination, biochemical profile, and Matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF-MS). Results showed that local markets and unpacked samples exhibited significantly higher total yeast counts, particularly in heart, gizzard, and liver samples. Yeasts were isolated from 96% (95% CI: 90-98%) of the samples, with an average count of 3.13±0.96 log colony-forming units (CFU)/g. All yeast isolates belonged to seven different genera, i.e., *Candida, Debaryomyces, Malassezia, Zygosaccharomyces, Rhodotorula, Yarrowia,* and *Cryptococcus*, which are commonly found in food and environmental samples. The yeast species identified included *Candida zeylanoides* (26.83%), *C. ciferrii* (2.44%), *Debaryomyces hansenii* (19.51%), *Zygosaccharomyces* sp. (7.34%), *Rhodotorula mucilaginosa* (9.76%), *Cryptococcus laurentii* (4.88%), *Malassezia pachydermatis* (2.44%), *Yarrowia lipolytica* (9.76%) and *Yarrowia galli* (2.44%). A yeast-like fungus, *Aureobasidium pullulans*, was also identified in one unpacked sample of feet obtained from the retail market, potentially introduced through contact with contaminated surfaces or handling equipment. Recognizing the prevalence and variety of yeasts in food is crucial for developing effective strategies to mitigate these spoilage agents and ensure food safety and suitability. In conclusion, this study provides valuable insights into the occurrence of yeasts in fresh chicken meat products, highlighting the importance of developing effective strategies to mitigate yeast spoilage throughout the poultry supply chain. Furthermore, identifying emerging health concerns associated with yeasts, such as *Y. galli* and *A. pullulans*, which are implicated in human infections, highlights the critical need for comprehensive contamination control and monitoring practices to ensure food safety and public health.

Keywords: Yeast, Poultry meat, Spoilage, Total count, Identification, MALDI-TOF

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Introduction

The term "offal" refers to the edible internal organs of animals, which possess significant nutritional value but are frequently discarded from the human food supply chain (Latoch et al., 2024). Offal consumption is a common practice in Portugal, particularly in the northern part of the country. The rich Portuguese gastronomic tradition includes recipes featuring chicken offal, such as chicken soup and gizzards, as well as chicken meat, including feet and blood, cooked with rice and flavored with vinegar and spices, resulting in a distinctive tangy taste (Cleto, 2008). Incorporating offal into diets could be an effective strategy for addressing the modern challenge of food waste, as it promotes the efficient use of all edible animal parts, enhances culinary diversity, and provides valuable nutritional benefits (Latoch et al., 2024).

Yeasts play a significant role in the spoilage of poultry products and processed meat (Deák, 2008, Riesute et al., 2021). Contamination of these edible products by yeasts can occur during various processing phases, including scalding, de-feathering, evisceration, cooling, packing, transportation, and storage, as several yeast species commonly associated with spoilage can grow at refrigeration temperatures (El-Matary and Zaki, 2016). Their proteolytic and lipolytic activities suggest that yeasts could play a significant role in the spoilage of poultry products (Deák, 2008). Moreover, yeasts can thrive across a wide range of pH levels, highlighting their potential for spoilage not only during storage but also during the processing of meat products (Jay et al., 2005). Such spoilage leads to off-flavors, unpleasant odors, and textural alterations, including increased sliminess (El-Matary and Zaki, 2016). Yeast activity also causes food discoloration, resulting in shades ranging from white or creamy to pink or brown due to pigment production (Feet, 1992). *Rhodotorula mucilaginosa* is one of the top 10 yeast species causing food spoilage, producing pink to red pigments, with most colonies appearing orange or salmon pink (Cerveny et al., 2019).

