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Microbial profile of keratitis: A retrospective review of South Africa's private microbiological laboratory results

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Background: Microbial keratitis (MK) is a vision-threatening infection whose empiric management depends on current, location specific antimicrobial susceptibility data. No nationwide analysis has yet characterised MK in South Africa's private healthcare sector.

Aim: The study aimed to describe the microbial profile of keratitis and antimicrobial resistance patterns within the private healthcare sector in South Africa.

Setting: This study was conducted within South Africa's private healthcare sector using the nationwide laboratory system of Lancet Laboratories, a large private pathology service.

Methods: This retrospective study reviewed microbiological reports of patients who underwent corneal scrape or pus swab processed by Lancet Laboratories between January 2016 and July 2024. Demographic details, microscopy results, culture isolates and antibiotic susceptibilities were extracted from laboratory reports.

Results: The corneal scrapes and/or swabs of 688 patients were analysed. The overall culture positivity rate was 35.0%. Median patient age was 46 years and 55.0% were female. Gram-positive bacteria accounted for 49.4% of positive cultures ($n = 132/267$), gram-negative bacteria for 46.8% ($n = 125/267$) and fungi for 3.7% ($n = 10/267$). *Pseudomonas aeruginosa* was the predominant pathogen (29.0% of all isolates; 62.0% of gram-negative), followed by *Staphylococcus epidermidis* (14.0%) and *Staphylococcus aureus* (13.0%). Resistance rates were highest for penicillin (74.0%; $n = 26/35$) and chloramphenicol (27.0%; $n = 36/134$); gentamicin and tobramycin each showed 11.0% resistance, while ciprofloxacin and moxifloxacin exhibited 14.0% and 12.0% resistance, respectively.

Contribution: This study provides private-sector, South Africa–specific microbial surveillance data for keratitis, informing empiric treatment choices and supporting judicious antibiotic use.

Conclusion: The private-sector MK profile is distinguished by a high prevalence of *P. aeruginosa* and appreciable resistance to chloramphenicol and penicillin, whereas fluoroquinolone and aminoglycoside activity remains largely preserved. These findings support the continued use of a fluoroquinolone or fortified aminoglycoside–cephalosporin combination as empiric therapy, while underscoring the need for ongoing regional surveillance to detect emerging resistance trends.

Keywords: eye; cornea; infection; microbial; keratitis; antibiotic; resistance.

Introduction

Microbial keratitis (MK) is an infection of the cornea that is caused by bacteria, protozoa and fungi.[1] It is a potentially sight threatening condition that is a primary contributor to ophthalmic morbidity and corneal blindness globally.[2] Developed countries report incidence rates of 3.6–52.1 per 100 000 persons per year,[3,4] whereas the incidence rates in developing countries are as high as 113 per 100 000 persons per year.[5]

Common risk factors for MK are contact lens wear, ocular surface disease, ocular trauma, lid abnormalities and prior ocular surgery.[2,6,7] The diagnosis of MK is based on clinical features and several special investigations. Clinically it is characterised by an epithelial defect, stromal infiltrate and conjunctival injection. There may be associated anterior segment inflammation. Patients generally present with pain and reduced visual acuity.[1,7,8,9] The gold standard for determination of

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causative organism in MK is microscopy and culture of multiple corneal swabs or scrapes.[1] Microscopy uses various staining techniques to aid in the identification of organisms.[10,11,12] Culture media includes blood agar, which is useful for most bacteria, and chocolate agar which cultures fastidious bacteria, for example, *Moraxella* and *Neisseria* spp.[10,13] Sabouraud agar is used for suspected fungal pathogens and non-nutrient agar with gram-negative seeding for *Acanthamoeba*.[1,14]

Both the incidence and aetiological organism of MK, as well as their susceptibility to antibiotics, vary widely by geographic location. This is likely because of variations in temperature, climate and regionally based risk factors as well as prevailing antibiotic prescribing practices.[1,2,7,15,16]

The initial treatment for MK worldwide is empiric broad spectrum topical antimicrobial treatment.[17,18] This is usually a topical fluroquinolone or a fortified aminoglycoside–cephalosporin combination. A 2014 review article found no difference in effectiveness of either option.[18] Subsequent treatment is adjusted based on clinical response, cultured organisms and their sensitivities. In South Africa, current first-line treatment for MK is doctor dependent – commonly used antibiotics are topical ciprofloxacin 0.3% or moxifloxacin 0.5% combined with chloramphenicol 0.5% – 1.0%.

