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RESEARCH ARTICLE

Collection of industrial microorganisms resources – molds isolated from food

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Abstract

Fungal spoilage remains a major challenge in the food industry, driven by the high adaptive capacity of molds and their ability to colonize diverse food matrices. Culture collections play a key role in documenting this diversity and providing access to well-characterized strains for research and industrial applications. This study presents a curated set of 60 mold isolates obtained from spoiled food products in Poland between 2019 and 2024 and subsequently deposited in the Collection of Industrial Microorganisms (KKP)—Microbiological Resources Center, Department of Microbiology, Prof. Wacław Dąbrowski Institute of Agricultural and Food Biotechnology—State Research Institute. The isolates originated from fruit-based products, cereal- and flour-derived items, dairy products and meat, reflecting the wide range of substrates susceptible to fungal contamination. Taxonomic identification based on ITS sequencing revealed representatives of common food spoilage genera, including Penicillium, Aspergillus, Mucor, Alternaria, Cladosporium and others, together with less frequently reported taxa and physiologically resilient species such as Xeromyces bisporus and Paecilomyces niveus. The dataset highlights the occurrence of xerophilic, psychrotolerant and otherwise stress-resistant molds capable of persisting under reduced water activity, low temperature or modified-atmosphere conditions. By documenting the diversity and origins of these isolates, this work expands the reference resources available for studies on fungal ecology, spoilage mechanisms and contamination pathways in food environments. The strains preserved in the KKP collection constitute a valuable foundation for future research aimed at improving food safety, developing targeted detection methods and assessing antifungal strategies.

KEYWORDS

food spoilage molds, fungal diversity, ITS identification, Collection of Industrial Microorganisms (KKP)

Introduction

The significance of mold contamination in food

Microbiological spoilage, including the growth of molds, is one of the key causes of losses in the global food chain. It is estimated that up to one third of the world's food production is wasted before consumption, amounting to approximately 1.3 billion tons per year [Garnier et al.; 2017]. Around 25% of the global food supply is lost due to secondary microbiological spoilage after harvest [Snyder and Worobo; 2018], and the combined pre- and post-harvest losses in major commodities may reach 30–50% [Pandey et al.; 2023]. In a substantial proportion of cases, this spoilage is caused by filamentous fungi present at every stage of the "farm-to-fork" chain. Most molds affect food safety primarily through the production of mycotoxins. Epidemiological data indicate that at least 25% of global crops are contaminated with

mycotoxins, and more recent analyses show that their traces can be detected in as many as 60–80% of agricultural products [Gouda et al.; 2024]. It is estimated that more than five billion people are exposed daily to mycotoxins present in food [Pandey et al.; 2023]. The most important ones include aflatoxins, ochratoxin A, fumonisins, deoxynivalenol, zearalenone, patulin and other secondary metabolites with documented hepatotoxic, nephrotoxic, immunotoxic, mutagenic and carcinogenic properties [Pandey et al.; 2023]. Mycotoxins are generally thermostable compounds that are difficult to remove during processing, meaning that once a batch of raw material or finished product becomes contaminated, it often has to be withdrawn from the market. In addition to toxicological concerns, the development of fungal mycelium leads to deterioration of sensory quality—changes in color and texture, surface growth, and undesirable odors and flavors—which results in product rejection by consumers even when no direct health risk is present [Garnier et al.; 2017; Snyder and Worobo; 2018]. Molds can metabolize organic acids, increasing the pH of the product and indirectly raising the risk of growth of pathogenic bacteria [Snyder and Worobo; 2018]. From a food safety perspective, contamination of raw materials with molds leads to reduced product quality and serious health hazards associated with the presence of mycotoxins.