Available data suggest that *Candida, Rhodotorula*, and *Debaryomyces* are the primary yeast genera involved in the spoilage of raw meat (Hernández et al., 2018). In addition, the role of *Y. lipolytica* and *C. zeylanoides* in the spoilage of fresh poultry meat has been highlighted in earlier studies, such as those by Ismail et al. (2000). Under aerobic conditions, *Candida* spp. and *Yarrowia* spp. are predominant in spoiled refrigerated poultry meat. However, under modified atmosphere packaging (MAP) or vacuum conditions, yeasts do not dominate the microflora, as noted by Cerveny et al. (2019). This highlights the influence of packaging methods on microbial communities in poultry products. *Debaryomyces* spp. are osmotolerant and can grow in environments containing up to 24% NaCl and at a water activity (a_w) as low as 0.65, and *Zygosaccharomyces* spp. can be isolated from a wide range of foods, including dry-cured meats and poultry (Cerveny et al., 2019). The identity of the spoilage yeast involved in the spoilage of raw ingredients or finished products depends on a combination of physical and chemical environmental factors (Snyder et al., 2019).

The relatively low incidence of pathogenic foodborne traits in yeasts has reduced scientific interest in them compared to bacteria. As a result, their significance as food-contaminating microorganisms has been underestimated for a long time. Research on the diversity of spoilage yeasts in chicken meat and products has been limited, creating gaps in our understanding of the range of species involved. This study aimed to investigate the total counts, yeast profile, and diversity of yeasts on chicken meat, offal, and edible feet randomly collected from retail markets and supermarkets in Portugal.

Materials and methods

Sample collection

In total, one hundred samples of fresh chicken edible feet, offal (gizzard, heart, liver), and meat (neck) were randomly collected (20 samples per food type) from supermarkets (54 samples) and retail markets (46 samples) in North Portugal between 1st March and 30th September 2023. The unpacked bulk products were placed in plastic bags and packed products were maintained in their original packaging. Samples were transported under refrigeration at 2°C in portable coolers and delivered to the laboratory within one hour of collection. All microbiological analyses were performed within two hours upon arrival at the laboratory.

Enumeration of yeasts

Ten grams of each sample were aseptically weighed and diluted in 90 mL of sterile tryptone

salt broth Solution (VWR, Belgium) and sterilized at 121°C for 15 minutes. This preparation created a 10^{-1} dilution, which was subsequently homogenized for 90 seconds using a laboratory blender (Stomacher®; Seward Ltd, Sussex, U.K.). At least two additional serial decimal dilutions were prepared in test tubes containing 9 mL of sterile tryptone salt broth (TSB; VWR, Belgium). A Vortex Mixer (Fisherbrand™ ZX3) was used to agitate the tubes at 2000 rpm for 5 to 10 seconds after each dilution. Then 0.1 mL from each dilution was spread plated on Yeast Glucose Chloramphenicol Agar (CGA; Himedia, India), and, then incubated at 25°C for 3 to 5 days. After incubation, typical creamy yeast colonies were counted, and the results were expressed as log colony-forming units (CFU)/g, taking into account the dilution factors of the original samples (Vanderzant and Splittstoesser, 1992; ISO 21527-1:2008). For statistical analysis purposes, in cases where yeast counts were below the limit of detection (LOD=100 CFU), the obtained result was recorded as "zero" log CFU/g.

Identification of yeasts

The morphological identification of yeast genera was based on the macroscopic and microscopic characteristics. The gross appearance of the isolated yeast colonies was evaluated in terms of size, consistency, and surface color, as described by Markey et al. (2013). For microscopy observation, a drop of sterile water was placed on a clean microscope slide. Using a sterile loop, a small amount of yeast was collected from the CGA plate, spread evenly in the water, and then covered with a cover slip. From the initial 96 isolates, 41 of them were selected for identification using the automated VITEK® 2 microbial ID/AST system (bioMérieux, Marcy l'Etoile, France). The selection was made considering the morphological characteristics (morphotypes) of isolates and their proportion. The isolates (41) respected the proportion present in the initial isolates. The manufacturer's instructions for the VITEK® 2 system were followed. The instrument automatically carried out all the subsequent steps, from the inoculation of the dedicated VITEK® 2 ID test cards for yeasts to the interpretation of the result. The Matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF) was applied to identify yeasts that could not be identified by the VITEK® 2 ID system or in cases of 'low discrimination' or 'low reactivity' biopattern observed using the VITEK® 2 system.

