

SANITARY AND HYGIENIC APPROACHES TO FUNGAL CONTAMINATION ASSESSMENT IN LIVESTOCK PRODUCTION FACILITIES

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Intensification of livestock farming creates conditions for the accumulation and circulation of pathogenic and opportunistic fungi with the development of antifungal resistance. The study aimed to perform comprehensive assessment of fungal contamination of production environment in various areas of livestock farms and determine sensitivity of the extracted isolates to common antifungal agent. The presence of fungal contamination in the air of all working areas of the studied production facility was established. Predominance of *Aspergillus niger* and *Candida albicans* was revealed. In 50% of cases, mixed contamination with different types of mold fungi was observed. The highest contamination levels were reported for the bedding material. Resistance of microorganisms to several antifungal drugs with different mechanisms of action at once has been revealed. The study confirmed systemic contamination of the livestock complex production environment with potentially pathogenic fungi forming stable communities in feed and bedding. The reported sanitary and microbiological approaches to assessing fungal contamination at livestock production facilities have a pronounced comprehensive preventive focus, which makes it possible to improve the farm employees' working conditions, as well as provide measures to improve the livestock complex production environment.

Keywords: livestock production, production environment, antifungals, yeast-like fungi isolates, sensitivity, working area

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САНИТАРНО-ГИГИЕНИЧЕСКИЕ ПОДХОДЫ К ОЦЕНКЕ ГРИБКОВОЙ КОНТАМИНАЦИИ НА ПРОИЗВОДСТВЕННЫХ ОБЪЕКТАХ ЖИВОТНОВОДСТВА

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Интенсификация животноводства создает условия для накопления и циркуляции патогенных и условно-патогенных грибов с формированием антимикотической резистентности. Целью исследования было выполнить комплексную оценку уровня грибковой контаминации производственной среды в различных зонах животноводческих предприятий с определением чувствительности выделенных изолятов к распространенным антимикотикам. Установлено наличие грибковой обсемененности в воздухе всех рабочих зон изученного предприятия. Выявлено доминирование *Aspergillus niger* и *Candida albicans*. В 50% случаев отмечена смешанная контаминация разными видами плесневых грибов. Наибольший уровень загрязнения выявлен в подстилочном материале. Выявлена устойчивость микроорганизмов одновременно к нескольким антимикотическим препаратам, имеющим различные механизмы действия. Исследование подтвердило системное загрязнение производственной среды животноводческих комплексов потенциально-патогенными грибами с формированием устойчивых сообществ в кормах и подстилке. Представленные в работе санитарно-микробиологические подходы оценки грибковой контаминации на производственных объектах животноводства имеют выраженную комплексную профилактическую направленность, позволяющую улучшить условия труда работников ферм, а также организовать мероприятия по оздоровлению производственной среды животноводческого комплекса.

Ключевые слова: животноводство, производственная среда, антимикотики, изоляты дрожжеподобных грибов, чувствительность, рабочая зона

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Intensification of livestock farming characterized by a high concentration of livestock in a limited space creates specific environmental conditions that promote the accumulation and circulation of various microorganisms [1, 2]. Among these fungi of are particular importance, which can not only

cause mycoses in animals, reducing productivity and leading to economic losses, but also act as sources of allergens and mycotoxins, thereby creating occupational and environmental risk for personnel [3, 4]. Contamination of livestock environments with molds and yeast-like fungi sets the stage for deterioration

of product sanitary and hygienic indicators and stable circulation of opportunistic species in the closed system of the production facility [5].

Air in the working area, surfaces of equipment and constructs, feed and bedding material represent the key reservoirs and vectors of mycobiota transmission in livestock complexes. The air environment is the main route of spore dissemination, while contaminated feed and bedding provide direct entry of micromycetes into the gastrointestinal tract and constant animal skin contamination [6, 7]. The difficulty of controlling fungal contamination is compounded by the formation of disinfectant-resistant biofilms on surfaces and the widespread use of antifungal drugs, which contribute to the resistant strain selection [8, 9].

Despite the relevance of the issue, comprehensive studies that simultaneously assess the contamination of various ecological niches (air, surfaces, feed, bedding) in livestock production facilities and provide phenotypic characteristics of the extracted fungal isolates remain underrepresented in the scientific literature. Such a systematic approach is necessary for the development of effective sanitary and preventive measures, as well as guidelines on mycological safety monitoring.

