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Bacteria recovered from ear swab samples of cats with otitis externa and their antimicrobial resistance profiles in Kayseri, Türkiye

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Abstract: This study aimed to isolate and identify bacteria from ear swab samples taken from cats with otitis externa and to determine the antimicrobial resistance profiles of the recovered isolates. For this purpose, ear swab samples from 100 domestic cats diagnosed with otitis externa were used. The samples collected from the animals were inoculated onto 7% defibrinated sheep blood agar and MacConkey agar, and the media were incubated at 37 °C for 24–72 h under aerobic/microaerobic conditions. The identification of the isolates was conducted by phenotypic tests, MALDI-TOF MS analysis, and 16S rRNA gene sequencing. Antimicrobial susceptibilities of the obtained isolates were determined via the disk diffusion method. Seventy-one samples were found to be positive for bacterial growth, and 75 isolates (2 isolates from 4 samples) were obtained. The most commonly identified genera were *Staphylococcus* (33.3%), *Enterococcus* (20%), and *Bacillus* (13.3%), while the most commonly identified species were *Enterococcus faecalis* (10.7%), *Staphylococcus felis* (8%), and *Staphylococcus epidermidis* (8%). The highest antimicrobial resistance among staphylococci isolates was observed against penicillin (48%) and trimethoprim/sulfamethoxazole (48%). All enterococci isolates were resistant to gentamicin, ciprofloxacin, clindamycin, penicillin, and trimethoprim/sulfamethoxazole. In addition, the multidrug resistance rates in the staphylococci and streptococci isolates were detected as 44% and 100%, respectively. In conclusion of the current study, in samples from cats with otitis externa, staphylococci and enterococci are obtained to be the dominant etiological agents, and these organisms exhibited high resistance rates to commonly used antimicrobials. Given the public health implications of these findings, the results obtained may be useful in the selection of drugs to be used in treatment.

Key words: 16S rRNA gene sequencing, antimicrobial resistance, cat otitis externa, cultural examination, identification

1. Introduction

Feline otitis externa (OE) is a condition of the external auditory canal in domestic and stray animals caused by multiple factors [1,2]. The main clinical symptoms consist of swelling, fibrosis, and calcification of the aural canal/pinna, as well as discomfort, pawing, intense pruritus, variable pain upon palpation of the aural region, and a foul odor, etc. [3,4]. The prognosis of the disease varies, and treatment may involve medication or surgery. On the other hand, a long-term protocol of the treatment may be required for cases that are refractory and tend to recur [3].

Primary factors of OE include congenital anatomical disorders, allergic reactions, foreign bodies, local trauma, autoimmune/immune-mediated diseases, endocrine/glandular disorders, etc. Secondary factors are microorganisms, including several bacteria and/or yeasts [3,5,6]. Although OE is a multifactorial disease, bacteria play a significant role in its etiology. Isolating and identifying the causative bacteria is crucial for determining an effective treatment protocol [7-9]. Cultural examinations of feline OE cases reveal a range of bacterial agents, with *Staphylococcus* spp., *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Escherichia coli*, and *Corynebacterium* spp. being the most frequently identified [5,10,11]. The most commonly identified gram-positive cocci are staphylococci species, but enterococci and streptococci species are also detected. Among gram-negative rods, multidrug-resistant *P. aeruginosa* and members of the *Enterobacteriaceae* are especially notable [7,11].

Antimicrobial treatment is important in the therapies of the feline OE cases caused by various bacteria. However, antimicrobial resistance (AMR) poses a major global threat to both animal and human health [12,13]. The presence of resistant isolates—particularly *Staphylococcus*

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spp. and *P. aeruginosa*—in feline OE can significantly complicate treatment efforts [3,7]. Therefore, conducting antimicrobial susceptibility testing is crucial for understanding resistance profiles and selecting effective therapeutic options [3,14].

In this study, we aimed to isolate and identify bacteria from ear swab samples from 100 domestic cats with OE and to characterize the antimicrobial resistance profiles of the recovered isolates.