Foods particularly susceptible to contamination include those with low water activity and nutrient content that support fungal growth, such as cereals and cereal-based products, corn, rice, legumes and oilseeds. These commodities are dominated by fungi of the genera *Fusarium*, *Aspergillus* and *Penicillium*, which are often responsible for the production of trichothecenes, fumonisins and zearalenone [Pandey et al., 2023]. Nuts and oil-rich seeds (including peanuts, pistachios and almonds), as well as spices and herbs, also constitute a significant source of exposure, since aflatoxins produced by Aspergillus flavus and ochratoxins produced by selected Aspergillus and Penicillium species are frequently detected in these products [Pandey et al.; 2023]. Another important group of products prone to fungal contamination are dried fruits such as raisins, figs and apricots, which, due to their high sugar content and nutrient availability, support the growth of microorganisms. In the study by Gouda et al. (2024), numerous filamentous fungi were isolated from dried fruits, mainly belonging to the genera *Aspergillus*, *Penicillium* and *Alternaria*. Among the analyzed isolates, selected Aspergillus strains (including A. flavus and A. parasiticus) demonstrated the ability to produce aflatoxins, whereas in the remaining genera no mycotoxin-producing ability was detected [Gouda et al.; 2024]. Despite the use of intensive technological barriers, dairy products and fermented beverages may also undergo mold spoilage, leading to significant economic losses [Garnier et al.; 2017]. The risk of contamination also applies to plant-derived raw materials intended for food and medicinal use (edible and medicinal substances). It has been shown that more than 90% of tested samples contain detectable levels of molds, mainly from the genera Aspergillus, Penicillium, Fusarium and Alternaria, and a substantial portion of them exceed the limits established in Europe [Chen et al.; 2025].

Molds represent a ubiquitous risk factor within the global food chain, affecting food safety, sensory quality, and the economics of production and distribution. The scale of this issue justifies the need for continuous monitoring of contamination and the development of effective mitigation strategies, which serves as the starting point for the subsequent sections of this study.

Molds as highly adaptive microorganisms

Molds exhibit an exceptional ability to adapt to diverse physicochemical conditions, which makes them one of the most difficult food spoilage agents to control [Snyder and Worobo; 2018]. Their growth is observed in both fresh and processed foods, including refrigerated, dried, high-sugar, acidic and modified-atmosphere-packaged products, with the dominant species determined by water activity, pH, temperature, oxygen availability and the preservatives applied [Garnier et al.; 2017; Leyva Salas et al.; 2017; Rico-Muñoz et al.; 2019]. A key adaptive trait is their capacity to grow at reduced water activity (xerophilicity) or in hyperosmotic environments. Such properties enable mold development in dried and high-sugar products—such as apricots, figs, grapes and confectionery—where Aspergillus species dominate, including xerophilic strains capable of producing mycotoxins even at very low aw levels [Rico-Muñoz et al.; 2019; Gouda et al.; 2024; Miliordos et al.; 2025].

Molds also colonize niches characterized by low pH, low temperature and limited oxygen availability. Many species prefer acidic environments and grow in fruits, juices, soft drinks and fermented dairy products [Mafe et al.; 2024]. In the dairy industry, numerous mold and yeast species can proliferate in refrigerated products at temperatures below 10°C and under reduced oxygen conditions, increasing the risk of spoilage in ripened cheeses, yogurts and vacuum-packaged cheeses [Souza et al.; 2023; Garnier et al.; 2017].

Herbal raw materials also constitute a significant contamination hotspot, as fluctuations in temperature and humidity during storage favor increased mold presence and exceedance of mycotoxin limits [Chen et al.; 2025].

The adaptive capacity of molds results from their tolerance to extreme environmental parameters and from their physiological and metabolic characteristics. Filamentous fungi secrete extracellular enzymes that enable substrate degradation and the colonization of diverse matrices [Garnier et al.; 2017; Snyder and Worobo; 2018]. They also produce resistant spores (conidiospores, ascospores) that exhibit high survival rates [Rico-Muñoz et al.; 2019; Snyder and Worobo; 2018].