The study aimed to perform comprehensive assessment of fungal contamination of the air and surfaces in various production areas of livestock farms and to characterize the isolated yeast-like fungi based on sensitivity to common antifungal agents.

METHODS

The study was conducted at several typical livestock farms in the Republic of Bashkortostan, specializing in dairy and beef cattle breeding.

Samples were collected in the main technological zones: premises for fattening cattle, calf houses, sections for keeping young animals, heifers and bulls, as well as in milking parlors and settling tanks. To monitor the indicators, administrative premises and the canteen were inspected.

The entire research cycle, from the procedures for collecting, transporting and storing samples to the laboratory stages of sowing, culturing, identifying fungal isolates and determining their sensitivity to antifungal drugs, was carried out in accordance with the current legislation.

Monitoring was carried out in a wide range of production areas, differing in key technological parameters: livestock density, age and sex groups of animals, diet specifics, and production purposes. Collection of samples for analysis was synchronized with the key technological cycles (distribution of feed, manure removal, loading and unloading of feed, etc.) to estimate actual operational contamination.

Air contamination was assessed by the open sedimentation method (Petri dishes with growth media: meat peptone agar, Endo agar, egg-yolk agar, blood agar, Enterococci agar, and Sabouraud agar (SRCAMB; Russia)) and aspiration methods involving the use of the microbiological sampler. Sampling was carried out at a height of 1.5 m from the floor in the central part of the room and in high-risk areas (at feed tables, manure aisles) with exposure time between 10 and 30 min.

Swab and swab blots were collected from the standard area (100 cm²) from the technological equipment (drinkers, feeders), fence elements, walls, floors and ventilation grilles using sterile tampons soaked in saline or peptone solution.

The "envelope" method was used to obtain a representative average sample of bulky and silage feeds. Single samples (8–10 units) were collected from different points within the test volume, including peripheral and central areas, as well as from

the upper, middle, and lower horizons. During sampling the 30–50 cm thick surface layer was previously removed from the silage and haylage to exclude the degraded mass. All single samples were combined in a sterile container, thoroughly homogenized to form an average laboratory sample. The number of feed samples ($n = 9$) was determined by the number of production zones allocated at the production facility in accordance with the technological regulations. Such a sample size ensured the coverage of all the main technological groups of animals and made it possible to conduct comparative assessment of contamination levels in different zones.

The bedding material (bedding) samples were collected in sterile hermetic containers using sterile instruments. The sampling scheme provided for sampling along the diagonal of the room from six points. At each point, material was collected after removing the top layer from the working depth of 5–10 cm characterized by maximum microbiological activity. A portion weighing about 100–200 g was taken from each point, after which all portions were combined into one common sterile container to form a combined sample. The number of bedding samples ($n = 7$) was determined by the number of sections in the production building that met all the inclusion criteria at once (identical maintenance conditions, operation term, physiological group of animals). The collection was carried out within one technological cycle of keeping, which excluded the time factor as an additional variable. Such a sample size enabled statistical analysis of the bedding mycobiota variability within homogeneous production environment. Exclusion criteria: areas with visible areas of moisture, mold or local disinfection (within less than 24 h).

Containers with samples were placed in a refrigerator bag; the time of delivery to the laboratory did not exceed 6 h from the time of sample collection.

To isolate and identify yeasts of the genus *Candida*, inoculation of the following microbiological media with the test material was performed: Sabouraud agar (SRCAMB; Russia), Sabouraud agar with glucose and chloramphenicol (HiMedia; India), Sabouraud agar with maltose (SRCAMB; Russia), and chromogenic agar (HiMedia; India) for yeast and mold. The yeast enzyme activity was determined in the media with the 1% peptone water and an indicator (Andrade, bromothymol blue (SRCAMB; Russia)) by the generally accepted methods. Culturing complied with the required conditions: dishes with cultures of yeast-like fungi was incubated at a temperature of 28 ± 2 °C for 48–72 h. Microbiological testing of mold fungi was performed using the growth medium No. 2 FPH (Sabouraud) (SRCAMB; Russia), chromogenic agar (HiMedia; India) for yeast and mold fungi at 25 °C. Culturing was performed for 5–7 years with the daily monitoring. The incubation time for slow-growing fungi was extended to 10 days. Identification was performed using identification guides for microscopic fungi by assessing morphology, shape, size, and the presence of characteristic structures.

To control the correctness of the yeast-like fungi (genus *Candida*) and mold fungi (genus *Aspergillus*) identification, reference strains from the State Collection of Pathogenic Microorganisms (SCPM) were used: *Candida albicans* ATCC 10231 и *Aspergillus niger* ATCC 16404. The proportion of confirmed isolates was at least 10% of the total number of isolated cultures.