2. Materials and methods

2.1. Ear swab samples and processing

One hundred ear swab samples collected from domestic cats that were brought to five different pet clinics in Kayseri, Türkiye, and the Erciyes University, Faculty of Veterinary Medicine, Department of Surgery, and were diagnosed with OE following clinical examinations of the ear pinnae and canals using an otoscope. The samples were transported to the Erciyes University, Faculty of Veterinary Medicine Microbiology Laboratory under cold chain conditions for the cultural examination and analyzed within one hour.

The ear swab samples collected were directly plated onto 7% defibrinated sheep blood agar (Neogen NCM2013A, USA) and MacConkey agar (Neogen NCM0017A, USA), and the media were incubated at 37 °C for 24–72 h under aerobic/microaerobic (MGC AnaeroPack-MicroAero, GB-255AE, Japan) conditions. The colonies grown on the media were evaluated for macroscopic/microscopic features, and biochemical tests, including colony morphology, hemolytic activity, Gram staining, motility, oxidase, catalase, coagulase, H_2S production, and oxidation-fermentation (O/F) tests were performed. Based on phenotypic tests, the isolates were defined at the genus level, and pure cultures were obtained for species-level identification and antimicrobial susceptibility testing.

2.2. Identification of the recovered isolates

2.2.1. Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS)

This method was used to identify isolates at the species level. Whole-cell samples for MALDI-TOF MS analysis were prepared as Dieckmann et al. [15] previously described. An Ultraflex II MALDI-TOF/TOF mass spectrometer (Bruker Daltonics, USA) equipped with an all-solid-state SmartBeamTM laser (Nd: YAG laser), operating at 100 Hz in the positive linear mode (100 ns, 25 kV, and 2.2–20 kDa) under control of the Flex Control software version 3.0 (Bruker Daltonics), was used to detect mass spectra. According to the manufacturer's criteria, scores ≥2.00, 1.70–1.99, and <1.70 indicated correct species identification, low consistency, and no consistency, respectively [16].

2.2.2. DNA extraction

The DNA isolation process from the isolates for use in molecular analysis was done with the classical single-cell lysis buffer protocol [17].

2.2.3. 16S rRNA gene sequencing

Isolates not identified at the genus/species level with MALDI-TOF MS were confirmed using 16S rRNA gene sequencing, as previously described by Lane [18]. In the amplification and sequence analysis, the universal 27F (AGAGTTTGATCMTGGCTCAG) and 1492R (GGTTACCTTGTTACGACTT) primers were used. A band of 1465 bp amplicon was expected. Chromatograms were evaluated using Finch TV (version V1.4), and sequences were aligned and compared with Rrna/ITS database of the National Center for Biotechnology Information using the Basic Local Alignment Search Tool. Sequences were deposited in the National Institutes of Health GenBank, following the necessary procedures.

2.3. Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was carried out via the disk diffusion method [19]. In the test, ampicillin (AM, 10 µg), amoxicillin/clavulanic acid (AMC, 30 µg), ciprofloxacin (CIP, 10 µg), clindamycin (DA, 2µg), erythromycin (E, 15 µg), gentamicin (CN, 10 µg), penicillin (P, 10 µg), tetracycline (TE, 30 µg), trimethoprim/sulfamethoxazole (SXT, 25 µg) and vancomycin (VA, 30 µg) (Bioanalyse, Türkiye) antimicrobial disks were used. A 0.5 McFarland suspension was prepared from the isolates' pure cultures, and 100 µL was inoculated onto 7% sheep blood agar. The discs were placed with sterile forceps, and the media were incubated aerobically at 37 °C for 24–48 h. Inhibition zone diameters (mm) were interpreted following the European Committee on Antimicrobial Susceptibility Testing (EUCAST)[1] guidelines. Isolates resistant to three or more different antimicrobials (≥3) were classified as multidrug-resistant (MDR) [11]. As the quality control strains, *S. aureus* ATCC 25923 and *E. coli* ATCC 25922 were used.