Antimicrobial resistance comprises of genetic traits that can be transferred between bacteria.[19] This global phenomenon is posing a challenge to the effectiveness of empiric treatment for MK.[1,17,20,21,22] A growing trend of corneal isolates showing resistance to fluoroquinolones, B-lactams and aminoglycosides is becoming evident.[19,22,23,24]

There is a relative paucity of data on MK in South Africa with no studies assessing the microbial profile and resistance patterns of keratitis in the private sector. Regular analysis of microbial trends is recommended to ensure that appropriate treatment is prescribed for MK.[15] Therefore, this research seeks to describe the demographics and microbial patterns of keratitis in the private health care sector.

Research methods and design

A retrospective analysis of microbiological laboratory records of patients with suspected MK in South Africa was conducted from 01 January 2016 to 05 July 2024. Data were obtained from Lancet Laboratories laboratory records, which receives specimens from private hospitals and outpatient facilities nationwide. All microbiological records during the study period where the specimen site or source was recorded as cornea, and where the request included microscopy and culture were included. These records represent specimens submitted at the discretion of the treating clinician for clinical suspicion of MK. For each eligible requisition, specimen date, gram stain, cultured organism, antibiotic sensitivity and demographic data were extracted from pathology reports. Data were exported in de-identified form for analysis. The data were divided into two periods (2016–2020 and 2021–2024) for comparison of trends.

Data were captured onto spreadsheet software. R version 4.4.1 was used for analysis. Individual organism and drug sensitivity profiles were analysed. The data were using the requisition number to describe demographics. Individual test data were used to describe the proportion of resistance and culture positivity rate. Frequencies and proportions, and median interquartile range (IQR) were used for categorical and continuous variables, respectively, to describe the sample population. The proportion of organisms isolated was described by year. Resistance species were represented as a proportion of the number of sensitivity tests for that organism. An epicurve of all cultured positive specimens was plotted by month. The trend was decomposed into seasonal and trend components. The culture positivity rate was calculated as the number of positive cultures divided by the number of specimens taken.

Ethical considerations

This research adhered to the Declaration of Helsinki. Ethics approval was granted by the Human Research Ethics Committee (Medical) of the University of the Witwatersrand, Johannesburg, South Africa (reference number: M240961), and the study was registered with the National Health Research Database of South Africa (GP_202408_010).

Results

There were 688 patients whose samples were sent to Lancet Laboratories over the 8 year study period. Table 1 illustrates the demographics of the study population. The median age was 46 years (IQR 34–60 years), and female patients comprised 55.0% of the sample. Most specimens originated from Gauteng (55.0%; n = 377/688), followed by KwaZulu-Natal (27.0%; n = 186/688).

The culture positivity rate for the study period was 35.0%. Table 2 shows the culture positivity rate per year. Higher rates were observed between 2023 and 2024, with both years recording a culture positivity rate of 43.0%. No discernible seasonal pattern emerged. gram-positive bacteria constituted 49.4% of positive cultures (n = 132/267), gram-negative bacteria 46.8% (n = 125/267) and fungi 3.7% (n = 10/267). A total of 214 patients yielded a single pathogen. Co-infection with two organisms was identified in 50 patients and with three organisms in eight patients.

Pseudomonas aeruginosa was the predominant gram-negative pathogen (62.0%; n = 77/125) and the most frequently isolated organism overall, except in Mpumalanga and Limpopo where *Staphylococcus aureus* predominated. *Staphylococcus aureus* made up 27.0% of the total gram-positive isolates (n = 35/132). *Serratia marcescens* was the second most common gram-negative isolate (11.0%; n = 14/125). Coagulase-negative staphylococci (CoNS) – all staphylococcal species other than *S. aureus* – accounted for 42.4% (n = 56/132) of gram-positive isolates, with *Staphylococcus epidermidis* representing 29.0% (n = 38/132). *Streptococcus pneumoniae* comprised only 7.6% (n = 10/132) of gram-positive isolates. *Candida albicans* was

TABLE 1: Demographic profile of patients with culture-positive versus culture-negative corneal specimens in the South African private healthcare sector, with confidence intervals.