To estimate the potential pathogen significance, the test results with a titer of at least 10^5 CFU/swab were considered.

Antifungal sensitivity testing was performed for all isolated yeast-like fungi of the genus *Candida* of the family *Saccharomycetaceae* from the air and production environment

Table 1. Number of strains of yeast-like fungi of the genus *Candida* isolated from the air and production environment samples at the livestock production facility in the studied period

Family	Genus	Species	Number of <i>Candida</i> strains				
			Air (n = 50)	Swabs (n = 100)	Feed (n = 9)	Bedding (n = 7)	Total (n = 166)
<i>Cryptococcaceae</i>	<i>Candida</i>	<i>C. albicans</i>	10	19	6	5	40
		<i>C. krusei</i>	0	13	3	0	16
		<i>C. glabrata</i>	1	4	2	2	9
Total			11	36	11	7	65

samples. A total of 65 isolates were tested, distributed as shown in Table 1.

To assess yeast sensitivity, the Mueller–Hinton agar (MHA) was used (HiMedia; India): modified, for antifungal sensitivity determination in accordance with the CLSI standard, recommended for diffusion of antifungal agents the paper discs are impregnated with in agar gel, as described in the CLSI standard. The antifungal activity criteria were determined by the disk diffusion method using commercial disks with antifungal agents for *in vitro* sensitivity testing (HiMedia; India). We used an extended panel of disks containing different concentrations of six antifungal drugs (fluconazole, clotrimazole, ketoconazole, nystatin, amphotericin B, itraconazole) measured in µg/disc or U. The results were assessed based on the diameter of the delayed (no) growth of microorganisms around the disks in accordance with the Instructions for Using Discs with Antifungal Drugs (Table 2) and tables from the IACMAC guidelines “Determination of the Sensitivity of Microorganisms to Antimicrobial Drugs” (version 2025-01, section 2: “Disc Diffusion Method to Assess Yeast Sensitivity to Antifungal Drugs”).

The 24-h culture (24 h at 35 ± 2 °C) for used to prepare the inoculum with the turbidity corresponding to the 0.5 McFarland standard for each strain, which corresponded to the cell content (1 × 10⁶–5 × 10⁶ CFU). A total of 1 mL of the resulting suspension was applied to the surface of the growth medium in Petri dishes in three directions. Discs with antifungals were placed onto the agar 15 min after inoculation.

The dishes were incubated at 35 ± 2 °C in the usual atmosphere for *C. albicans* and in the 5% CO₂ atmosphere for *C. krusei* and *C. glabrata*. The results were considered reliable with the almost flush growth of the culture and uniformly round zones of growth inhibition in the cups. If this was not observed after 20–24 h of growing, the results after 48 h were considered. A ruler was used to measure the zones of inhibition. The Petri dishes with the closed lids were placed upside down on a dark matte surface so that the light fell on it at an angle of 45° (counting using reflected light).

The testing quality control at all stages was accomplished in accordance with the IACMAC guidelines “Determination of the Sensitivity of Microorganisms to Antimicrobial Drugs” (version 2025-01). The yeast antifungal sensitivity testing quality

control involved the use of specific reference strains obtain from commercial sources (SRCAMB) that were recommended in accordance with the CLSI standard: *C. albicans* ATCC 10231, *C. albicans* ATCC 24433. Reference strains were included in each testing series. Inoculation and reference cultures and test isolates was performed under the same condition using the same batches of growth media. The series of tests was considered valid, when the diameters of the zones of inhibition for reference strains corresponded to the ranges determined by the disc manufacturer (Table 3). When the values were beyond the reference range limits, the series results were not taken into account, and the analysis was repeated.

When using the disc diffusion method for the *C. albicans* ATCC 10231 culture, the diameter of the zone of inhibition was as follows: amphotericin B — 15.9 ± 1.7 mm, nystatin — 19.6 ± 2.6 mm, clotrimazole — 15.5 ± 1.7 mm, ketoconazole — 19.6 ± 1.3 mm, itraconazole — 19.6 ± 1.2 mm, fluconazole — 32.7 ± 3.7 mm. As for the *C. albicans* ATCC 24433 culture, the zones of inhibition were as follows: amphotericin B — 14.8 ± 1.6 mm, nystatin — 20.9 ± 1.4 mm, clotrimazole — 22.2 ± 3.3 mm, ketoconazole — 24.4 ± 3.8 mm, itraconazole — 18.9 ± 0.9 mm, fluconazole — 32.1 ± 3.3 mm. The values obtained correspond to reference ranges for the reference strain, thereby confirming the experiment validity.