3. Results

Seventy-one samples showed bacterial growth, and 75 isolates (2 isolates from 4 samples) were obtained. Based on phenotypic tests, 63 and 12 isolates were classified as gram-positive and gram-negative, respectively. MALDI-TOF MS analysis identified 64 isolates at the species level and one of the genus levels (*Exiguobacterium* spp.); ten could not be identified. In the MALDI-TOF MS analysis, 64 of 75 isolates were defined at the species level and one at the genus level (*Exiguobacterium* spp.), while 10 isolates could not be identified. The confirmation of the eleven isolates was performed by 16S rRNA gene sequencing. The sequence data of the isolates (n = 11) were deposited

[1] EUCAST (2025). Website https://www.eucast.org/ [accessed 15 Feb 2025].

in GenBank under accession numbers from PV104452 to PV104462. Nine isolates were confirmed at the species level; *Staphylococcus lentus* (n = 2), *S. pseudintermedius* (n = 1), *S. sciuri* (n = 1), *Jeotgalicoccus nanhaiensis* (*J. nanhaiensis*) (n = 1), *Corynebacterium stationis* (*C. stationis*) (n = 1), *Bacillus amyloliquefaciens* (*B. amyloliquefaciens*) (n = 1), *Exiguobacterium artemiae* (*E. artemiae*) (n = 1), and *Dermabacter hominis* (*D. hominis*) (n = 1). The remaining two isolates were defined as *Bacillus* spp. at the genus level.

Of the 75 isolates obtained in the study, 50 belonged to the genera *Staphylococcus* (25/75, 33.3%), *Enterococcus* (15/75, 20%), and *Bacillus* (10/75, 13.3%), respectively. The remaining 25 isolates belonged to 15 different genera. The number of isolates included in these genera was 4 *Pseudomonas*, 4 *Micrococcus*, 3 *Escherichia*, 2 *Proteus*, 2 *Streptococcus*, 1 *Jeotgalicoccus*, 1 *Aerococcus*, 1 *Paenibacillus*, 1 *Corynebacterium*, 1 *Actinomyces*, 1 *Dermabacter*, 1 *Exiguobacterium*, 1 *Acinetobacter*, 1 *Klebsiella*, and 1 *Moraxella*, respectively (Figure).

Enterococcus faecalis (8), *S. felis* (6), *S. epidermidis* (6), *S. pseudintermedius* (5), and *E. faecium* (5) were the most commonly identified species. Other species detected were *S. hominis* (2), *S. simulans* (2), *S. lentus* (2), *S. haemolyticus* (1), *S. sciuri* (1), *E. hirae* (2), *Bacillus oceanisediminis* (*B. oceanisediminis*) (4), *B. licheniformis* (2), *B. amyloliquefaciens* (2), *Bacillus* sp. (2), *Micrococcus luteus* (*M. luteus*) (4), *P. aeruginosa* (4), *E. coli* (3), *P. mirabilis* (2), *Streptococcus lutetiensis* (*Str. lutetiensis*) (2), *J. nanhaiensis* (1), *Aerococcus viridans* (*A. viridans*) (1), *Paenibacillus lautus* (*P. lautus*) (1), *C. stationis* (1), *Actinomyces oris* (*A. oris*) (1), *D. hominis* (1), *E. artemiae* (1), *Acinetobacter schindleri* (*A. schindleri*) (1), *Klebsiella oxytoca* (*K. oxytoca*) (1), and *Moraxella osloensis* (*M. osloensis*) (1) (Figure).

The highest antimicrobial resistance in 25 staphylococci isolates was observed against P (48%), SXT (48%), VA (40%), and CN (40%). All 15 *Enterococcus* isolates were found to be resistant to CIP, CN, DA, P, and SXT. Of the 10 *Bacillus* isolates, 70%, 70%, 10%, and 10% were determined to be resistant to DA, P, CN, and SXT, respectively. When evaluating the antimicrobial resistance at the species level, the whole of the 8 *E. faecalis* isolates were resistant to CN, CIP, DA, E, P, SXT, and TE. It was detected that 33.3%, 33.3%, 16.7%, 16.7%, and 16.7% of 6 *S. felis* isolates were resistant to SXT, VA, CN, DA, and P, respectively. While the highest antimicrobial resistance in 6 *S. epidermidis* isolates was determined against E, P, and SXT at a rate of 66.7%, in 5 *S. pseudintermedius* isolates was determined against CN (80%), P (60%), TE (60%), and SXT (60%). Detailed results regarding the antimicrobial resistance profiles are shown in Table 1. MDR rates in the *Staphylococcus*, *Enterococcus,* and *Bacillus* isolates were detected as 44% (11/25), 100% (15/15), and 10% (1/10), respectively. The highest MDR, involving resistance to nine antimicrobials was observed in four isolates (n = 4) (Table 2).

