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Assessment of fungal contamination in *dangke*, a traditional cheese product from small-scale producers in Enrekang, South Sulawesi

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Abstract. *Syah SP, Sudarwanto MB, Sudirman I, Mukhlisah AN, Ningtyas WD, Irfan M. 2025. Assessment of fungal contamination in dangke, a traditional cheese product from small-scale producers in Enrekang, South Sulawesi. Biodiversitas 26: 3324-3333.* *Dangke* is a traditional soft cheese produced in Enrekang, South Sulawesi, Indonesia, using household-scale methods that can pose significant food safety risks due to inadequate hygiene practices. This study assessed the level and diversity of fungal contamination in *dangke* collected from small-scale producers across Enrekang Regency. A total of 20 samples were collected aseptically and analyzed using the Total Plate Count (TPC) method on Sabouraud Dextrose Agar. The results showed that the average fungal count was 5.2×10^6 CFU/g, which greatly exceeded the maximum acceptable limit for solid dairy products (10 CFU/g) according to Codex Alimentarius guidelines. Phenotypic identification revealed the presence of both yeasts (75%) and molds (25%), with nine fungal genera detected. *Candida* sp. was the dominant genus (30%), followed by *Saccharomyces* sp. (16%), *Geotrichum* sp. (11%), *Microsporum* sp. (13%), *Cladosporium* sp. (9%), *Penicillium* sp. (9%), *Aspergillus* sp. (6%), *Rodotorula* sp. (5%), and *Fusarium* sp. (2%). Several of these genera, such as *Aspergillus* and *Fusarium*, are known producers of mycotoxins that pose potential health risks. These findings highlight the urgent need for improved hygiene practices, proper handling, and better storage conditions in traditional *dangke* production to reduce fungal contamination and ensure product safety for consumers.

Keywords: *Dangke* cheese, food safety, fungal contamination, microbial identification

INTRODUCTION

Dangke is a traditional soft cheese from Enrekang, South Sulawesi, with deep cultural and economic significance. Produced since 1905, it reflects local wisdom and heritage, serving as a primary livelihood for many households in the region (Syah et al. 2017; Zakariah et al. 2022; Malaka et al. 2023). Despite its economic importance, *dangke* production still relies heavily on traditional methods, which lack standardization and present persistent food safety challenges. While the product contains beneficial microorganisms like Lactic Acid Bacteria (LAB) that contribute to its flavor and health benefits (Syah et al. 2017, 2024; Syah 2022; Widyadhana et al. 2024), harmful pathogens such as fungi and bacteria are also a concern (Hatta et al. 2013; Zakariah et al. 2019). Therefore, efforts to sustain, improve, and further develop the industry must address these concerns while preserving its cultural value.

One key factor contributing to *dangke's* vulnerability to microbial contamination is its physicochemical composition. As a fresh, unripened cheese, *dangke* typically has a high moisture content (above 60%) and a mildly acidic to neutral pH (approximately pH 6.06-6.73) (Malaka et al. 2024). These characteristics, combined with the absence of standardized preservation and using coconut shells as molds is unhygienic, create an ideal environment for the growth of spoilage microorganisms, including fungi. Traditional *dangke* is also produced using fresh cow's milk coagulated with crude papaya (*Carica papaya*) sap, which contains the enzyme papain (Zakariah et al. 2022; Malaka et al. 2024). If the sap or milk is contaminated or handled under poor hygienic conditions, fungi and other pathogens can enter the product at multiple stages.

The traditional handling of *dangke* further increases its susceptibility to contamination. Production typically occurs in open, non-sterile household kitchens, where the cheese is often molded by hand or shaped in coconut shells molds that are rarely sterilized (Malaka et al. 2024). Finished cheese is commonly stored at ambient temperature and sold unpackaged in local markets, exposing it to airborne spores and contact with contaminated surfaces and utensils. These conditions resemble those reported for other artisanal cheeses and fermented dairy products produced under traditional settings in tropical climates. Previous research has demonstrated that traditional dairy products produced under artisanal conditions in warm, humid climates are highly susceptible to microbial contamination, including spoilage yeasts and toxin-producing molds. For instance, *wara*, a soft cheese made in Nigeria, has been reported to contain high levels of molds such as *Aspergillus* and *Penicillium* due to unhygienic handling and ambient storage (Shiawoya et al. 2006; Ndudi et al. 2024).

Similarly, *amasi* Zimbamwe traditional fermented milk product popular in southern Africa, has been found to carry a range of spoilage fungi when produced using non-standardized household methods (Gadaga et al. 2000). Furthermore, wagashi, a traditional cheese from Kozah municipalities in Togo, has been reported to be contaminated by yeast and mould (Taale et al. 2025). Yahyapour et al. (2023) also documented significant fungal loads in Iranian traditional cheeses, highlighting the presence of *Candida*, and *Geotrichum* spp.. These examples underline that in tropical and subtropical settings, where temperatures and humidity are high, artisanal dairy products often present increased microbiological risks if hygienic practices and temperature control are lacking (Fleet 1990). Despite these known risks, there is still very limited published data specifically examining the fungal safety of *dangke*, which remains an important but under-researched local food product.