Statistical data processing was performed using the Statistica 10.0 software package (StatSoft; USA) and Microsoft Excel (Microsoft; USA). Significance of the associations between categorical variables (fungal species, object type, resistance level) was assessed using the Pearson’s chi-squared test (χ²) for contingency tables. The two-tailed Fischer’s exact test was used in cases of violation of the assumption of sufficient expected frequencies (when more than 20% of the cells had the expected frequency < 5, or at least one cell had E < 1).

RESULTS

The microbiota of the air in the working area of the premises is represented by two major groups: yeast-like and mold fungi (Fig. 1).

Microbiological testing of the samples collected from different premises of the working area showed that the mycobiota

Table 2. Zones of inhibition of the growth of yeast-like fungi cultures by antifungal drugs

Antifungal agents in the disk	Content in the disk	Diameter of the zones of inhibition, mm		
		resistant	intermediate (sensitivity depends on the dose)	sensitive
Amphotericin B	100 U	< 18	–	≥ 18
Nystatin	100 U	< 25	–	≥ 25
Clotrimazole	10 µg	< 18	–	≥ 18
Ketoconazole	10 µg	< 22	–	≥ 22
Itraconazole	10 µg	< 22	–	≥ 22
Fluconazole	25 µg	≤ 30	15–18	≥ 30

Table 3. Zones of inhibition (mm) by antifungals for reference strains

Antifungal	Symbol	Содержание в диске	Zone diameter (mm)			Control strains	
			R or less	S-DD*	S or more	<i>C.albicans</i> ATCC 10231	<i>C.albicans</i> ATCC 24433
Amphotericin B	AP	100 U	–	–	–	10–18	10–17
Nystatin	NS	100 U	–	–	–	15–23	19–23
Clotrimazole	CC	10 µg	–	–	–	12–18	18–32
Ketoconazole	KT	10 µg	–	–	–	18–22	20–32
Itraconazole	IT	10 µg	–	–	–	18–22	16–20
Fluconazole	FU	25 µg	14	15–18	19	28–39	28–39

Note: the reference ranges are provided in accordance with the instructions of the disk manufacturer (HiMedia; India) and confirmed during the method validation in laboratory settings; * — sensitive dose-dependent.

generic and species composition was almost the same, but the percentage varied depending on the department. The typical representatives of pathogenic and opportunistic mycobiota often detected during screening were as follows: *Aspergillus flavus*, *Aspergillus fumigatus*, *A. niger*, *C. albicans*, *C. krusei*, *C. grabrata*, *Candida tropicalis*. The distribution of the specified microorganisms based the frequency of their detection in the samples, as well as the share in the opportunistic microflora structure were similar in the premises with similar environmental conditions and similar indicators of agrobiocenosis contamination (Fig. 2).

Assessment of the working area swabs showed that mold and fungi represented mainly by *A. niger* and *C. albicans* were present in all working areas of the complex. *A. niger* was most often isolated in the calf house premises (35.7% of cases) and in the section for keeping bulls (24.3%); *C. albicans* was most often isolated in the section for keeping young animals (42.81% of cases) and in the settling tank (45.39% of cases).

In terms of species, among mold fungi together with *A. niger* such mold fungi, as *A. flavus*, *A. fumigatus*, were identified, and *C. krusei*, *C. grabrata*, *C. tropicalis* were isolated together with *C. albicans*. Furthermore, all these fungal species were found in all premises of the working environment, but the percentage was different. Other representatives of fungal microbiota, *Mucor spp.*, *Penicillium spp.*, *Fusarium*, were detected in less than 1% of samples.

The analysis conducted suggests that all the tested feed samples are contaminated with mold and yeast-like fungi. *A. niger* was identified in 90% of samples, while *A. flavus* and *A. fumigatus* were found in 10%. In a half of cases (50% of samples), mixed contamination represented by two species of mold fungi at once was reported.

The most complex microbial cenosis represented by two- and three-component associated was reported for feed samples collected from the premises for keeping young animals, bulls, and the settling tank. Associations of *Pseudomonas aeruginosa*, *Citrobacter freundii*, and *Enterobacter aerogenes* were identified in the samples from the section for keeping young animals. *Escherichia coli*, *Proteus vulgaris*, and *Enterobacter aerogenes* were isolated from feeds from the premises for keeping bulls; *E. coli* and *Citrobacter freundii* were isolated from samples from the settling tank. *E. aerogenes* was also identified in the structure of microorganisms isolated: 20% of samples.