Variable	Overall				Negative					Positive					*P*-value
	n	%	Median	IQR	*n*	%	Median	IQR	95% CI	*n*	%	Median	IQR	95% CI	
Total	688	100	-	-	448	65	-	-	-	240	35	-	-	-	-
Age (years)	-	-	46	34–60			46	33–59	44, 48	-	-	47	35–61	45, 49	0.48†
Unknown	88	-	-	-	59	-	-	-	-	29	-	-	-	-	-
Sex	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.90‡
Female	331	55	-	-	215	55	-	-	50, 60	116	54	-	-	48, 61	-
Male	273	45	-	-	176	45	-	-	40, 50	97	46	-	-	39, 52	-
Unknown	84	-	-	-	57	-	-	-	-	27	-	-	-	-	-
Province															
Free State	20	2.9	-	-	7	1.6	-	-	0.69, 3.3	13	5.4	-	-	3.0, 9.3	-
Gauteng	377	55	-	-	246	55	-	-	50, 60	131	55	-	-	48, 61	-
KwaZulu-Natal	186	27	-	-	129	29	-	-	25, 33	57	24	-	-	19, 30	-
Limpopo	2	0.3	-	-	1	0.2	-	-	0.01, 1.4	1	0.4	-	-	0.02, 2.7	-
Mpumalanga	20	2.9	-	-	11	2.5	-	-	1.3, 4.5	9	3.8	-	-	1.8, 7.2	-
North West	71	10	-	-	50	11	-	-	8.5, 15	21	8.8	-	-	5.6, 13	-
Western Cape	12	1.7	-	-	4	0.9	-	-	0.29, 2.4	8	3.3	-	-	1.6, 6.7	-

CI, confidence interval; IQR, interquartile range.
†, Wilcoxon rank sum test; ‡, Pearson's Chi-squared test.

the leading fungal pathogen. Table 3 presents the principal organisms cultured during the 8-year study period; the full isolate profile is available in Appendix 1, Table 1-A1. Note that species-level identification of CoNS was not uniformly undertaken across laboratories.

Table 4 summarises the absolute number and proportion of antimicrobial-resistant isolates during the first surveillance period (2016–2020) versus the second (2021–2024) and provides cumulative resistance rates for the full 8-year period. No statistically significant temporal shift in resistance was detected; however, several agents demonstrated appreciable resistance burdens. Chloramphenicol resistance was identified in 27.0% (n = 36/134) of tested isolates, and penicillin exhibited a markedly high resistance rate of 74.0% (n = 26/35). By contrast, the aminoglycosides gentamicin and tobramycin each showed resistance rates of 11.0% (n = 23/216; n = 20/177, respectively). Among fluoroquinolones, resistance was observed in 14.0% (n = 19/135) of isolates for ciprofloxacin and 12.0% (n = 9/74) for moxifloxacin. No resistance to vancomycin was observed (n = 0/107). Table 5 illustrates the proportion of organisms that are resistant to respective antibiotics. Figure 1 depicts the same information in a heatmap. To avoid alarm of the high proportion of resistance resulting from 1/1 specimen being resistant, the midpoint of the confidence interval (CI) is used for the heatmap to assist in interpretation. Interpretation must be in conjunction with the knowledge of the sample size.