Fungi are common spoilage organisms in dairy products and can also pose serious health risks due to the production of mycotoxins. Molds such as *Aspergillus*, *Penicillium*, and *Fusarium* are of particular concern as they produce toxic secondary metabolites, including aflatoxins, ochratoxins, and sterigmatocystin, which are stable under typical food processing conditions (Kure and Skaar 2019; Dey et al. 2023; Pandey et al. 2023). Long-term consumption of contaminated dairy products may increase the risk of carcinogenic, nephrotoxic, or immunosuppressive effects (Chen et al. 2020; Tebbi 2023). Despite the significance of these risks, fungal contamination in *dangke* has not been well documented, whereas research has focused mainly on its beneficial Lactic Acid Bacteria (LAB) that contribute to desirable fermentation properties (Syah et al. 2024; Widyadhana et al. 2024).

Given its physicochemical properties, traditional processing methods, and handling practices, *dangke* is highly susceptible to fungal spoilage and potential mycotoxin contamination. To date, no comprehensive study has investigated the level and diversity of fungal contaminants in this traditional cheese. Therefore, this study aims to (i) assess the extent of fungal contamination in *dangke* collected from various small-scale producers in Enrekang District, South Sulawesi, Indonesia; (ii) identify dominant fungal genera present; and (iii) provide evidence to inform improvements in hygiene practices to safeguard public health and support the sustainability of this culturally significant product.

MATERIALS AND METHODS

Study area

Data collection was conducted in Enrekang District, South Sulawesi, Indonesia, across 20 traditional *dangke*-producing industries distributed throughout the region. The sampling sites represented diverse production areas and were georeferenced using a Global Positioning System (GPS), with coordinates ranging from approximately 3°27′-3°45′ South Latitude and 119°40′-120°07′ East Longitude. Enrekang District is situated in a mountainous area with elevations varying between 100 to over 1,000 meters above sea level. The region experiences a tropical monsoon climate, with an average annual temperature of 20-27°C and relative humidity levels of 70-95%, creating favorable conditions for microbial activity and potential fungal contamination. A detailed map of the sampling locations is presented in Figure 1.

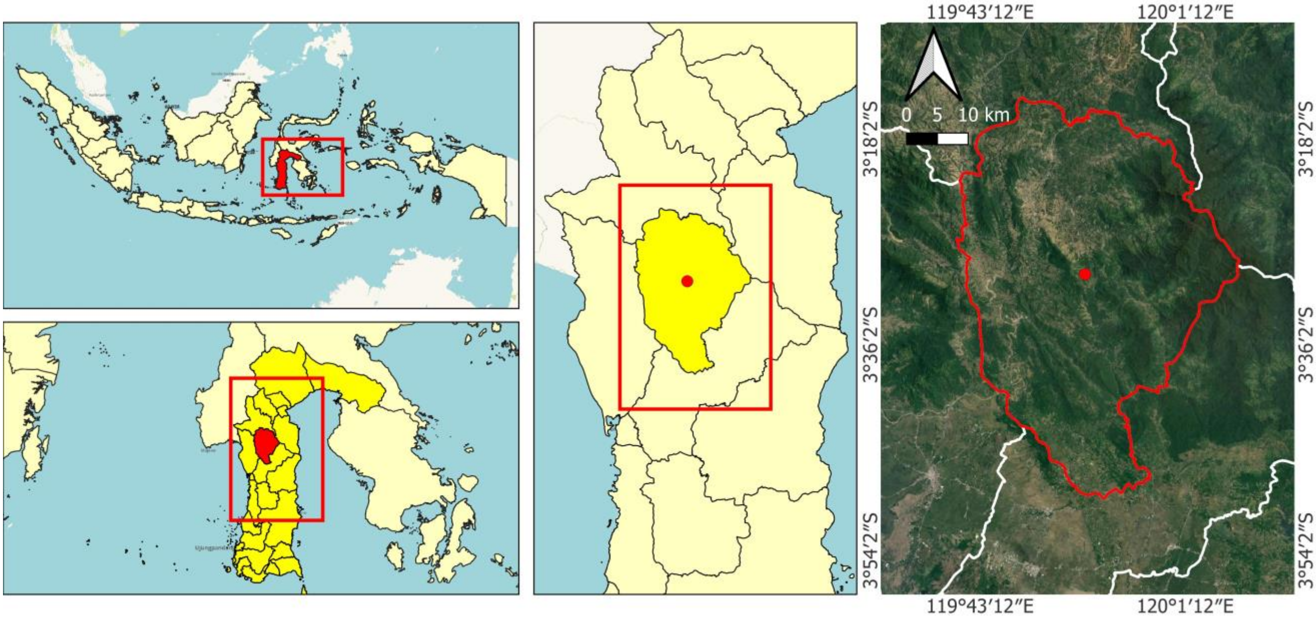

Figure 1. Location of Enrekang District, South Sulawesi, Indonesia indicating the sampling sites for *dangke* soft cheese (3°29'41.6"S 119°52'11.1" E)