Among all isolated opportunistic microorganisms, mold and yeast-like fungi have the highest relative importance, which may indicate unsatisfactory feed storage and insufficient sanitary processing of the production environment working areas (Fig. 3).

The bedding material fungal microflora is represented by mold fungi: *A. flavus*, *A. fumigatus*, and *A. niger* were isolated from 100% of samples. As for yeast fungi, *C. albicans* was isolated from 100% of samples. *C. krusei* and *C. grabrata* were detected less often. *C. tropicalis* was not detected in any of the bedding material samples (Fig. 4).

The analysis of the rate of the *Candida* yeast-like fungi isolation revealed considerable differences depending on the studied object. The maximum contamination (100%) was reported for feed and bedding material samples. In swabs, the rate was 36%, which was higher compared to air samples, in which the isolation rate was minimal and reached 22%. The determined dependence of the *Candida spp.* Detection rate from the substrate type is significant ($p < 0.001$), which suggests the significantly higher likelihood of detecting fungi in the feed and bedding compared to the air and swabs. All the microorganisms isolated

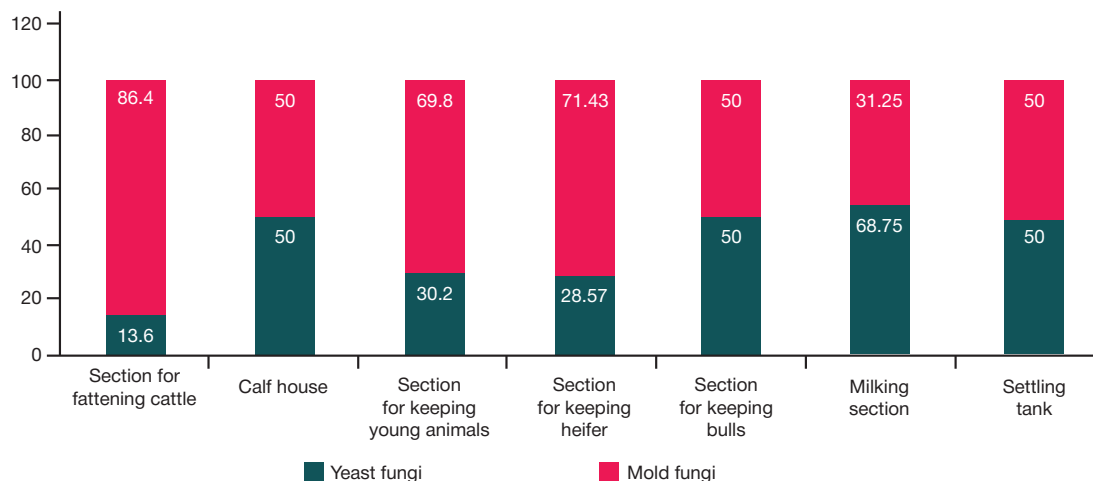


Fig. 1. Mycobiota of the air in the working area of the livestock complex premises (% of isolated samples)