Statistical analysis

Samples were grouped into five categories (feet, gizzard, heart, liver, and neck) to analyze statistical differences in yeast counts among diverse samples. Regarding retail sampling points, the samples were categorized into small retail (local market with 46 samples) and large retail (supermarket with 54 samples). Regarding packaging, the samples were grouped into two categories: packed (44 samples) and bulk (unpacked) (56 samples). Statistical analyses were conducted using one-way ANOVA, and mean comparisons were performed using Tukey's HSD test ("Honestly Significant Difference") with a significance level of $p<0.05$. The statistical analysis was conducted using SPSS Statistics Software (version 21, IBM, New York, USA).

Results

The total yeast counts (log CFU/g) of the examined chicken samples (n=20 per food category) are presented in Table 1. Yeasts were isolated from 96% of the tested samples (95% CI: 90-98%) with an average count of 3.13±0.96 log CFU/g (range 0–5.64 log CFU/g).

Table 1: Total yeast counts (log CFU/g) observed in the analyzed samples, including feet, gizzard, heart, liver, and neck (n = 20 per food matrix).

Sample	Yeast counts (log CFU/g)*				p-value
	Mean	Std Dev	Min	Max	
Feet	3.02	1.03	0	4.98	NS**
Gizzard	3.27	0.88	2	4.60	
Heart	2.81	1.19	0	4.65	
Liver	2.96	0.44	2	3.50	
Neck	3.57	0.97	2.3	5.64	
Total	3.13	0.96	0	5.64	

*CFU= colony forming unit; **NS: non-significant

The statistical analysis of total yeast counts (log CFU/g) in the tested sample types revealed mean values (±SD) ranging from 2.81±1.19 in heart samples to 3.57±0.97 in neck samples. No significant differences were observed among the groups (Table 1). The total yeast counts in the tested samples per type of retail sampling point (supermarket vs. local market) and packaging status (packed vs. bulk) are presented in Table 2. Significant differences in the total yeast counts (log CFU/g) were observed between retail sampling points. Samples from local markets exhibited higher counts for gizzard (p=0.049), heart (p=0.034), and liver (p=0.003). Packaging conditions also influenced yeast counts, with unpackaged heart (p=0.004), gizzard (p<0.001), liver (p=0.006), and neck (p=0.048) samples showing significantly higher counts. However, yeast counts in feet samples did not significantly vary by establishment type or packaging conditions. Local markets (3.06±0.58) and packaged (3.27±1.08) products showed overall higher yeast counts.

Table 2: Average yeast counts (log CFU/g) by type of retail sampling point and packaging status.

Sample	Establishment			Packaging		
	Supermarket	Local market	p-value	Packed	Bulk	p-value
Feet	3.00 ± 1.23^{AB**}	3.06 ± 0.58	NS	3.27 ±1.08^{AB}	2.83 ± 1.00	NS*
Gizzard	2.96 ± 0.91^{AB}	3.74 ± 0.63	0.049	2.48 ± 0.54^{AB}	3.79 ± 0.64	0.000
Heart	2.31 ± 1.26^{A}	3.42 ± 0.79	0.034	1.84 ± 1.39^{A}	3.33 ± 0.66	0.004
Liver	2.66 ± 0.46^{AB}	3.21 ± 0.23	0.003	2.61 ± 0.52^{AB}	3.15 ± 0.26	0.006
Neck	3.70 ± 1.01^{B}	3.35 ± 0.92	NS	3.06 ± 0.56^{B}	3.92 ± 1.05	0.048
Total	2.96 ± 1.11	3.35 ± 0.65	0.040	2.69 ± 0.98	3.41 ± 0.84	0.001
p-value	0.013	NS		0.001	NS	

*NS: non-significant. **Different superscript letters in the same column indicate a significant difference (p<0.05) between different food matrix