As a consequence, traditional preservation methods such as pH reduction, lowering of water activity, refrigeration or the addition of preservatives often lead to the selection of species that are best adapted to the newly created conditions [Snyder and Worobo; 2018; Rico-Muñoz et al.; 2019]. Even complex multi-hurdle systems combining heat treatment, modification of aw and pH, modified atmosphere packaging and chemical agents do not always guarantee complete elimination of molds, particularly in long-shelf-life products [Leyva Salas et al.; 2017; Mafe et al.; 2024]. The persistence of contamination despite rigorous hygienic and technological procedures observed in dairy processing plants, in the production of dried fruits, and in herbal raw materials highlights the need to consider the high adaptive capacity of molds when designing food safety strategies [Souza et al.; 2023; Chen et al.; 2025; Miliordos et al.; 2025].

Pathways and sources of mold contamination in food

Contamination of food with molds results from overlapping routes of exposure present at every stage of the production chain from the field environment, through storage and processing, to packaging and distribution [Snyder and Worobo; 2018; Souza et al.; 2023]. Molds may enter the food system both as part of the natural microbiota of raw materials and through secondary contamination in processing facilities. The pre-harvest stage constitutes the first critical point of risk. Cereals, legumes and other plant-derived raw materials may be colonized in the field by Fusarium sp., Alternaria sp., Cladosporium sp. and other molds, depending on the presence of inoculum, plant residues and environmental stresses such as humidity, rainfall or tissue damage [Pandey et al.; 2023; Deligeorgakis et al.; 2023]. Similar mechanisms apply to herbal raw materials, where delayed harvesting, contaminated soil and improper agricultural practices promote colonization by Aspergillus sp., Penicillium sp. and Fusarium sp. [Chen et al.; 2025]. In fruits intended for drying, molds are often detected even before processing, increasing the likelihood of their presence in the final product due to the high resistance of fungal spores [Gouda et al.; 2024].

The storage stage is particularly critical. Elevated humidity and temperature, poor ventilation and condensation favor the growth of storage molds, which dominate the mycobiota of stored grains, seeds and dried products [Pandey et al.; 2023; Deligeorgakis et al.; 2023]. Aerosols in storage facilities may act as vectors for spores, as confirmed by environmental studies in dairy-processing plants [Souza et al.; 2023]. During processing, contamination may originate from spores present in the air, ventilation systems, process water and on food-contact surfaces. Open exposure of products during handling, cooling or pre-packaging facilitates the deposition of spores [Snyder and Worobo; 2018; Souza et al.; 2023]. Technological equipment, conveyors, containers and machinery can serve as reservoirs of molds when cleaning and disinfection procedures are insufficient [Snyder and Worobo; 2018; Leyva Salas et al.; 2017].

The packaging and distribution stages also pose contamination risks. Contaminated packaging materials or surfaces may transfer spores that subsequently develop during storage [Snyder and Worobo; 2018]. In low–water-activity products, improperly selected packaging may promote moisture absorption and growth of xerophilic molds [Rico-Muñoz et al.; 2019; Gouda et al.; 2024]. Fluctuations in temperature and humidity during transport determine whether spores remain dormant or initiate spoilage [Pandey et al.; 2023; Mafe et al.; 2024].

Viewed as a whole, the routes and sites of contamination form a complex network of interactions between the natural environment, storage conditions, logistics and the design and operation of processing lines [Snyder and Worobo; 2018; Souza et al.; 2023; Deligeorgakis et al.; 2023].

Increasing attention is being directed toward the monitoring and documentation of molds isolated from food, which enables a better understanding of their diversity, origins and technological relevance. One of the tools that facilitates such activities is microbial culture collections, which serve as reference repositories providing access to well-characterized and stably preserved isolates. The Collection of Industrial Microorganisms (KKP) preserves microorganisms of importance to the agri-food industry, including a broad set of molds isolated from food products analyzed as part of routine laboratory testing.