Procedures

Collection of samples

A total of 20 samples of *dangke* were randomly collected from different small-scale processing houses distributed across Enrekang District, South Sulawesi, Indonesia, over a period of two months (February-Maret 2012) to account for possible seasonal variation in production and hygiene conditions. From each processing house, one sample (approximately 250 g) was collected. Sampling was conducted in triplicate, meaning each sample was subdivided into three subsamples for independent analysis to ensure data reliability and reproducibility. Standard aseptic sampling techniques were followed throughout. Sterile gloves were worn, stainless steel knives and scoops were sterilized by autoclaving or flaming after treatment with 70% ethanol, and sterile polyethylene bags or autoclaved containers with ice gel packs were used for immediate storage. Samples were transported to the laboratory in insulated cooling boxes maintained at 4°C and processed within 6 hours of collection to minimize changes in the microbial load.

Isolation and enumeration of fungi

Fungal contamination was quantified using the Total Plate Count (TPC) method, adapted from Ryu and Wolf-Hall (2015). For each sample, 25 g of *dangke* were aseptically transferred into 225 mL of 0.1% Buffered Peptone Water (BPW) and homogenized using a stomacher (BagMixer, Interscience, France) for 1 minute. Serial decimal dilutions ranging from 10^{-1} to 10^{-6} were prepared using sterile BPW as the diluent. From each dilution, 0.1 mL was pipetted and spread evenly onto Sabouraud Dextrose Agar (SDA; Oxoid, UK) using a sterile bent glass or metal spreader. SDA was selected due to its suitability for supporting the growth of a broad range of fungi, including both yeasts and filamentous molds. Triplicate plates were prepared for each dilution to ensure statistical accuracy. The inoculated plates were incubated aerobically at 25°C for 48 hours. Colony forming units (CFUs) were counted on plates containing between 30 and 300 colonies and expressed as CFU per gram of sample. Representative colonies were selected and purified by double streaking on fresh SDA plates.

Phenotypic characterization and identification of fungi

Distinct fungal colonies were first distinguished by their macroscopic characteristics, including colony color, texture, surface appearance, margin, elevation, growth rate, and pigmentation on the reverse side of the agar. Colonies with visually different traits were selected for further characterization. Purification was carried out by subculturing each distinct colony type at least twice on fresh Sabouraud Dextrose Agar (SDA) to ensure pure isolates. After purification, each isolate was grown on SDA at 25°C for 3-5 days. Microscopic examination was performed using the slide culture method, following Fisher and Cook (1999) and Weber and Pitt (2000).

A sterile microscope slide was prepared by placing a small block (1 cm²) of sterile SDA in the center. A fragment of fungal mycelium was carefully inoculated onto the sides of the agar block using a sterile needle. A sterile coverslip was gently placed on top of the inoculated agar block. The slide was placed in a sterile moist chamber (e.g., a Petri dish lined with moist filter paper) to maintain humidity. The chamber was incubated at 25°C for 3-5 days, allowing the fungi to grow out onto the coverslip. After incubation, the coverslip was carefully removed, stained with lactophenol cotton blue, and placed on a clean glass slide for microscopic observation.

Microscopic features, including the shape and arrangement of spores (conidia or sporangia), presence and type of hyphae (septate or non-septate), conidiophores, phialides, sporangia, and other reproductive structures, were examined under light microscope at 400× and 1000× magnifications. Isolates were identified to genus level by comparing morphological characteristics with standard identification keys and atlases (Fisher and Cook 1999; Barnett and Hunter 1972; Ahmed and de Hoog 2023). When features were unclear, additional cultures were grown on Potato Dextrose Agar (PDA) to encourage sporulation and pigmentation as needed.

Data analysis

All obtained data, including fungal colony counts (CFU/g), morphological characteristics of isolates, and frequency of fungal genera, were analyzed using descriptive statistical methods. Colony count data were expressed as mean ± standard deviation, and the frequency distribution of fungal genera was presented in percentages. The results were summarized and presented in the form of tables and figures to illustrate the level and diversity of fungal contamination in *dangke* samples.

RESULTS AND DISCUSSION

Enumeration of contaminant fungi in *dangke*

The initial test in this study focused on quantifying the number of contaminant fungi presented in 20 samples of *dangke*, a traditional cheese obtained from small-scale household production businesses in Enrekang District. The Total Plate Count (TPC) method was used for this test and is a widely accepted technique for assessing microbial contamination by counting microbial colonies in samples subjected to serial dilutions, was used for this test. This method provided a clear estimate of the number of microorganisms, including fungi, in a food product. The results from this test were then compared to established standards for fungal contamination in dairy products that were similar to *dangke*. As outlined in Table 1, the study's findings revealed that the average TPC of fungi was 5.2×10^6 CFU/g, significantly exceeding the threshold set by the US Army Public Health Command (USAPHC) Circular 40-1, Appendix O (Department of Defense Food Safety and Quality Assurance Laboratory Action Levels 2016).