Discussion

This 8-year review characterises the microbiological spectrum and antimicrobial susceptibility of corneal scrapings submitted to Lancet Laboratories in South Africa for microscopy, culture and sensitivity testing. The microbial profile identified differs from other South African studies,[8,9,25,26] demonstrating a greater proportion of gram-negative organisms. Whereas public-sector studies by Anderson,[8] Koetsie[25] and Proxenos[26] identified gram-positive bacteria – principally CoNS, *S. aureus* and *S. pneumoniae* – as dominant pathogens, this study found *P. aeruginosa* to be the leading isolate, accounting for 29.0% of cultures, followed by *S. epidermidis* and *S. aureus*. This is in contrast to the most recent South African study where *P. aeruginosa* made up 6.0% of the organisms isolated.[8] The prominence of *P. aeruginosa* is consistent with some studies in developed countries, such as the United Kingdom, France and Australia,[15,27,28] yet contrasts with United States data, where gram-positive organisms, including *Staphylococcus* spp. remain more common.[7] These geographical variations highlight the importance of understanding the local microbial epidemiology to guide empirical treatment. The prevalence of *P. aeruginosa* observed here could potentially be linked to contact lens usage in the private-care population of this study.

Fungal isolates accounted for 3.7% of the cultured organisms in this study, a proportion comparable to findings from other South African studies, including Koetsie et al.[25] (3.0%) and Proxenos et al.[26] (2.5%). The most common fungal isolate was *C. albicans* (n = 8/10). This is in contrast to both Indian and Chinese studies where a fungal isolate predominance was described, with *Fusarium* spp. and *Aspergillus* spp. being the most isolated fungi.[1,5,29]

The global rise in methicillin-resistant *S. aureus* (MRSA) infections is a concern.[21] In a study conducted in San Francisco, Peng et al. reported a 1.13-fold increase in the odds of isolating MRSA with each successive year.[22] Chang et al.[21] also found a high proportion of MRSA (30.7%). In this study, there were no cases of MRSA isolated, comparable to the 2018 study by Anderson et al.[8] This is reassuring, given that the study encompassed a longer time frame and included patients from diverse regions across the country, suggesting that MRSA does not currently pose a significant threat in South Africa.

Climate and seasonal variations influence which organisms are likely to be cultured over a given time period. In the UK, gram-positive bacteria have been reported to grow at

TABLE 2: Culture-positivity rate of corneal specimens processed by Lancet Laboratories, South Africa (2016–2024).

Characteristic	Overall		2016			2017			2018			2019			2020			2021			2022			2023			2024			*P*-value†
	n	%	*n*	%	95% CI	*n*	%	95% CI	*n*	%	95% CI	*n*	%	95% CI	*n*	%	95% CI	*n*	%	95% CI	*n*	%	95% CI	*n*	%	95% CI	*n*	%	95% CI	
Total	688	-	89	-	-	79	-	-	107	-	-	80	-	-	69	-	-	63	-	-	77	-	-	75	-	-	49	-	-	-
Culture positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.067
Negative	448	65	56	63	52, 73	61	77	66, 86	65	61	51, 70	61	76	65, 85	46	67	54, 77	38	60	47, 72	50	65	53, 75	43	57	45, 69	28	57	42, 71	-
Positive	240	35	33	37	27, 48	18	23	14, 34	42	39	30, 49	19	24	15, 35	23	33	23, 46	25	40	28, 53	27	35	25, 47	32	43	31, 55	21	43	29, 58	-

CI, Confidence Interval.
†, Pearson's Chi-squared test.

warmer temperatures.[16,17] Filamentous fungi such as *Fusarium* spp. and *Aspergillus* spp. thrive in tropical conditions.[1] In contrast, *Candida* spp. are more common in temperate zones.[1,16] Uneven yearly distributions of fungal keratitis have been noted with peaks in the windy and harvest seasons in India and China.[30,31] A surge in *Acanthamoeba* keratitis has been seen in the UK, Hong Kong, Australia and Canada during the summer months.[14,32,33] This can be attributed to the microorganism thriving in warmer temperatures, as well as increased exposure through swimming. Seasonal variations have been shown in MK;[17] however, no seasonal variation was found in this study.