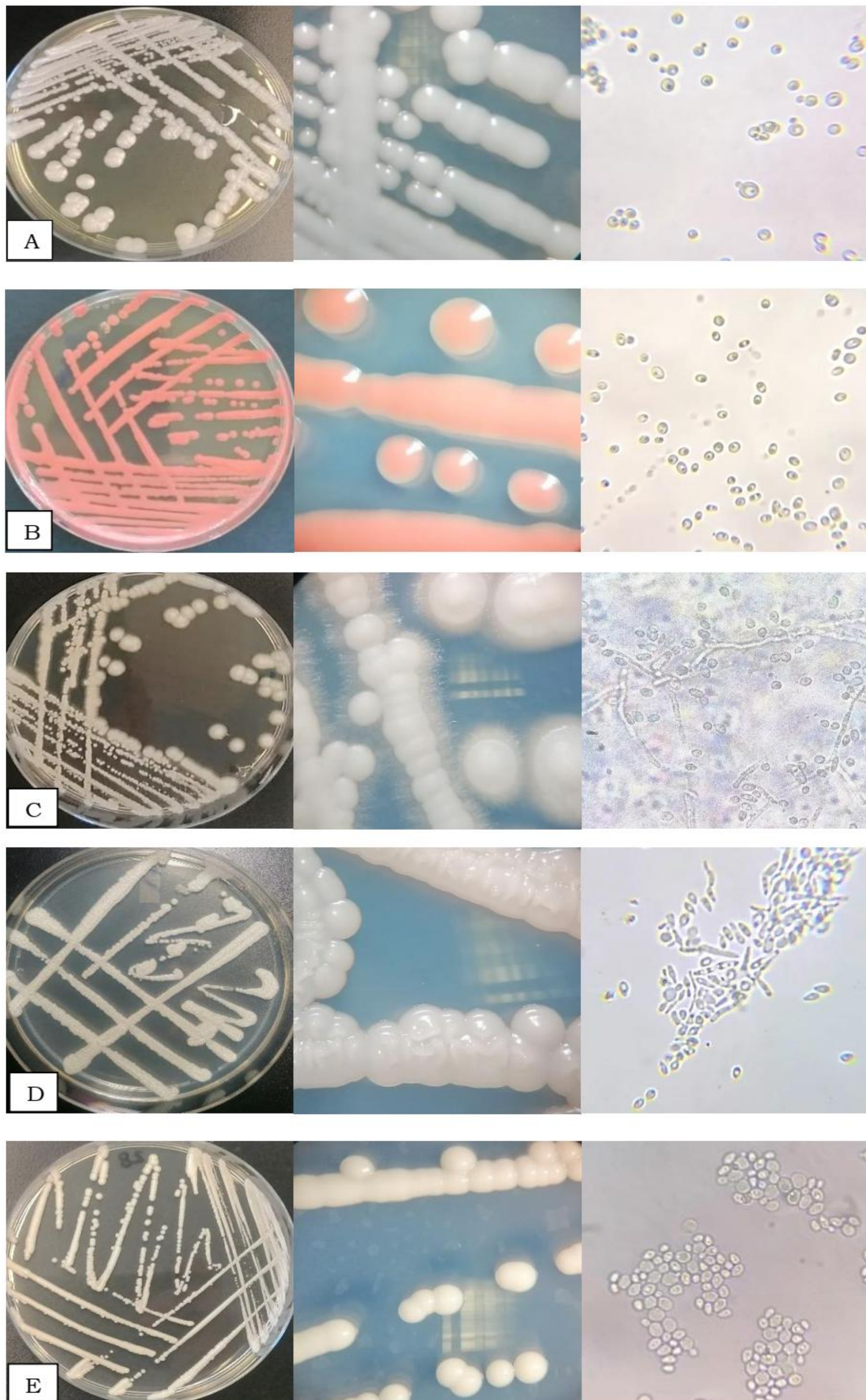
According to Tukey's post hoc test, neck samples (3.70±1.01) obtained the highest yeast count in supermarkets but only differed significantly from heart samples (2.31±1.26). Feet, gizzard, and liver share the label "AB" in most cases, indicating no significant differences among them or between the neck and heart results. Similar results were obtained in the packaged products. The yeast species identified by VITEK® 2 or MALDI-TOF in the tested samples (feet, gizzard, heart, liver, and neck) are presented in Table 3. Out of the 41 isolates, 20 were identified by VITEK® 2, 16 by MALDI-TOF, and five were not identified by any method.