According to these guidelines, the maximum allowable limit for contaminant fungi in solid and semi-solid dairy products was 10 CFU/g. This comparison highlighted a concerning level of fungal contamination in all the *dangke* samples tested, far surpassing safe consumption levels and indicating a potential risk for consumers (Department of

Defense Food Safety and Quality Assurance Laboratory Action Levels 2016).

The investigators hypothesized that this high level of fungal contamination could be attributed to poor hygiene and sanitation practices during the production process. *Dangke* production, especially in household-scale businesses, could not always adhere to stringent food safety protocols, resulting in elevated contamination risks. Factors such as improper cleaning of equipment, lack of personal hygiene among workers, and unsanitary working conditions could all contribute to the spread of fungi. The data suggested that more current management practices within these household businesses were not sufficient to ensure the microbial safety of the product.

In addition, dairy products must meet established microbial contaminant limits, including those for bacteria and fungi, to ensure that all fungi are safe for consumption (El-Sayed et al. 2022; Silva et al. 2023). In the case of *dangke*, the findings pointed to an urgent need for improved sanitation and hygiene measures in the production process to align with food safety standards. Without such improvements, the safety of *dangke* as a consumable product remained at risk, which could have broader implications for both public health and its sustainability.

Types of contaminant fungi in *dangke*

The analysis conducted on 20 *dangke* samples sourced from Enrekang District revealed significant fungal contamination, as detailed in Table 2. Remarkably, every sample tested positive for fungi, underscoring a pervasive issue within the production process. The overall fungal composition included both yeasts and molds, which accounted for yeasts 75% and molds 25% of contamination, respectively. A total of 9 distinct mold strains were identified, including species of *Candida*, *Saccharomyces*, *Geotrichum*, *Rhodotorula*, *Microsporum*, *Cladosporium*, *Penicillium*, *Aspergillus*, and *Fusarium*. Among these fungal contaminants, *Candida* sp. was the most prevalent yeast, identified in a staggering 30% of the samples (Figure 2).

Table 1. Average number of contaminant fungi in *dangke*

n	The number of fungi (CFU/g)			Standard deviation	The percentage of contamination exceeds the threshold* (%)
	Minimum	Maximum	Average		
20	3.2×10^{6a}	7.6×10^{6a}	5.2×10^{6a}	1.212	100

Note: *Exceeds the threshold for contaminant fungi (mold/yeast) in USAPHC Circular 40-1, Appendix<10 CFU/g (Department of Defense Food Safety and Quality Assurance Laboratory Action Levels 2016)