The aim of this study was to present the resources of filamentous fungi deposited in the Collection of Industrial Microorganisms (KKP) and to illustrate the taxonomic diversity of molds isolated from various categories of food products. Between 2019 and 2024, the Microbiology Department of the Institute of Agricultural and Food Biotechnology – State Research Institute (IBPRS-PIB, Warsaw) isolated numerous fungal strains originating from spoiled food items, including fruit beverages, fruits and fruit-derived products, cereal-based foods, meat products, dairy items, and high-sugar foods.

In this paper, we present a set of 60 selected, representative strains that best capture the taxonomic spectrum of molds isolated during this period. All strains have been deposited in the Collection of Industrial Microorganisms (KKP), forming a curated reference resource for future research on food-associated molds and their relevance to food quality and safety.

MATERIALS AND METHODS

The molds included in this study were isolated from food products exhibiting visible signs of spoilage, originating from categories such as fruit-based beverages (e.g., juices, flavored drinks), fruit-based solids (e.g., mousses, jams), dairy products, flour-based products, meat products, and several less frequent types of food items. Initially, the isolates were obtained using classical culture-based methods and subsequently subjected to molecular identification based on sequencing of the internal transcribed spacer (ITS) region. The strains selected for further characterization were deposited in the Collection of Industrial Microorganisms (KKP).

Fungal Isolation from Food Samples.

Samples selected for analysis were food products exhibiting visible signs of spoilage, such as surface growth, discoloration, or changes in texture. Material from these products was plated onto Dichloran Rose Bengal Chloramphenicol Agar (DRBC) or DG-18, both of which reduce bacterial growth and support the recovery of molds with differing growth rates. This created favorable conditions for the recovery of slower-growing colonies that might otherwise be overgrown. Plates were incubated aerobically at 25 °C for 5–7 days according to EN-ISO 21527-1:2009 or EN-ISO 21527-2:2009.

Distinct fungal colonies were subsequently transferred onto Sabouraud Agar (SA) to promote more robust mycelial growth and allow detailed morphological assessment. This standard two-step protocol generally allowed for efficient isolation and purification. In cases where isolates failed to grow under these conditions due to specific ecological or physiological requirements alternative media or modified incubation parameters (e.g., temperature, pH, water activity) were applied, depending on the suspected characteristics of the strain.

All purified isolates were preserved by cryopreservation at −80 °C and in liquid nitrogen in growth medium supplemented with

glycerol (final concentration 10%, v/v), according to standard KKP preservation procedures, to ensure their stability for further identification and long-term archiving.

Molecular identification

Fungal DNA was extracted using the commercial DNeasy PowerFood Microbial Kit (Qiagen GmbH, Hilden, Germany). Amplification of the internal transcribed spacer (ITS) region was performed using the ITS1 (5'–TCCGTAGGTGAACCTGCGG–3') and ITS4 (5'–TCCTCCGCTTATTGATATGC–3') primers [White et al., 1990]. PCR conditions were as follows: initial denaturation at 95°C for 2 minutes, followed by 35 cycles consisting of denaturation at 94°C for 30 seconds, annealing at 53°C for 35 seconds, and extension at 72°C for 1 minute. The reaction concluded with a final extension at 72°C for 10 minutes, conducted using the SimpliAmp™ Thermal Cycler (Applied Biosystems™, ThermoFisher Scientific, Waltham, MA, USA). The amplification products were separated by electrophoresis on a 2% agarose gel containing SimplySafe™ DNA stain (5 µL/100 mL; EURx, Gdańsk, Poland). A DNA Ladder with a size range of 100–3000 bp (A&A Biotechnology, Gdańsk, Poland) was used as a molecular size marker. Electrophoresis was carried out at 110 V for 60 minutes using the Sub-Cell GT Horizontal Electrophoresis System (Bio-Rad, Madrid, Spain). Bands were visualized using the GeneFlash Network Bio Imaging System (Syngene, Wales, UK). Sequencing of the amplicons was outsourced to Genomed S.A. (Warsaw, Poland). The obtained chromatograms were inspected and trimmed for quality, and the edited sequences were subsequently analyzed using the BLASTn tool from NCBI. Species assignments based solely on ITS sequences were accepted only when the top BLAST hits showed clear separation from closely related taxa; otherwise, strains were identified to the genus level.