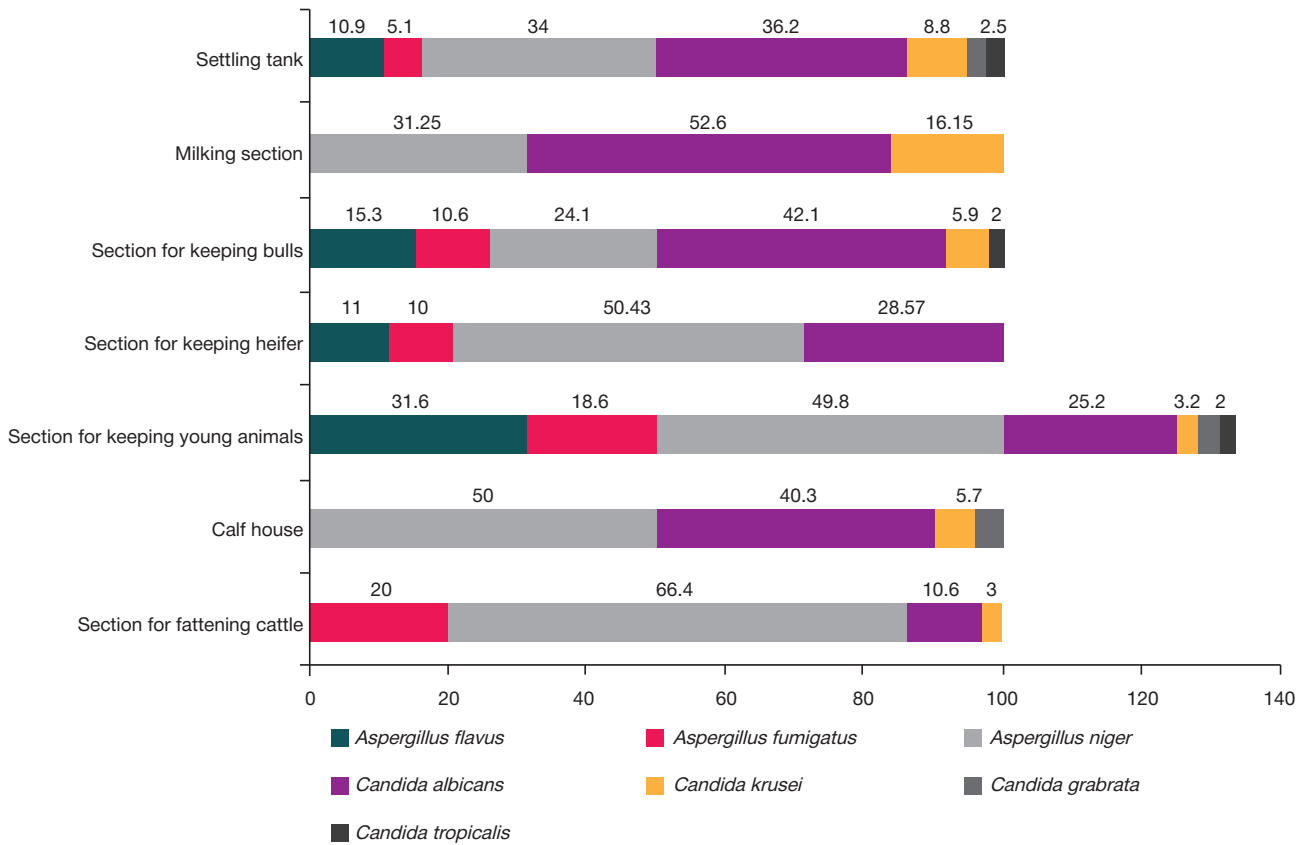


Fig. 2. Content of fungal flora in swabs from the working area (% of isolated samples)

were found in the form of multicomponent associations with other bacterial species.

The analysis of the resistance of 65 isolated strains of *Candida fungi* to six antifungal drugs revealed significant interspecies variability. No significant differences were found when comparing sensitivity of different *Candida* species (A vs. G and K vs. G) (Table 4; $p > 0.05$ in all cases).

The highest *in vitro* efficacy was reported for nystatin and clotrimazole. The share of *C. albicans* sensitive to nystatin was 92.5% (95% CI: 80.1–97.4), to clotrimazole — 87.5%

(95% CI: 73.9–94.5). As for *C. Krusei*, the maximum activity was reported for ketoconazole (93.8%; 95% CI: 71.7–98.9) and nystatin (93.8%; 95% CI: 71.7–98.9).

Fluconazole showed the lowest efficacy: the share of resistant *C. albicans* strains reached 70.0% (sensitivity was only 30.0%; 95% CI: 18.1–45.4). Sensitivity of non-albicans species (*C. krusei* and *C. glabrata*) to fluconazole was also low (56.3 and 55.6%, respectively). High *C. krusei* sensitivity to ketoconazole (93.8%) attracts attention; the value reported for *C. albicans* is 77.5%.