4. Discussion

The OE is known as a multifactorial condition with a complex etiology. The bacterial (primarily staphylococci species) agents are frequently responsible for the cases in cats. The detection of OE in cats is performed by physical examination of the ear region and microbial culture of clinical samples, such as ear discharge or swabs [3,20].

Globally, studies investigating bacterial culture results and antimicrobial resistance profiles from feline OE cases remain limited. For instance, Hariharan et al. [7] reported that the 75 most frequently identified isolates among

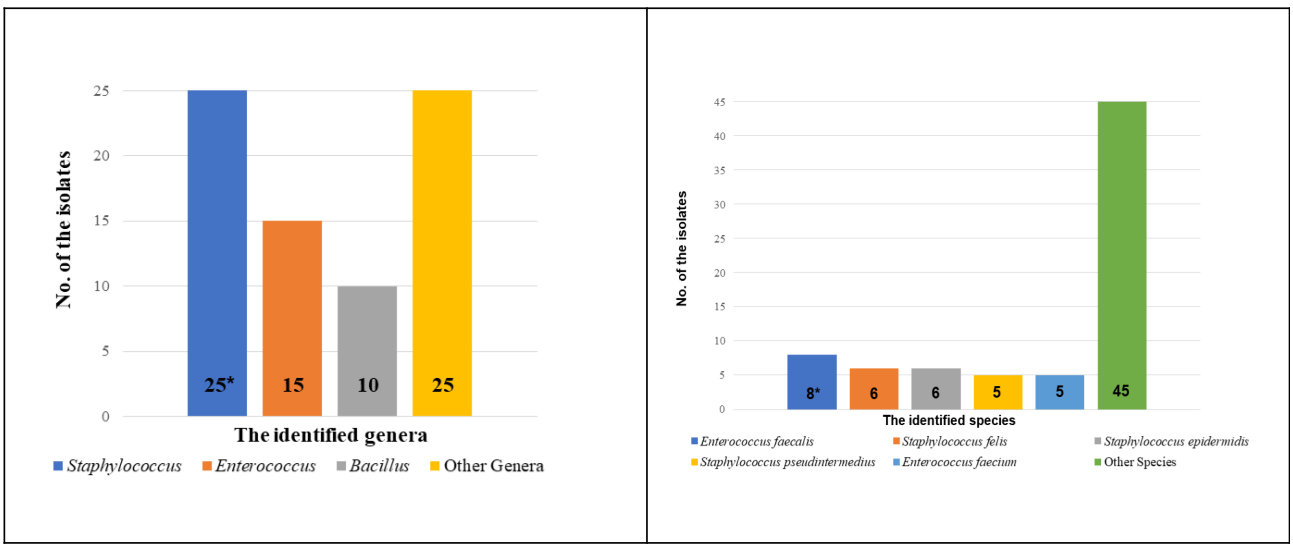


Figure. The percentage distribution at genus and species level of the isolates recovered from ear swab samples. *: No. of the isolates identified at the genus and species level.

Table 1. The antimicrobial resistance profiles of the isolates from cat ear swab samples.