Table 3: Identified yeast species in the tested samples.

Yeast species \ Samples	Feet	Gizzard	Heart	Liver	Neck	Total
	N (%)	N (%)	N (%)	N (%)	N (%)	N (%)
*Aureobasidium pullulans**	1 (2.44)					1 (2.44)
Candida ciferrii complex		1 (2.44)				1 (2.44)
Candida zeylanoides	2 (4.88)	3 (7.34)	1 (2.44)	2 (4.88)	3 (7.34)	11 (26.83)
Cryptococcus laurentii				1 (2.44)	1 (2.44)	2 (4.88)
Debaryomyces hansenii	2 (4.88)	2 (4.88)	1 (2.44)	1 (2.44)	2 (4.88)	8 (19.51)
Malassezia pachydermatis		1 (2.44)				1 (2.44)
Rhodotorula mucilaginosa		1 (2.44)	1 (2.44)		2 (4.88)	4 (9.76)
Yarrowia galli	1 (2.44)					1 (2.44)
Yarrowia lipolytica	1 (2.44)		1 (2.44)	1 (2.44)	1 (2.44)	4 (9.76)
Zygosaccharomyces sp.		1 (2.44)		1 (2.44)	1 (2.44)	3 (7.34)
Unidentified		1 (2.44)	1 (2.44)	2 (4.88)	1 (2.44)	5 (12.20)

N= Number of isolates per yeast species. *Yeast-like fungus

The different yeast colony morphologies obtained on CGA, along with the respective microscopy images, are presented in Figure 1. Table 4 summarizes the key characteristics of isolates, including colony features (shape, color, elevation, and surface texture) and cell attributes (shape and the presence of pseudohyphae).