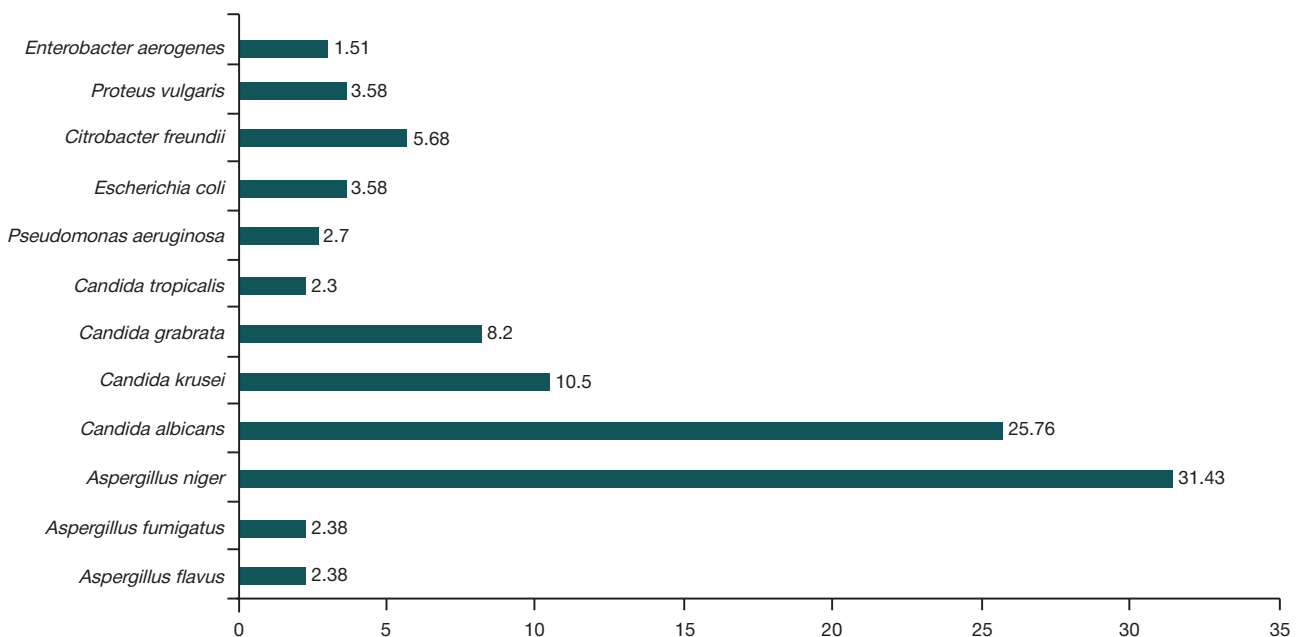


Fig. 3. Typical composition of microbial communities of feeds collected in the livestock complex working areas (% of samples)

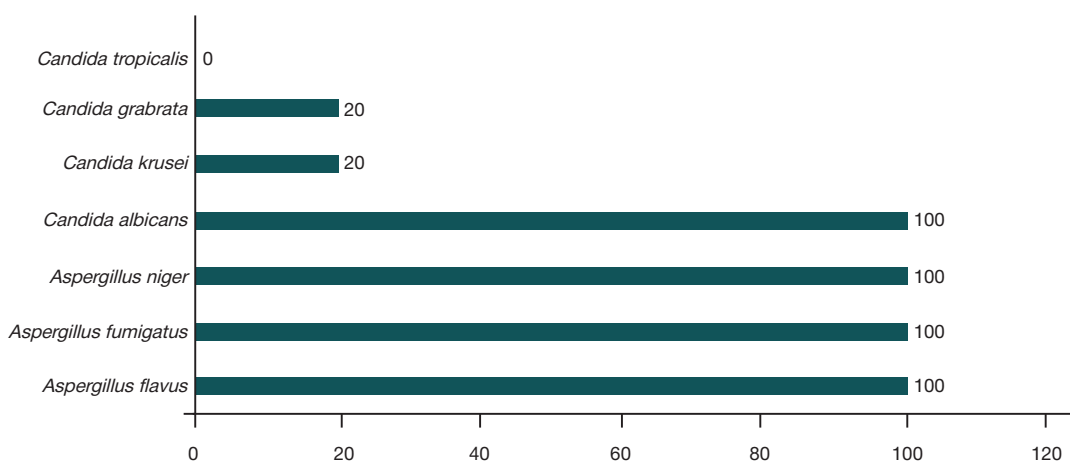


Fig. 4. Species composition of fungal microorganisms isolated from the bedding material in the livestock complex working areas (% of the total number of isolates)

DISCUSSION

Microbiological testing of swabs from the production environment surfaces confirmed fungal contamination of all the complex working areas.

Feeds represent a significant reservoir and vector of microorganism transmission. All the tested feed samples were contaminated with mold and yeast-like fungi. In addition to mycobiota, bacteria *P. aeruginosa*, *C. freundii*, and *E. aerogenes* were identified in feed samples, *E. coli*, *P. vulgaris* were also isolated.