RESULTS AND DISCUSSION

The mycobiota of food encompasses numerous genera of filamentous fungi, among which Aspergillus sp., Penicillium sp., Fusarium sp., Alternaria sp., Cladosporium sp., Mucor sp. and Rhizopus sp. are particularly relevant due to their frequency of occurrence and their impact on food quality and safety [Leyva Salas et al., 2017; Garnier et al., 2017; Deligeorgakis et al., 2023; Souza et al., 2023; Chen et al., 2025; Rovetto et al., 2023]. Our results are consistent with this general pattern: the most frequently isolated genus in our collection was Penicillium (28.3%), followed by Aspergillus (16.7%) (Table 1). Both genera are widely recognized as common food spoilage molds and are associated with a broad range of matrices, including fruit-based products, cereal-derived items, dairy products and meat.

Table 1. Most frequently isolated mold genera.

Genus of mold	Number of cases	Relative frequency (%)
Penicillium	17	28.3%
Aspergillus	10	16.7%
Alternaria	3	5%
Cladosporium	2	3.3%
Paecilomyces	3	5%
Fusarium	3	5%
Talaromyces	2	3.3%
Didymella	3	5%
Mucor	4	6.7%
Trichoderma	2	3.3%
Other (1 case each)	11	18.4%

The largest group of isolates in our dataset originated from fruit-based products, including both beverages (e.g., juices, flavored drinks) and solid fruit-derived items such as mousses, jams, purées and jelly-based confectionery (Table 2).

Table 2. Distribution of mold isolates according to food category of origin.

Source	Number of cases	% of all isolations (n=60)
Fruit-based beverages (juices, drinks)	21	35%
Fruit-based solids (mousses, jams, purées, jelly beans)	9	15%
Flour and flour-based products	9	15%
Meat and meat products	6	10%
Dairy products and production environment	4	6.7%
Coffee and tea	2	3.3%
Bread	2	3.3%
Other	7	11.7%

According to the literature, fruit-based products with high sugar content and reduced water activity tend to favor the growth of xerophilic species of Aspergillus and Penicillium [Miliordos et al., 2025; Gündüz et al., 2020]. In dried fruits and other high-sugar matrices, the mycobiota is typically dominated by xerophilic molds from these genera, although the exact species composition varies depending on the fruit type, geographical origin and conditions of drying and storage [Miliordos et al., 2025]. In our dataset, several isolates belonging to Penicillium sp. and Aspergillus sp. were recovered from fruit-based products, which is consistent with their documented ability to colonize low-aw, sugar-rich environments. Citrus products, including fresh oranges, are often associated with species of Alternaria, Colletotrichum and Penicillium, even in asymptomatic fruits [Rovetto et al., 2023]. The presence of molds in raw materials lacking visible defects highlights the importance of monitoring the entire production chain. All isolates included in this study are listed in Table 3.

Another group of isolates in our dataset originated from cereal- and flour-based products. According to the literature, molds most frequently associated with grains and flours include species of Fusarium, Penicillium, Aspergillus and Alternaria, which are considered important contaminants in these matrices [Deligeorgakis et al., 2023]. In our collection, isolates belonging to Penicillium and Aspergillus were recovered from flour-based products, in line with the documented occurrence of these genera in stored cereals and milling environments. Literature reports further indicate that species capable of tolerating low water activity and preservative agents such as Aspergillus pseudoglaucus and Penicillium roqueforti may persist despite thermal or chemical treatments commonly applied in bakery systems [Garcia et al., 2019a; Garcia et al., 2019b; Vytrasová et al., 2002; dos Santos, 2016; Morassi et al., 2018]. Such findings help explain recurring spoilage issues in high-sugar and flour-rich products, even when preservation measures are in place.