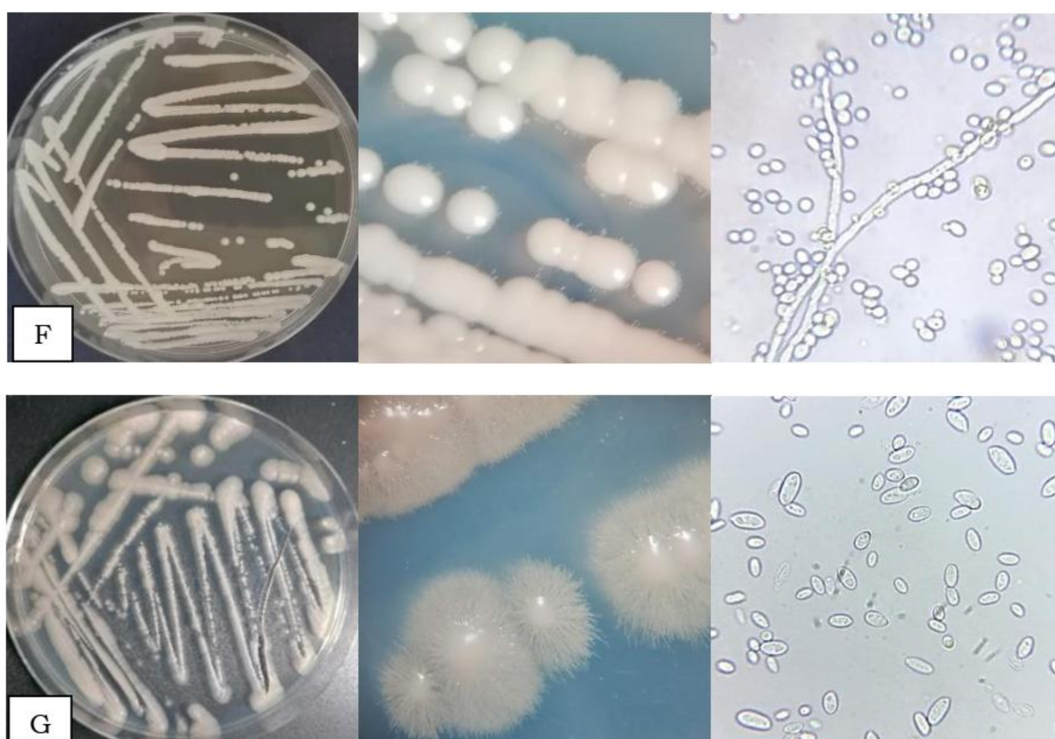


Figure 1: Yeast isolates colonies on CGA medium and under the microscope: A) *Debaryomyces hansenii.* B) *Rhodotorula mucilaginosa.* C) *Candida lypolitica.* D, E) *Candida zeylanoides*. F) *Yarrowia galli.* G) *Aureobasidium pullulans.*

Table 4: Morphological characteristics of yeast isolates.

Yeast species	Colony characteristics (shape, color, elevation, and surface texture)	Cell characteristics (shape, and pseudohyphae + or -)
Aureobasidium pullulans	Irregular, Creamy-brown, Flat, Smooth	Oval-elongate; Pseudohyphae +
Debaryomyces hansenii	Circular, White, Raised, Smooth	Spherical; Pseudohyphae -
Yarrowia lipolytica	Circular, White, Raised, Smooth	Oval; Pseudohyphae +
Candida ciferrii	Circular, White, Raised, Smooth	Oval; Pseudohyphae -
Yarrowia galli	Circular, White, Raised, Smooth	Oval; Pseudohyphae +
Candida zeylanoides	Circular or Irregular, Creamy, Convex or Undulate, Smooth or Rough	Spherical or apiculate; Pseudohyphae -
Zygosaccharomyces sp.	Circular, White, Raised, Smooth	Spherical-oval; Pseudohyphae -
Cryptococcus laurentii	Circular, Creamy-rose, Raised, Smooth	Oval; Pseudohyphae -
Malassezia pachydermatis	Circular, Creamy-green, Raised, Smooth	Oval; Pseudohyphae -
Rhodotorula mucilaginosa	Circular, Rose, Raised, Smooth	Oval; Pseudohyphae -

Pseudohyphae (+): Present; pseudohyphae (-): Absent

Discussion

Food spoilage poses a significant challenge for the food industry and consumers, as it renders food unfit for human consumption, leading to substantial food waste and economic losses. Microbial activity is a major contributor to food spoilage (Karanth et al., 2023). Nine yeast species associated with spoilage were identified in the present study, representing the genera *Debaryomyces, Candida, Malassezia, Zygosaccharomyces, Rhodotorula, Yarrowia,* and *Cryptococcus*. These findings align with previous studies, which also highlighted *Candida, Rhodotorula, Debaryomyces,* and *Yarrowia* as the primary yeast genera involved in raw poultry spoilage (Jay et al., 2005). Hinton et al. (2002) identified at least seven yeast genera on broiler carcasses stored at 4°C for up to 14 days, with *Candida* being the most prevalent, followed by *Cryptococcus* and *Yarrowia*. Similarly, in the present study, *Candida* was also the most dominant genus, represented by *C. zeylanoides, C. lipolytica*, and the *C. ciferrii* complex, which

together accounted for 29.27% of the identified yeasts.

A study in South Africa examining yeasts on both fresh and spoiled poultry carcasses also highlighted *Candida* and *Debaryomyces* as the dominant genera on both carcass types, while *Rhodotorula* was notably absent from spoiled carcasses (Viljoen et al., 1998). In the current study, *C. zeylanoides* (26.83%) and *D. hansenii* (19.51%) emerged as the most abundant species, consistent with the findings of Viljoen et al. (1998), who also reported these species as the most prominent on both fresh and spoiled poultry carcasses. Ozturk (2015) found that yeast species, such as *C. zeylanoides*, can originate from external sources during the handling and initial processing stages, confirming the key role of environmental exposure. Therefore, the presence of *C. zeylanoides* on carcasses or unpackaged meat and offal is attributed to environmental contamination.