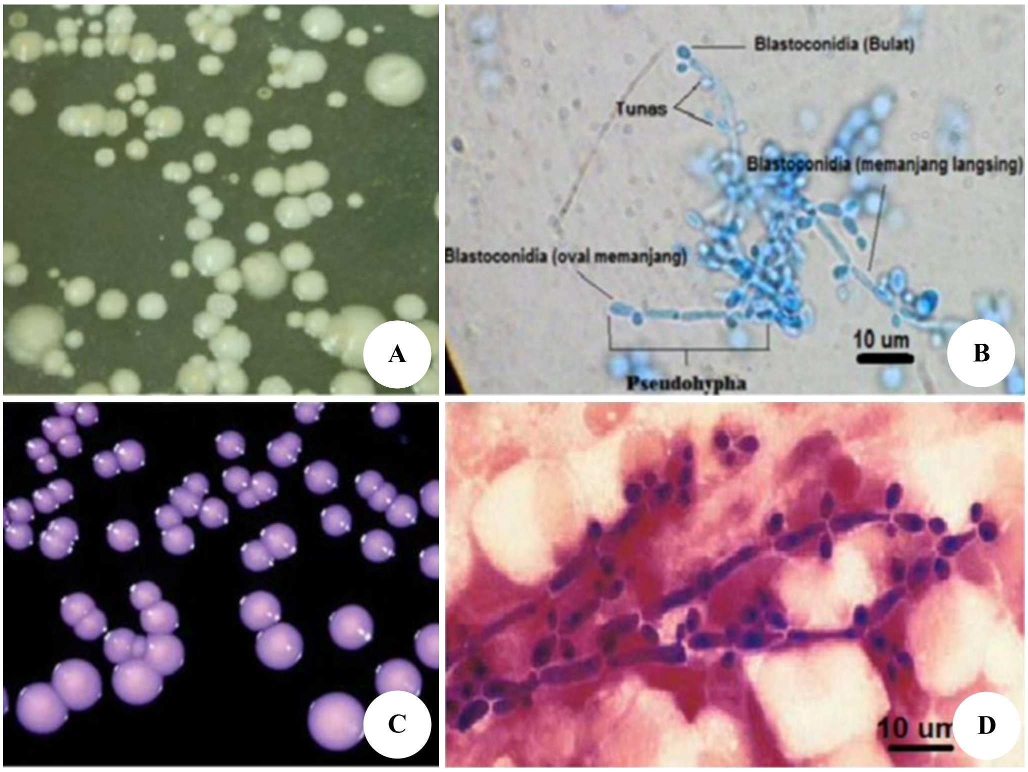

Figure 2. A. Macroscopic and microscopic *Candida* sp., B. The study results, C-D. Figure from Ellis et al. 2007. A and C are growth of *Candida* sp. colonies on Sabouraud dextrose agar (SDA) after 3 days of incubation at 25°C, B and D are Microscopic *Candida* sp. magnification 100×

Table 2. The type of fungi found in *dangke* samples from several *dangke* processing household industries in Enrekang District

Samples (n)	**The type of fungi**									**Total (%)**
	Yeast				**Mold**					
	***Candida* sp.**	***Saccharomyces* sp.**	***Geotrichum* sp.**	***Rodotorula* sp.**	***Microsporum* sp.**	***Cladosporium* sp.**	***Penicillium* sp.**	***Aspergillus* sp.**	***Fusarium* sp.**	
1	+	+	-	-	-	-	-	-	-	
2	+	+	+	-	-	-	-	-	-	
3	+	+	-	+	-	-	-	-	-	
4	+	-	-	-	-	-	-	-	-	
5	+	-	+	-	-	-	-	-	-	
6	+	-	-	-	-	+	+	+	+	
7	+	+	+	-	+	-	-	-	-	
8	+	-	+	-	+	-	+	-	-	
9	+	-	-	-	-	-	+	-	-	
10	+	+	-	+	-	+	-	-	-	
11	-	-	+	-	-	-	-	-	-	
12	+	-	+	-	+	-	-	-	-	
13	+	+	-	-	+	-	-	+	-	
14	+	+	+	-	+	+	+	+	-	
15	+	+	-	-	-	-	+	+	-	
16	+	+	-	-	+	+	-	-	-	
17	+	+	-	-	-	-	-	-	-	
18	+	-	-	-	+	+	-	-	-	
19	+	-	-	-	-	+	+	-	-	
20	+	-	-	+	+	-	-	-	-	
Percentage (%)	30	16	11	5	13	9	9	6	2	100

Note: + : there was fungi, - : there was no fungi

This high prevalence raised questions regarding the conditions under which *dangke* was produced, as it could indicate inadequate hygiene practices. Furthermore, the most common molds detected were *Cladosporium* sp. and *Penicillium* sp., each found in 9% of the samples. The presence of these fungal contaminants not only posed potential health risks to consumers but also threatened the overall quality and shelf life of *dangke*. In addition, this highlighted an urgent need for better sanitation protocols and management practices within household-scale production businesses in Enrekang District. By addressing these issues, producers could enhance the safety and quality of *dangke*, thereby preserving its cultural significance while ensuring that it remained safe for consumption.

Discussion

The relationship between the quantity of microscopic fungi presented in dairy products was a topic that had not been extensively studied and is of utmost importance for ensuring food safety and quality. Fungi, including molds and yeasts, were commonly found in raw milk, also known as fresh milk. However, these microorganisms were generally eliminated during the pasteurization process, a heat treatment designed to kill harmful pathogens and extend the shelf life of dairy products. This process played a crucial role in reducing the risks associated with fungal contamination in dairy products before this process occurred (Torkar and Vengušt 2008; Garnier et al. 2017; Awasti and Anand 2020). The contamination of raw milk with fungi could occur through various pathways, with animals being a significant source. Fungi could reside on the skin of dairy cows and be transferred to the milk during the milking process. Furthermore, animal excreta could introduce these microorganisms into the milk, especially when hygienic practices were not strictly followed. The milking process could also be a critical point of contamination, where the hands of the milkers and equipment harbored fungi, contributing to the microbial load.