Dairy products constituted another category from which fungal isolates were recovered. According to the literature, the mycobiota of dairy environments is typically dominated by species of Penicillium, Mucor and Cladosporium, along with several Aspergillus species [Garnier et al., 2017; Pitt and Hocking, 2009]. In our dataset, isolates obtained from dairy matrices included Mucor nidicola (KKP 4069), Mucor circinelloides (KKP 4091) and Paecilomyces

Table 3. Mold isolates from food samples collected between 2019 and 2024.

No	Mold	KKP Accession Number	Source of isolation
1	*Fusarium sporotrichum*	3059	sugar beet juice
2	*Penicillium* sp.	3365	pasta salad with mozzarella and basil sauce
3	*Alternaria alternata*	3368	water with collagen
4	*Cadophora malorum*	3423	water with collagen
5	*Penicillium* sp.	3526	Tortilla
6	*Aspergillus niger*	3557	hot dog bun
7	*Dothiora*	3562	Flour
8	*Cladosporium* sp.	3564	Flour
9	*Penicillium* sp.	3609	Juice
10	*Aspergillus* sp.	3625	green coffee
11	*Lichtheimia corymbifera*	3665	green coffee
12	*Paecilomyces niveus*	3725	cream cheese
13	*Monascus* sp.	3727	apple juice
14	*Alternaria infectoria*	3728	apple juice
15	*Paecilomyces niveus*	3733	apple juice
16	*Paecilomyces variotii*	3775	fruit mousse
17	*Cladosporium* sp.	3783	apple juice
18	*Fusarium sambucinum*	3786	apple juice
19	*Alternaria* sp.	3794	apple juice
20	*Penicillium* sp.	3804	isotonic drink
21	*Xeromyces bisporus*	3865	fruit jelly beans
22	*Didymella* sp.	3875	Beverage
23	*Trichoderma* sp.	3883	Beverage
24	*Penicillium* sp.	3884	Beverage
25	*Penicillium* sp.	3885	apple-seabuckthorn juice
26	*Penicillium corylophilum*	3886	Beverage
27	*Trichoderma* sp.	3926	Beverage
28	*Talaromyces* sp.	3927	Beverage
29	*Aspergillus* sp.	3946	jelly beans
30	*Penicillium* sp.	3947	jelly beans
31	*Cytospora* sp.	3951	apple juice
32	*Schizophyllum commune*	3952	apple juice
33	*Petriella* sp.	3958	apple drink
34	*Aspergillus* sp.	3960	Beverage
35	*Penicillium aeneum*	3965	tomato paste
36	*Penicillium* sp.	3966	jelly beans
37	*Aureobasidium pullulans*	3972	haskap berry
38	*Didymella* sp.	3973	Beverage
39	*Aspergillus flavus*	3974	Beverage
40	*Didymella* sp.	3977	Beverage
41	*Chaetomium* sp.	3978	Beverage
42	*Rhizopus stolonifer*	4030	Beverage
43	*Aspergillus brasiliensis*	4036	black berry
44	*Fusarium* sp.	4052	fruit juice
45	*Cytospora pruinosa*	4053	apple juice
46	*Aspergillus turcosus*	4062	bottled water
47	*Mucor nidicola*	4069	food- milk products
48	*Mucor circinelloides*	4091	dairy production environment
49	*Aspergillus* sp.	4110	Flour
50	*Penicillium buchwaldii*	4111	Flour
51	*Aspergillus jensenii*	4112	Flour
52	*Mucor circinelloides*	4113	rye bread
53	*Hyphopichia burtonii*	4119	wheat flour
54	*Mucor racemosus*	4122	Sausage
55	*Penicillium expansum*	4125	Sausage
56	*Penicillium glabrum*	4126	Sausage
57	*Penicillium* sp.	4129	Chorizo
58	*Penicillium polonicum*	4133	Meat
59	*Penicillium expansum*	4164	Raspberries
60	*Talaromyces trachyspermus*	4172	frozen strawberries