The culture positivity rate denotes the proportion of specimens that demonstrate microbial growth on culture. Reported positivity rates in cases of clinically diagnosed MK vary widely in the literature, ranging from 32.6% to 79.4%, depending on the study referenced.[1] In this study, the overall culture positivity rate was 35%, which is lower than rates reported in both local and international studies. In South Africa, Koetsie et al., Anderson et al., and Proxenos et al. reported positivity rates of 52.0%, 63.0%, and 51.3%, respectively.[8,25,26] Studies from Malaysia, Australia, and the United States have reported rates ranging from 61.4% to 69.0%.[34,35,36] The reason for the significantly lower culture positivity rate is uncertain. It may be related to prior antimicrobial use before the corneal sample was taken. Sample collection may have been inadequate – failing to obtain enough infected material, especially if the infiltrate was small. The gold standard for identifying the causative organism in MK is microscopy and culture of material obtained from multiple corneal scrapes and plated at the time of consultation. In the South African private healthcare sector, however, a single pus swab placed in Amies transport medium is often used for culture. This practice is largely influenced by the relative infrequency of MK cases and the logistical challenges associated with obtaining fresh culture media on short notice. In a prospective study by Pakzad-Vaezi et al.,[37] the diagnostic utility of a single-sample, liquid-based collection system (ESwab) was compared to the conventional multi-sample corneal scraping method for identifying the causative organism in MK. The findings demonstrated that the ESwab method was non-inferior to the traditional approach, with comparable culture positivity rates and diagnostic agreement.[37]

Antimicrobial resistance has become a pivotal consideration in the empiric management of MK, as treatment failure directly threatens visual prognosis. Numerous studies now document a progressive rise in fluroquinolone resistance among MK isolates worldwide.[20,21,22,23,24,38] The Steroids for Corneal Ulcers Trial demonstrated that bacteria isolated from individuals who had previously been exposed to topical fluroquinolones required significantly higher minimum inhibitory concentration than those from the treatment naïve group.[24] In a study by Peng et al.[22] each additional year of the 20 year study was associated with a 1.26-fold increase in the odds of isolating a moxifloxacin-resistant organism. Chang et al.[21] linked escalating resistance to the drugs widespread

TABLE 3: Spectrum of organisms cultured from corneal specimens in South African private-sector patients (N = 267†).

Organism name	Overall		2016		2017		2018		2019		2020		2021		2022		2023		2024	
	n	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%
Total	**267**	-	**37**	-	**20**	-	**45**	-	**19**	-	**29**	-	**27**	-	**31**	-	**34**	-	**25**	-
Pseudomonas aeruginosa	77	29	8	22	7	35	9	20	6	32	10	34	8	30	11	35	10	29	8	32
Staphylococcus epidermidis	38	14	4	11	3	15	2	4.4	7	37	4	14	6	22	8	26	2	5.9	2	8.0
Staphylococcus aureus	35	13	4	11	3	15	8	18	0	0	6	21	3	11	5	16	4	12	2	8.0
Serratia marcescens	14	5.2	2	5.4	1	5.0	2	4.4	1	5.3	0	0	3	11	0	0	5	15	0	0
Streptococcus pneumoniae	10	3.7	2	5.4	0	0	4	8.9	0	0	1	3.4	1	3.7	0	0	2	5.9	0	0
Klebsiella pneumoniae	4	1.5	0	0	0	0	2	4.4	0	0	0	0	0	0	0	0	0	0	2	8.0
Proteus mirabilis	3	1.1	2	5.4	0	0	1	2.2	0	0	0	0	0	0	0	0	0	0	0	0
Staphylococcus warneri	4	1.5	0	0	2	10	1	2.2	0	0	1	3.4	0	0	0	0	0	0	0	0
Streptococcus viridans	6	2.2	3	8.1	0	0	0	0	1	5.3	0	0	0	0	2	6.5	0	0	0	0
Enterococcus faecalis	7	2.6	0	0	0	0	1	2.2	1	5.3	0	0	2	7.4	1	3.2	0	0	2	8.0
Escherichia coli	4	1.5	0	0	0	0	1	2.2	0	0	3	10	0	0	0	0	0	0	0	0
Other	65	24	12	32	4	20	14	31	3	16	4	14	4	15	4	13	11	32	9	36

†, Total isolates including co-infections.

TABLE 4: Temporal trends in antimicrobial resistance: number and proportion of resistant isolates overall, and in 2016–2020 versus 2021–2024.