In the context of *dangke*, a traditional Indonesian cheese made from cow's milk, the fungal contamination observed in this study aligned with the findings of Torkar and Vengušt (2008) and Garnier et al. (2017). These studies suggested that the source of contamination often lay in the raw materials used during processing, which included the cow's milk itself as well as additional ingredients such as papaya fruit sap. The papain enzyme derived from papaya sap could also harbor microbial contaminants, which may survive and persist throughout the production stages, posing a risk to the final product's safety (Opiyo et al. 2013). Moreover, recontamination during the processing of *dangke* is a critical concern. Environmental factors, including unclean equipment, airborne spores, and handling practices, play a significant role in introducing fungi into dairy products (Fleet and Mian 1987; Kalamaki and Angelidis 2023; Aranda et al. 2025). For instance, the hands of workers, the molds used for shaping the cheese, and other processing tools can act as vectors of contamination (Kure and Skaar 2019). The presence of fungi not only compromises food safety, but also affects sensory attributes such as flavor, texture, and shelf-life, which are critical for consumer acceptability (Garnier et al. 2017; Wikandari et al. 2021). Given these risks, there is a pressing need for the implementation of Good Hygienic Practices (GHP) and Hazard Analysis and Critical Control Points (HACCP) systems throughout dairy production to control microbial hazards (FAO-WHO 2011). This includes ensuring proper sanitation during milking, sterilization of equipment, and personnel hygiene training. By addressing these contamination risks, dairy producers can improve product quality and meet both consumer expectations and regulatory standards. Understanding the dynamics of fungal contamination in traditional dairy products is thus essential for advancing food safety and public health.

Milk and fermented milk products serve as a favorable environment for the growth of yeasts and molds, microorganisms that could lead to food spoilage and fermentation (Awasti and Anand 2020; Ntuli et al. 2022; Shekhar 2024). This characteristic made these products particularly susceptible to fungal contamination, which posed significant challenges for dairy producers and consumers alike. A notable example was *dangke*, a traditional Indonesian cheese known for its unique flavor and texture. However, the presence of fungal contaminants could severely compromise the quality and shelf life of *dangke*, drastically affecting its safety for consumption. This study indicated that contaminated *dangke* had a remarkably short shelf life, and it could only remain safe for 1 to 2 days at room temperature (around 27 to 30°C) and up to 5 days when stored in a refrigerator at a temperature of 4°C. This limited duration highlighted the importance of proper handling and storage conditions for maintaining the integrity of the product. Similar observations were made with Dadiah, another dairy product from West Sumatra, which also exhibited a limited shelf life when subjected to microbial contamination. According to a study by Herlina and Setiarto (2024), dadiah could last only 3 days at room temperature before becoming unfit for consumption.

The short shelf life of these products was not merely a logistical concern, but it raised significant health risks. Fungal contamination could lead to the development of mycotoxins, which were toxic compounds produced by certain fungi. When consumed, these toxins could cause a variety of foodborne diseases in humans, posing a serious public health threat (Bintsis 2017; Gallo et al. 2020; Long et al. 2023). Symptoms of foodborne illnesses could range from mild gastrointestinal discomfort to severe health complications, depending on the type of fungi involved and the individual's susceptibility. This underscored the necessity for strict hygiene and quality control measured in the dairy industry to mitigate the risk of fungal contamination.

The contamination of cheese products by fungi posed a significant risk to food safety, primarily due to the presence of various molds and yeasts. The fungi most frequently associated with cheese contamination belonged to several genera, including *Penicillium*, *Aspergillus*, *Cladosporium*, *Geotrichum*, *Mucor*, and *Trichoderma* (Hymery et al. 2014; Izzo et al. 2022). These genera of molds could be particularly hazardous because nearly all of these molds had the potential to produce mycotoxins and secondary metabolites. These toxic compounds were significant contributors to food spoilage, making it a primary concern in the dairy industry. The presence of mycotoxins could lead to poisoning in humans, posing a serious health risk when contaminated cheese products are consumed (Kure and Skaar 2019; Izzo et al. 2022; Aasa et al. 2023; Pandey et al. 2023).

A specific yeast species also contributed to the contamination of milk and dairy products. However, the genera *Kluyveromyces*, *Saccharomyces*, and *Candida* were frequently found in these products (Moubasher et al. 2018; Akinyemi et al. 2023). The presence of these yeast genera could lead to fermentation issues, off-flavors, and spoilage, further complicating the production and storage of dairy products. A study conducted by Torkar and Vengušt (2008) in Slovenia provided valuable insights into the prevalence of different yeast and mold species in raw milk and cheese. Their study revealed significant findings such as *Geotrichum* present in 51.5% of the samples, followed by *Aspergillus* at 33.8%, *Mucor* at 5.9%, *Fusarium* at 2.9%, and *Penicillium* also at 2.9%. These results highlighted the widespread nature of fungal contamination in dairy products, emphasizing the need for rigorous quality control measures to mitigate these risks. Similarly, a study by Akinyemi et al. (2023) focused on raw milk samples in Nigeria, identifying the dominant yeast species present. Their findings showed that *Kluyveromyces* accounted for 28% of the yeast population, followed by *Saccharomyces* at 24% and *Candida* at 18%. This data underscored the global nature of fungal contamination issues in dairy products, which could vary by region but share common genera.