Four isolates (9.76%) of *R. mucilaginosa* were detected in this study in fresh heart (2.44%), neck (4.88%), and gizzard (2.44%) samples, a result also in line with the survey by Viljoen et al. (1998). *Rhodotorula* is typically detected in environmental samples, such as soil, air, and water, and is not commonly involved in meat spoilage (Kabisch et al., 2016). On the other hand, species such as *Y. lipolytica* and *C. zeylanoides* are increasingly recognized for their role in poultry spoilage due to their ability to metabolize lipids and proteins, resulting in off-flavors, discoloration, and reduced shelf life. Ismail et al. (2000) describe how specific yeasts can dominate the spoilage microbiota under certain conditions. For example, *Y. lipolytica* thrives in lipid-rich environments and can produce enzymes, such as lipases, which contribute to rancidity in poultry. Additionally, *C. zeylanoides* can impact quality by producing volatile compounds that affect the sensory attributes of the meat. In the present study, *C. zeylanoides* was commonly detected (26.83%), and almost 10.0% of isolates were identified as *C. lipolytica*. The sources of contamination can be various, including soil and feces of livestock origin, facilities and equipment used during slaughter and processing, the hands of personnel, and indirect contamination via air (Kabisch et al., 2016).

Airflow in industrial facilities further facilitates the dissemination of spoilage yeasts, as microorganisms can travel by adhering to dust particles, droplets, or single particles (Curiel et al., 2000). These findings align with the present study, emphasizing the widespread presence of yeasts in poultry products and the importance of proper handling and packaging to mitigate spoilage.

Yeast populations across different chicken parts were found to be similar, with mean values ranging from 2.81±1.19 log CFU/g in the heart to 3.57±0.97 log CFU/g in the neck, showing no significant differences observed among the samples. Kabisch et al. (2016) reported yeast counts ranging from 2 to 7 log CFU/g in minced or ground meat, while Samaha (2013) documented a mean yeast count of 4 log CFU/g in retail frozen meats from Egypt, which is slightly higher than the mean values reported in the current study. The most prevalent genera detected were *Candida* (64.9%), *Torulopsis* (24.5%), and *Rhodotorula* (17%).

There were significant differences in total yeast counts (CFU/g) between types of establishments, with local markets showing higher counts. For instance, establishments with better hygiene practices may have lower yeast contamination, but packaging still plays a role in preventing additional contamination post-processing. The findings of the present study indicate that yeast counts are generally higher in bulk chicken carcass samples (3.41±0.84) compared to packed ones (2.69±0.98), with significant differences observed across most sample types (gizzard, liver, heart, neck). The protective role of packaging in limiting yeast growth is consistent with the fact that most yeasts are obligate aerobes, requiring oxygen for growth and metabolism (Fleet, 1998). Moreover, heart ($p=0.004$), gizzard ($p<0.000$), liver ($p=0.06$), and neck ($p=0.048$) samples presented significantly higher yeast counts if unpackaged. The higher yeast counts in unpackaged samples could be due to increased exposure to environmental contamination. Packaging typically acts as a barrier, protecting the product from contact with air, surfaces, and microorganisms during handling and storage. In a survey of retail samples of vacuum-packed beef from Germany, psychrophilic yeasts were detected in 30% of the samples, with a mean count of 3.76 CFU/cm^2 (Kabisch et al., 2016). The exception in this study is the yeast counts in

the feet samples, where higher counts were found in the packed feet, although no significant packaging effect was observed. This could align with studies suggesting that packaging can sometimes trap moisture, or poor air evacuation can create an environment conducive to enzymatic activity and microbial growth, particularly in cuts with a high surface area, which are more prone to spoilage. Studies, such as those by Prasad and Kochhar (2014) have highlighted that the presence of air and liquid in packaging can accelerate deterioration by promoting microbial activity and affecting texture, particularly during extended storage.