Antibiotic	Overall				2016–2020				2021–2024				*P*-value†
	n	*N*	%	95% CI	*n*	*N*	%	95% CI	*n*	*N*	%	95% CI	
Chloramphenicol	36	134	27	20, 35	22	75	29	20, 41	14	59	24	14, 37	0.47
Tetracycline	33	109	30	22, 40	24	69	35	24, 47	9	40	23	11, 39	0.18
Penicillin	26	35	74	56, 87	16	19	84	60, 96	10	16	63	36, 84	0.25
Gentamicin	23	216	11	7.0, 16	16	124	13	7.8, 20	7	92	7.6	3.4, 16	0.21
Tobramycin	20	177	11	7.2, 17	10	92	11	5.6, 20	10	85	12	6.1, 21	0.85
Ciprofloxacin	19	135	14	8.9, 21	7	68	10	4.6, 21	12	67	18	10, 30	0.20
Cefuroxime	16	31	52	33, 69	7	17	41	19, 67	9	14	64	36, 86	0.20
Moxifloxacin	9	74	12	6.1, 22	5	44	11	4.3, 25	4	30	13	4.4, 32	> 0.99
Cefepime	5	87	5.7	2.1, 14	3	42	7.1	1.9, 21	2	45	4.4	0.77, 16	0.67

CI, Confidence Interval.

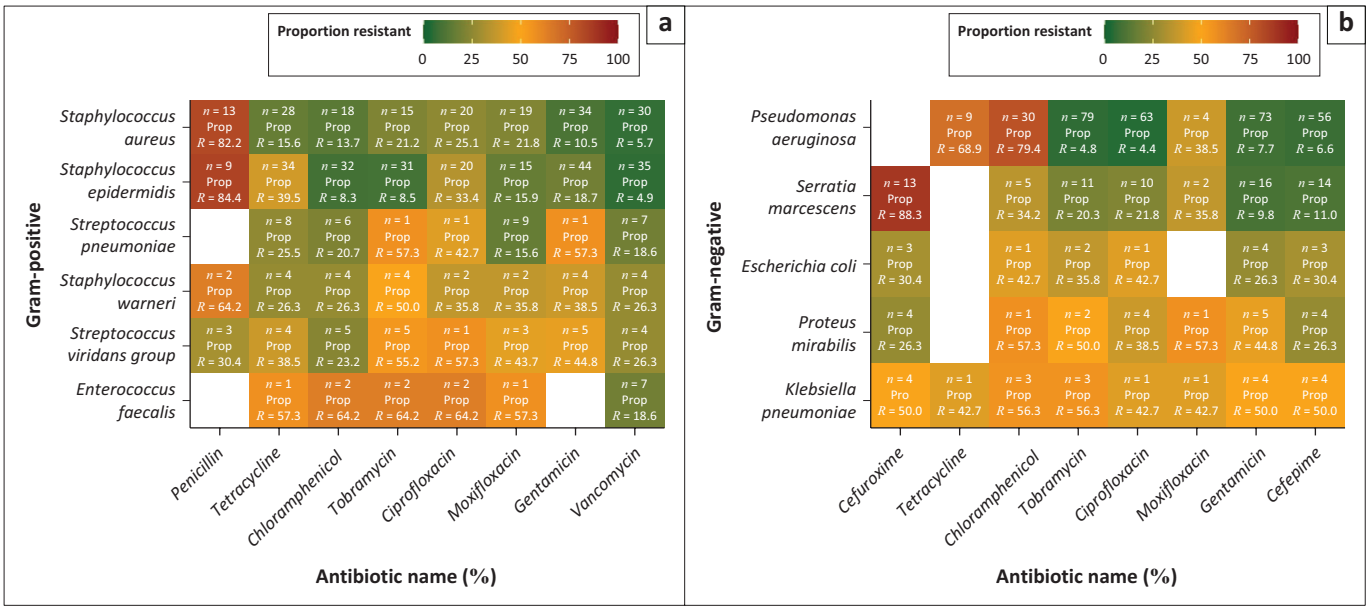
†, Pearson's Chi-squared test; Fisher's exact test.