The highest microbial contamination levels are reported for the bedding material, in which the communities are represented by both micromycetes and various Gram-negative bacteria. Among yeast fungi, *C. albicans* was isolated from all samples (100%).

Comparative assessment of the *Candida* yeast-like fungi isolation rate revealed considerable intergroup differences. The feed and bedding material samples were characterized by the 100% contamination. Fungi were more often found in swabs (36%), than in air samples (22%). The differences obtained are highly significant ($p < 0.001$), which suggests the priority role of feeds and the bedding material as a reservoir of *Candida* spp. compared to the air environment objects and swabs.

The findings confirm natural resistance of *C. krusei* to fluconazole (sensitivity is 56.3%, that is considered a relatively high indicator for this species against the background of the literature data) and low sensitivity of *C. albicans* to this azole (30.0%), which can indicate selection of resistant strains in the population. The lack of significant differences between species ($p > 0.05$) is likely to result from the small size of the *C. glabrata* ($n = 9$) and *C. krusei* ($n = 16$) samples.

Table 4. Sensitivity of *Candida* spp. clinical isolates to antifungal drugs, % (abs.) [95% CI]

Drug	<i>C. albicans</i> ($n = 40$)	<i>C. krusei</i> ($n = 16$)	<i>C. glabrata</i> ($n = 9$)	p (A vs. G)	p (K vs. G)
Amphotericin B (AP)	75.0 (30) [59.8–85.8]	68.8 (11) [44.4–85.8]	77.8 (7) [45.3–93.7]	1.000*	0.683*
Nystatin (NS)	92.5 (37) [80.1–97.4]	93.8 (15) [71.7–98.9]	77.8 (7) [45.3–93.7]	0.199*	0.245*
Clotrimazole (CC)	87.5 (35) [73.9–94.5]	81.3 (13) [56.9–93.4]	77.8 (7) [45.3–93.7]	0.598*	1.000*
Ketoconazole (KT)	77.5 (31) [62.5–87.7]	93.8 (15) [71.7–98.9]	77.8 (7) [45.3–93.7]	1.000*	0.267*
Itraconazole (IT)	60.0 (24) [44.6–73.7]	37.5 (6) [18.5–61.4]	55.6 (5) [26.7–81.1]	1.000*	0.433*
Fluconazole (FU)	30.0 (12) [18.1–45.4]	56.3 (9) [33.2–76.9]	55.6 (5) [26.7–81.1]	0.242*	1.000*

Note: n — number of strains tested; the percentage of sensitive strains is specified in the cells, absolute numbers are specified in parenthesis, 95% confidence intervals are specified in square brackets; p (A vs. G) — comparison of *C. albicans* and *C. glabrata*; p (K vs. G) — comparison of *C. krusei* and *C. glabrata*; * — non-significant differences ($p > 0.05$).

The literature data in the *C. krusei* itraconazole sensitivity are controversial and demonstrate significant inter-strain variability: from the high *in vitro* activity to the complete resistance. This suggests that there is no species-specific susceptibility [10–12].

The *C. glabrata* fluconazole resistance is multifactorial, it is realized through overexpression of efflux pumps (resulting from the PDR1 mutations) and mutation on the *ERG11* target gene. Active elimination of the drug from the cell is the leading mechanism, and the *ERG11* alteration increases resistance. This determines the frequent lack of clinical response to fluconazole and requires prescription of echinocandins [13–15].

CONCLUSIONS

The results obtained demonstrate systemic contamination of the livestock complex production environment with potentially pathogenic fungi with the formation of stable microbial communities in key facilities (feeds, bedding). The determined multi-resistance of the circulating strains of yeast-like fungi to common antifungals (resistance to more than four drugs) suggests the need to develop specialized control measures.

The yeast antifungal sensitivity in the context of CLSI standards is the ability of microorganisms to inhibit visible growth under certain test conditions *in vitro*. The determined resistance to the azole class of drugs necessitates exclusion of those from preventive regimens for livestock farming in order to avoid the decrease in antifungal measure efficacy. Polyene group drugs and echinocandins can be offered as alternative antifungal drugs.

Considering the potentially reversible nature of the yeast resistance to antifungals and the positive experience of rotation of agents in adjacent areas, strategy of sequential change

of antifungal drugs so overcome the resistance of *Candida spp.* in candidiasis seems justified.

The reported sanitary and microbiological approaches to assessment of fungal contamination in livestock production

facilities have a pronounced complex preventive orientation, allowing one to improve the working conditions of farm workers, as well as organize measures to improve the livestock complex production environment.

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