Isolates	n	β-Lactams			Quinolone	Macrolide	Lincosamide	Aminoglycoside	Sulfonamide	Tetracycline	Glycopeptide
		AM	AMC	P	CIP	E	DA	CN	SXT	TE	VA
S. felis	6	-	-	1	-	-	1	1	2	-	2
S. epidermidis	6	1*	-	4	2	4	2	2	4	3	3
S. pseudintermedius	5	-	-	3	-	1	2	4	3	3	2
S. hominis	2	-	-	2	1	1	1	-	1	1	1
S. simulans	2	-	-	-	-	-	-	1	-	-	1
S. lentus	2	-	-	1	1	2	2	1	1	1	-
S. haemolyticus	1	1	1	1	1	-	1	1	1	-	1
S. sciuri	1	-	-	-	-	-	-	-	-	-	-
***Staphylococcus* spp.**	**25**	**2**	**1**	**12**	**5**	**8**	**9**	**10**	**12**	**8**	**10**
E. faecalis	8	-	-	8	8	8	8	8	8	8	5
E. faecium	5	4	4	5	5	5	5	5	5	4	-
E. hirae	2	-	-	2	2	1	2	2	2	-	1
***Enterococcus* spp.**	**15**	**4**	**4**	**15**	**15**	**14**	**15**	**15**	**15**	**12**	**6**
B. oceanisediminis	4	-	-	4	-	-	4	-	1	-	-
B. licheniformis	2	-	-	2	-	-	2	-	-	-	-
B. amyloliquefaciens	2	-	-	-	-	-	-	-	-	-	-
Bacillus sp.	2	-	-	1	-	-	1	1	-	-	-
***Bacillus* spp.**	**10**	**-**	**-**	**7**	**-**	**-**	**7**	**1**	**1**	**-**	**-**
Pseudomonas aeruginosa	4	4	4	ND	1	ND	4	2	4	4	4
Micrococcus luteus	4	-	-	-	1	-	-	-	-	-	2
Escherichia coli	3	1	1	ND	1	ND	1	-	1	1	1
Proteus mirabilis	2	2	-	ND	2	ND	2	-	2	2	2
Streptococcus lutetiensis	2	-	-	-	2	-	-	2	2	-	-
Jeotgalicoccus nanhaiensis	1	-	-	-	1	-	1	-	1	-	-
Aerococcus viridans	1	-	-	-	1	-	-	1	1	-	1
Paenibacillus lautus	1	-	-	1	-	-	1	-	1	1	-
Corynebacterium stationis	1	-	-	-	-	-	-	-	-	-	-
Actinomyces oris	1	-	-	-	-	-	-	1	-	-	-
Dermabacter hominis	1	-	-	-	-	1	-	1	1	-	-
Exiguobacterium artemiae	1	-	-	-	-	-	-	1	-	-	-
Acinetobacter schindleri	1	-	-	ND	-	1	1	-	-	-	1
Klebsiella oxytoca	1	1	-	ND	-	ND	1	1	-	-	1
Moraxella osloensis	1	-	-	ND	-	-	-	-	-	-	-
Total	**75**	**14**	**10**	**35**	**29**	**24**	**42**	**35**	**41**	**28**	**28**

n: No. of the isolates, *: No. of the resistant isolates, -: The antimicrobial resistance is not observed, **ND:** Not determined, **AM:** Ampicillin, **AMC:** Amoxicillin/clavulanic acid, **CIP:** Ciprofloxacin, **CN:** Gentamicin, **DA:** Clindamycin, **E:** Erythromycin, **P:** Penicillin, **SXT:** Trimethoprim/sulfamethoxazole, **TE:** Tetracycline, **VA:** Vancomycin.

Table 2. Multidrug resistance patterns of the isolates from cat ear swab samples.

Genus	Species	No. of the resistant isolates	Antimicrobial resistance patterns
Staphylococcus	*S. epidermidis*	1	DA-P-SXT
		1	CN-E-P-SXT-TE-VA
		1	CIP-DA-E-P-SXT-TE-VA
		1	AM-CIP-CN-E-P-TE-VA
	S. pseudintermedius	2	CN-P-SXT-TE-VA
		1	CN-DA-E-P-SXT-TE
	S. felis	1	CN-DA-P-SXT
	S. hominis	1	CIP-P-SXT-VA
	S. lentus	1	CIP-CN-DA-E-P-SXT-TE
	S. haemolyticus	1	AM-AMC-CIP-CN-DA-P-SXT-VA
Enterococcus	*E. faecalis*	3	CIP-CN-DA-E-P-SXT-TE
		5	CIP-CN-DA-E-P-SXT-TE-VA
	E. faecium	1	CIP-CN-DA-E-P-SXT
		4	AM-AMC-CIP-CN-DA-E-P-SXT-TE
	E. hirae	1	CIP-CN-DA-E-P-SXT
		1	CIP-CN-DA-P-SXT-VA
Bacillus	*B. oceanisediminis*	1	DA-P-SXT
Pseudomonas	*P. aeruginosa*	1	AM-AMC-DA-SXT-TE-VA
		2	AM-AMC-CN-DA-SXT-TE-VA
		1	AM-AMC-CIP-DA-SXT-TE-VA
Escherichia	*E. coli*	1	AM-AMC-CIP-DA-SXT-TE-VA
Proteus	*P. mirabilis*	2	AM-CIP-DA-SXT-TE-VA
Streptococcus	*Str. lutetiensis*	2	CIP-CN-SXT
Jeotgalicoccus	*J. nanhaiensis*	1	CIP-DA-SXT
Aerococcus	*A. viridans*	1	CIP-CN-SXT-VA
Paenibacillus	*P. lautus*	1	DA-P- SXT-TE
Dermabacter	*D. hominis*	1	CN-E-SXT
Acinetobacter	*A. schindleri*	1	DA-E-VA
Klebsiella	*K. oxytoca*	1	AM-CN-DA-VA