niveus (KKP 3725). As previously reported, Mucor species are well known as common spoilage molds in dairy systems [Garnier et al., 2017], while the occurrence of Paecilomyces in dairy products has also been documented [Souza et al., 2022]. These findings indicate that both typical dairy-associated molds and less frequently reported species may be present in such products, underscoring the importance of monitoring fungal contaminants in the context of food quality and safety. Literature sources further note that certain molds are capable of surviving pasteurization or entering the product through post-processing contamination, which may explain their detection in heat-treated samples.

The isolates obtained from meat and meat-derived products in our dataset included Mucor racemosus (KKP 4122), Penicillium expansum (KKP 4125), Penicillium glabrum (KKP 4126), Penicillium sp. (KKP 4129) and Penicillium polonicum (KKP 4133). Literature reports indicate that airborne contamination in processing environments is the primary source of mold spoilage in meat products, with Penicillium and Aspergillus frequently cited as key genera involved [Battilani et al., 2007; Sørensen et al., 2008; Parussolo et al., 2019; Bernardi, 2019]. Our observations are consistent with these findings in terms of the prominence of Penicillium, while the absence of Aspergillus in our subset likely reflects the limited number of meat-associated samples analyzed.

Particularly noteworthy within our collection are isolates representing extreme fungi, including xerophilic and xerotolerant species. An example is Xeromyces bisporus (KKP 3865), recovered from fruit jelly confectionery. According to the literature, this species exhibits the lowest known water activity level permitting fungal growth (aw 0.61–0.62), and its ascospores display pronounced heat resistance [Pitt and Christian, 1968; Hocking and Pitt, 1999; Grant, 2004; Leong et al., 2011, 2015; Williams and Hallsworth, 2009; Hocking, 2001]. The detection of X. bisporus in our dataset aligns with previous reports identifying dried fruits, spices and other very low–water-activity products as common sources of contamination [Pitt and Hocking, 2009; Leong et al., 2011].

Overall, our results illustrate the wide taxonomic diversity of molds that may be encountered in different food matrices. As documented in previous studies, both the richness and composition of the food mycobiota are strongly influenced by matrix characteristics such as water activity, sugar content and processing or storage conditions. The patterns observed in our set of isolates are consistent with these established trends reported in the literature.

CONCLUSIONS

This study provides a curated overview of 60 representative mold strains isolated from spoiled food products in Poland between 2019 and 2024 and subsequently deposited in the Collection of Industrial Microorganisms (KKP). The isolates encompassed a broad taxonomic range, including both commonly reported food-spoilage genera such as Penicillium, Aspergillus, Mucor, and Alternaria, as well as several less frequently encountered taxa. Their occurrence across diverse food categories, including fruit-based products, cereal-derived items, dairy products and meat, reflects the heterogeneous nature of fungal contamination in food systems.

The presence of xerophilic and other physiologically resilient fungi, such as Xeromyces bisporus and Paecilomyces niveus, highlights the capacity of certain molds to persist in environments characterized by low water activity or other restrictive conditions. These findings underscore the importance of maintaining comprehensive reference collections that preserve taxonomically diverse strains relevant to food spoilage.

By documenting the diversity and origins of these isolates, this work expands the available resources for future studies on fungal ecology, spoilage mechanisms and contamination pathways in food environments. The strains deposited in the KKP collection constitute a valuable foundation for further research, including physiological characterization, risk assessment, development of detection methods and evaluation of antifungal strategies.

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