A yeast-like fungus identified in a poultry feet sample was *A. pullulans* (Figure 1, G), commonly associated with environmental sources such as soil, plants, and air. *A. pullulans* can produce extracellular polysaccharides, such as pullulan, which may play a role in biofilm formation and its persistence in host tissues (Chi et al., 2009¸Gostinčar et al., 2014). Different strains of *Aureobasidium pullulans* can produce a wide range of biotechnologically valuable compounds and enzymes, including amylase, protease, lipase, cellulase, xylanase, mannanase, various transferases, pullulan, siderophores, and single-cell protein (Chi et al., 2009). Nevertheless, *A. pullulans* has also been implicated in opportunistic infections, including rare cases of skin and soft tissue infections, peritonitis, and catheter-related fungemia in certain human hosts (Verdecia et al., 2022). A case of peritonitis caused by *A. pullulans* and associated with a dialysis catheter may have resulted from poor hand hygiene by the caregiver (Chamroensakchai et al., 2019). Its adaptability to diverse environments and ability to thrive under different conditions raise concerns about its dual role as a food spoilage organism and a potential agent of human infection (Babič et al., 2016; Gostinčar et al., 2011).

The detection of *A. pullulans* and other fungi with opportunistic pathogenic capabilities on poultry products emphasizes the need for rigorous monitoring, especially in food production and processing environments (Gostinčar et al., 2011; Hernández et al., 2018). Further research into the ecology and pathogenicity of *A. pullulans* is necessary to better understand its transmission routes, interactions with other microbial populations, and potential impact on public health.

In the present study, one sample of feet transported in bulk was identified as belonging to the *C. ciferrii* complex using VITEK® 2. This complex includes *C. ciferrii, C. allociferrii,* and *C. mucifera*. These species share similar macroscopic and microscopic characteristics, challenging their discrimination (Agin et al., 2011; Danielescu et al., 2017). The *C. ciferrii* complex has been implicated in various human infections, including endophthalmitis, intraorbital abscess, systemic mycosis, and otitis media (Agin et al., 2011; Danielescu et al., 2017). *Yarrowia galli* (previously known as *Candida galli*) was identified in another sample of feet (Figure 1, F), in this case, using MALDI-TOF for confirmation of its identification. *Y. galli* can be differentiated from *Y. lipolytica* based on several phenotypic traits, including the non-assimilation of N-acetyl glucosamine, the absence of urease activity, growth in a medium containing 10% NaCl and 5% glucose, and the ability to grow in vitamin-free conditions (Galán-Sánchez et al., 2014). Interestingly, this species has rarely been reported in poultry-related food products. The presence of *Y. galli* in chicken breast and liver was first documented in 2004 (Péter et al., 2004). Since then, this species has also been isolated from clinical settings, with its genome revealing several gene families associated with virulence (Bing et al., 2020). Bing et al. (2020) described the genomic and biological characteristics of *Y. galli* isolated for the first time in a facial granuloma. The genome of *Y. galli* contains several gene families essential for virulence, and, like major pathogenic fungi, it can undergo morphological transitions in response to environmental changes a critical feature for fungal pathogens (Bing et al., 2020). These results raise concerns about its presence in poultry products and potential health implications (Gostinčar et al., 2011). Moreover, *Y. lipolytica*, a closely related species, has also been implicated in infections in severely polytraumatized patients (Bahloul et al., 2017). Genomic and biological analyses suggest that *Y. galli* has the potential to act as an opportunistic fungal pathogen in humans (Bing et al., 2020).

Conclusions

The study reveals a high prevalence of yeasts in poultry products, particularly in local retail and unpacked samples. *C. zeylanoides* was the most prevalent, with notable occurrences *of D. hansenii, Y. lipolytica*, and *R. mucilaginosa.*

Emerging opportunistic pathogens such as *Y. galli* and *A. pullulans*, which can pose health risks, were also identified. These findings highlight the importance of improving contamination control measures and monitoring practices throughout the poultry supply chain to minimize spoilage and safeguard food safety.

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Authors contribution. S.S.: laboratory analysis and drafted the manuscript. C.S., T.L., and S.C.: laboratory analysis and manuscript review. J.R.M., A.C.C., and P.P. reviewed and supervised this study.

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