AM: Ampicillin, **AMC:** Amoxicillin/clavulanic acid, **CIP:** Ciprofloxacin, **CN:** Gentamicin, **DA:** Clindamycin, **E:** Erythromycin, **P:** Penicillin, **SXT:** Trimethoprim/sulfamethoxazole, **TE:** Tetracycline, **VA:** Vancomycin.

103 isolates were 31 coagulase-negative staphylococci, 17 coagulase-positive staphylococci (10 *S. aureus* and 7 *S. intermedius*), 15 *Pasteurella* spp. (14 *P. multocida* and 1 *P. dagmatis*), and 12 coliforms (9 *E. coli* and 3 other coliforms), respectively. In addition, the researchers stated that the remaining isolates (≤5 each) consisted of streptococci, enterococci, *P. aeruginosa*, *Proteus* spp., and *Trueperella pyogenes*. In Türkiye, Özener [21] detected that the most commonly defined bacteria were 11 coagulase-negative staphylococci, 4 *S. aureus*, 4 *Corynebacterium* spp., 2 *E. coli*, 2 *Pseudomonas* spp. and 1 *Bacillus* spp. Dégi et al. [22] performed the isolation of the staphylococci from 45 ear swab samples and identified 43.75% of the 32 staphylococci isolates as *S. intermedius*, 15.6% as *S. aureus*, 12.5% as *S. felis*, 12.5% as *S. haemolyticus*, 9.4% as *S. epidermidis* and 6.25% as *S. hyicus*. Nardoni et al. [10] defined three isolates recovered from 16 cats with OE as *S. pseudintermedius*, *Str. canis*, and *E. coli*. Hiblu et al. [3] reported that the isolates from feline OE cases were identified as 18 *Staphylococcus* spp., 4 *Proteus* spp., and 2 *Pseudomonas* spp. Kumar et al. [20] isolated and identified *Staphylococcus* spp. from an ear swab sample from a cat with OE. Li et al. [12] determined that the isolates from cats with OE were mostly in the *Staphylococcus*, *Streptococcus*, *Pseudomonas*, *Corynebacterium*, and *Escherichia* genera, respectively. Martins et al. [11] defined coagulase-positive staphylococci (40.2%), *Enterobacteriaceae* (16.5%), *Pseudomonas* spp. (13%), coagulase-negative staphylococci (11.3%), and *Corynebacterium* spp. (5.2%) as the most common species in the results of cultural examination of cat/dog ear swab samples, and *Proteus* spp. (13/30) was the most common among 30 *Enterobacteriaceae* isolates.

In the present study, 75 isolates were obtained from 71 samples based on the results of the cultural examination of ear swab samples from 100 cats with OE. As a result of the identification of 75 isolates, the three most identified genera were *Staphylococcus* (33.3%), *Enterococcus* (20%), and *Bacillus* (13.3%), respectively. In addition, the five most identified species were *E. faecalis* (10.7%), *S. felis* (8%), *S. epidermidis* (8%), *S. pseudintermedius* (6.7%), and *E. faecium* (6.7%), respectively. Compared to the aforementioned studies, these results show variation in isolate distribution, likely due to differences in geography, climate, age of the animals, habitat, season, sanitary conditions, number of samples analysed, and methodological approach [1,23].

Antimicrobial resistance remains a major concern for both public and animal health problems worldwide. The widespread and unnecessary use of various antimicrobials has contributed to an increase in antibiotic-resistant bacteria [24,25]. Companion animals are increasingly recognized as potential reservoirs and vectors of antimicrobial-resistant bacteria due to their close relationship with humans. Therefore, antimicrobial susceptibility testing is crucial for both the provision of public/animal health and the treatment of several clinical diseases (otitis externa, etc.) in animals [26].