Candida sp. emerged as the most prevalent fungal genus found in a study of 20 *dangke* samples, with a remarkable detection rate of 30% (Table 2). This finding aligned with numerous studies that indicated the *Candida* genus as the dominant type of fungus contaminating milk and dairy products. According to Awasti and Anand (2020), *Candida* was frequently reported as a significant contaminant in dairy. Subsequently, around 24 different species of *Candida* were linked to the spoilage of dairy products, highlighting the importance of monitoring this genus in the dairy industry. Fleet and Mian (1987) reported that the highest populations of yeast, often reaching up to 10^6-10^7 cells/g, were found in yogurt and cheese samples. The most frequently isolated species included *Candida famata, Kluyveromyces marxianus, Candida diffluens*, and *Rhodotorula glutinis*. These findings underscored the significance of *Candida* spp. in contributing to the microbial load in dairy products. Furthermore, Ahmed et al. (2020) reported that as many as 29.2% of the isolated species from various dairy products were identified as *Candida* spp., indicating a widespread issue across different dairy items. In addition, studies on traditional dairy products like Thairu from India have also revealed a high prevalence of *Candida* species, as noted by Chandran et al. (2022). This observation suggested that *Candida* contamination was a common challenge in both industrial and artisanal dairy production settings.

The high fungal load observed in *dangke* samples in this study (average 5.2×10^6 CFU/g) is consistent with reports for other traditional dairy products produced under similar tropical or subtropical conditions. For example, *wara* cheese in Nigeria and wagashi a traditional cheese from Kozah municipalities in Togo, has been reported to contain fungal counts ranging from 10^4 to 10^7 CFU/g (Shiawoya et al. 2006; Ndudi et al. 2024; Taale et al. 2025), and mainly due to poor handling and ambient storage. Furthermore, Yahyapour et al. (2023) reported comparable contamination levels in Iranian local cheeses, with dominant genera including *Candida*, and *Geotrichum*, similar to those detected in *dangke* in this study. These comparisons highlight that high moisture content, neutral pH, and non-standardized production methods remain major risk factors for fungal growth across different artisanal dairy contexts. Moreover, the presence of genera such as *Aspergillus*, *Penicillium*, and *Fusarium* raises concern because these molds are capable of producing mycotoxins, such as aflatoxins and ochratoxins, which pose serious food safety risks (Pandey et al. 2023). Chronic exposure to mycotoxins through dairy products may lead to carcinogenic, nephrotoxic, or immunosuppressive effects in consumers, particularly when dairy products are consumed without further heat treatment (Chen et al. 2020; Tebbi 2023).

The high level of contamination from the genus *Candida* was likely attributable to poor hygiene practices among workers in processing factories. *Candida* sp. was a ubiquitous fungal contaminant that naturally resides in the lining of the oral cavity, digestive tract, and vagina in humans (Alhussein and AL-Yasiri 2019; Rudramurthy and Singh 2020; Malik et al. 2022). In healthy individuals, *Candida* was present in small quantities and was typically kept in check by other normal microbial flora, contributing to the balance of the body's microflora (Cauchie et al. 2017; Ciurea et al. 2020). However, when conditions favored its overgrowth, such as in environments with poor sanitation and hygiene practices, the risk of contamination increased significantly.

In Figure 2, the microscopic examination of *Candida* sp. revealed that the cells exhibited an elongated, oval shape and were characterized by the formation of blastoconidia and reproduced through elongated, multilateral shoots that resembled hyphae, commonly referred to as pseudohyphae. Occasionally, *Candida* sp. cells could also develop true hyphae and were Gram-positive and typically measured between 2-3 µm in width and 4-6 µm in length (Ellis et al. 2007; Howell and Hazen 2022). The colonies of *Candida* sp. were distinctly round and could be cultured on SDA. After 3 days of incubation, the colony morphology became visible, displaying smooth and shiny appearance accompanied by a characteristic yeast-like odor. When incubated at temperatures ranging from 25 to 37°C for approximately 7 days, the colonies became compact and soft, with a yellowish-white coloration. These typically had a diameter of 1 to 5 mm and continued to exhibit a smooth texture along with a distinct yeast-like smell (Fisher and Cook 1999; Ahmed and de Hoog 2023). This detailed observation of the morphology and growth characteristics of *Candida* sp. was essential for accurate identification and understanding of its potential implications in food safety and spoilage. (Fisher and Cook 1999; Ahmed and de Hoog 2023).

Given these findings, the fungal contamination levels in *dangke* clearly indicate a pressing need for improved hygiene and quality control during production. Producers should adopt Good Manufacturing Practices (GMP) and hygiene training to minimize recontamination from equipment, molds, and handlers. Implementing simple measures such as sterilizing coconut shell molds, using clean water, storing finished products under refrigeration, and introducing safer packaging could substantially reduce fungal loads and extend shelf life. For local authorities and extension services, these results emphasize the importance of outreach and training programs targeting small-scale *dangke* producers to safeguard public health while sustaining this valuable cultural product.