As with prevalence data, there is limited research on the antimicrobial susceptibility results of isolates with cats with OE. Hariharan et al. [7] reported that 31.9%, 31.3%, 4.2%, 4.2%, 2.1%, and 2.1% of the 48 staphylococci isolates were resistant to P, AM, E, CN, SXT, and DA, respectively. The researchers also found a resistance to DA (100%), AM (25%), CN (17%), and ENR (9%) in 12 coliform isolates, including 9 *E. coli*. Özener [21] determined the resistance rates of 15 staphylococci isolates to SXT, AM, AMC, CN, and E as 80%, 80%, 73.3%, 60%, and 13.3%, respectively. In addition, the researchers found that all of *E. coli*, *Pseudomonas* spp., and *Bacillus* spp. isolates were resistant to SXT, AM, AMC, and CN. Dégi et al. [22] observed E (46.87%) and AMC (25%) resistance in 32 *Staphylococcus* isolates. Hiblu et al. [3] reported that 94.4%, 83.3%, 33.3%, and 11.1% of 18 *Staphylococcus* spp. isolates were resistant to amoxicillin, P, CN, and norfloxacin, respectively. The researchers determined that two *Pseudomonas* spp. isolates were resistant to amoxicillin, while four *Proteus* spp. isolates were resistant to amoxicillin (50%), norfloxacin (50%), and CN (25%). Kumar et al. [20] reported that one *Staphylococcus* isolate was resistant to amoxicillin, CIP, CN, and P. Martins et al. [11] determined that the *Staphylococcus* isolates were resistant to P (68.2%), SXT (50%), E (40.9%), AM (20.9%), CIP (20.8%), CN (19.6%), and AMC (4%). The researchers reported that 40%, 33.3%, 33.3%, 20%, and 20% of *Bacillus* spp. isolates were resistant to SXT, E, P, AM, and AMC, respectively, *Pseudomonas* spp. isolates were resistant to CN (32%), and CIP (8.3%), and 41.7%, 41.7%, 16.7%, 8.3% and 7.1% of *Proteus* spp. isolates were resistant to AM, SXT, AMC, CN, and CIP, respectively.

In our study, antimicrobial resistance in *Staphylococcus* isolates was most frequently observed against P (48%), SXT (48%), VA (40%), and CN (40%). All 15 *Enterococcus* isolates were found to be resistant to CIP, CN, DA, P, and SXT. Of the 10 *Bacillus* isolates, 70%, 70%, 10%, and 10% were determined to be resistant to DA, P, CN, and SXT, respectively. When the data we obtained are compared with the studies mentioned above, it is seen that there are differences in the resistance rates of the isolates to various antimicrobials. For example, the P resistance rates in the staphylococci isolates were determined as 31.9% [7], 68.2 [11], and 83.3 [3], while the SXT resistance rates were detected as 2.1% [7], 50% [11], and 80% [21]. It is thought that this difference may be related to the number of analyzed isolates, methods employed, the intensive use of antimicrobials, and the geographical distribution of the isolates.

The MDR rates observed in this study were 44% (11/25) for *Staphylococcus*, 100% (15/15) for *Enterococcus*, and *Bacillus* isolates were detected as 10%, respectively. Although antimicrobial resistance was reported in the isolates from the ear swab samples belonging to cats with OE, our findings showed the number of studies reporting MDR is quite limited. Thus, in the current study, the MDR rate (44%) obtained for *Staphylococcus* was consistent with the data reported by Martins et al. [11], while it was observed to be lower than the MDR rate reported for *Bacillus*.

In conclusion, this study demonstrates that the *staphylococci* and *enterococci* species are the predominant bacterial agents in the feline otitis externa and exhibit high resistance rates to antimicrobials used in treatment. These findings highlight the importance of performing microbial culture and antimicrobial susceptibility testing prior to treatment. Tailoring therapy based on laboratory results may improve treatment outcomes and help mitigate the development of resistance.

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Conflict of interest
The authors declare that they have no conflict of interest.

Ethical approval
Ethics committee approval is not required within the scope of this study.

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