The lack of proper sanitation and hygiene among *dangke* processors was a crucial factor that facilitated the contamination of this fungal genus. Inadequate cleaning protocols, insufficient training for workers on hygiene practices, and environmental factors within production facilities could all contribute to the proliferation of *Candida* spp.. This highlighted the urgent need for improved sanitation measures and training programs for workers in the dairy industry. By implementing rigorous hygiene standards and monitoring for microbial contamination, producers could help mitigate the risks associated with *Candida* contamination in *dangke* and other dairy products, ensuring a safer product for consumers. Understanding the prevalence and implications of *Candida* contamination was essential for maintaining the quality and safety of dairy products in both commercial and traditional production contexts.

Candida sp. is a genus of fungi that is frequently responsible for fungal infections in humans, making it a significant concern in medical mycology. Among the various fungal genera, *Candida* was often noted for its role in causing mycosis, an infection that could arise in individuals with compromised immune systems. This opportunistic fungal pathogen could cause diseases that typically did not affect healthy individuals, highlighting its capacity to exploit vulnerabilities in the human body. Under normal circumstances, *Candida* species existed in small amounts as part of the body's natural flora. These were commonly found in areas such as the oral mucosa, respiratory tract, digestive tract, vagina, skin, and even under the nails of healthy individuals. In these instances, it coexists peacefully with the body's microbiota without causing any symptoms or harm (Cauchie et al. 2017; Ciurea et al. 2020). However, when conditions change, whether due to physical, chemical, or environmental factors, *Candida* could proliferate excessively, leading to various health issues. For example, an overgrowth of *Candida* on the surface of the tongue and cheeks could result in canker sores, causing discomfort and pain (Singh et al. 2013; Ciurea et al. 2020). The transition from a saprophytic formed to a pathogenic one was usually triggered by predisposing factors that weakened the immune system. Several conditions could lower the body's defenses, making it more susceptible to *Candida* infections. These factors included diabetes, AIDS, prolonged exposure to high humidity, continuous use of antibiotics, and obesity (Oliveira et al. 2023). Each of these conditions could create an environment where *Candida* could thrive, leading to opportunistic infections.

As an opportunistic pathogenic fungus, *Candida* could cause a wide range of diseases in humans. Some of the more common infections included oral thrush, characterized by painful mouth ulcers (Terai et al. 2018), skin lesions that could occur in various areas of the body (Espinosa-Hernández et al. 2020), and vulvovaginitis, which affected the vaginal area (Arechavala et al. 2021). Another significant manifestation of *Candida* infection was candiduria, where *Candida* was presented in the urine, indicating a urinary tract infection (Kauffman 2005). Additionally, gastrointestinal candidiasis could occur, leading to conditions such as gastritis and ulcers (Ciurea et al. 2020; Alonso-Monge et al. 2021).

In more severe cases, *Candida* could even be associated with complications arising from cancer treatment or immunosuppressive therapies, which could significantly increase the risk of opportunistic infections (Vázquez-Olvera et al. 2023; Wang et al. 2023). These complications underscored the need for heightened vigilance in individuals undergoing such treatments. The management of *Candida* infections typically involves addressing the underlying predisposing factors and could include the use of antifungal medications. Maintaining a healthy immune system was crucial for preventing overgrowth and subsequent infections. Awareness of the conditions that could lead to *Candida* proliferation was essential for both patients and healthcare providers, allowing for timely intervention and effective management of potential infections.

Candida sp. represented a significant challenge in the realm of fungal infections due to its opportunistic nature. Additionally, its ability to transition from harmless flora to a pathogenic entity underscored the importance of understanding the predisposing factors and the conditions that allowed for its overgrowth. By recognizing the signs and symptoms of *Candida* infections, individuals and healthcare providers could work together to implement preventive measures and appropriate treatments, ensuring better health outcomes.

In conclusion, this study demonstrated that the level of fungal contamination in *dangke* produced in Enrekang District far exceeded the recommended safety threshold of 10 CFU/g, with an average fungal load of 5.2×10^6 CFU/g. Both yeasts (75%) and molds (25%) were detected, with *Candida* sp. (30%) identified as the dominant genus, followed by *Saccharomyces* sp., *Geotrichum* sp., *Microsporum* sp., *Cladosporium* sp., *Penicillium* sp., *Aspergillus* sp., *Rhodotorula* sp., and *Fusarium* sp. Several of these genera are known spoilage agents and potential mycotoxin producers, posing clear food safety risks if contamination remains unchecked. These findings highlight the urgent need for household-scale *dangke* producers to adopt stricter hygiene and sanitation measures at every production stage, from milking to packaging and storage. Implementing Good Hygiene Practices (GHP) and Good Manufacturing Practices (GMP), such as using sterilized equipment, wearing protective clothing, regularly cleaning molds and utensils, and introducing hygienic packaging, can significantly reduce fungal contamination. In addition, local food safety authorities should develop clear guidelines and provide training to producers on safe handling and storage conditions. Establishing local standards for microbial quality and routine monitoring could help ensure that *dangke* meets acceptable food safety criteria. Finally, educating consumers about safe storage and consumption practices, such as refrigeration and limiting shelf life, is essential to protect public health and maintain trust in this culturally significant product.

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