TABLE 5: The proportion of organisms that are resistant to respective antibiotics.

Organism name	Penicillin		Cefuroxime		Tetracycline		Chloramphenicol		Tobramycin		Ciprofloxacin		Moxifloxacin		Gentamicin		Cefepime		Vancomycin	
	n	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%
Staphylococcus aureus	12	92	-	-	3	11	1	5.0	2	12	4	20	3	14	2	5.9	-	-	0	0
Pseudomonas aeruginosa	-	-	-	-	7	78	25	83	2	2.5	1	1.6	1	25	4	5.5	2	3.6	-	-
Staphylococcus epidermidis	9	100	-	-	13	38	1	3.1	1	3.1	6	30	1	5.6	7	16	-	-	0	0
Serratia marcescens	-	-	13	100	-	-	1	20	1	8.3	1	10	0	0	0	0	0	0	-	-
Enterococcus faecalis	-	-	-	-	1	100	2	100	2	100	2	100	1	100	-	-	-	-	0	0
Streptococcus pneumoniae	0	0	-	-	2	20	0	0	3	100	0	0	0	0	3	100	-	-	0	0
Klebsiella pneumoniae	-	-	2	50	0	0	2	67	2	67	0	0	0	0	2	50	2	50	-	-
Streptococcus viridans	0	0	-	-	1	25	0	0	3	60	1	100	1	33	2	40	-	-	0	0
Escherichia coli	-	-	3	100	-	-	1	100	2	100	1	100	-	-	4	100	3	100	-	-
Proteus mirabilis	-	-	0	0	-	-	1	100	1	50	1	25	1	100	2	40	0	0	-	-
Staphylococcus warneri	2	100	-	-	0	0	0	0	2	50	0	0	0	0	1	25	-	-	0	0

Note: Only the top 10 organisms and antibiotics are shown.

empiric use since its introduction in 2003. Although fluoroquinolone resistance remains uncommon in North Europe and the UK,[15,39] several Asian centres are seeing sharp increases. Shi et al.[38] observed a decline in moxifloxacin susceptibility from 93% to 79% and in ciprofloxacin susceptibility from 94.0% to 82.0% over a single decade. A second Chinese study reported susceptibilities of 66.5% and 68.8%, respectively. Parallel Indian data likewise show steadily worsening resistance to both agents.[23,40] In our cohort, 12.0% of isolates (n = 9/74) were moxifloxacin resistant, with no significant trend found over the study period. This contrasts modestly with earlier South African studies, which reported one resistant isolate (10.0%) in 2018,[8] and none in 2008.[25] Ciprofloxacin resistance was detected in 14.0% of isolates (n = 19/135), again with no statistically significant trend observed over time. Prior local rates were 4.2%



Note: Only the top 10 organisms and antibiotics are shown.

FIGURE 1: Heatmap depicting the proportion of organisms that are resistant to respective antibiotics: (a) gram-positive organisms (b) gram-negative organisms.

(n = 3/72)[8] and 9.2% (n = 5/54).[25] Taken together, these data suggest that while fluroquinolone efficacy in our setting remains acceptable, the disparate international experience underscores the need for continued regional surveillance.

Chloramphenicol is often prescribed at a primary healthcare level in South Africa for ocular infections. It is also used as part of first line empiric therapy for MK. Anderson et al.[8] found that 14.6% of all cultured organisms at St John Eye Hospital were resistant to chloramphenicol. Much higher rates of chloramphenicol resistance have been reported in other parts of the world: 51% in China, 74.1% in the UK and 69.6% in Nigeria.[41] In our study, it was found that 27.0% (n = 36/134) of the organisms tested for susceptibility to chloramphenicol were resistant to it. The higher rate of resistance observed in this study, compared to the findings of Anderson et al.,[8] may be explained by the greater proportion of *P. aeruginosa* isolates, which are intrinsically resistant to chloramphenicol and therefore not expected to demonstrate susceptibility. Some specimens did nevertheless undergo susceptibility testing, likely in accordance with routine laboratory protocols. Additionally, the widespread empirical use of chloramphenicol in the primary healthcare setting may facilitate the emergence and persistence of resistant strains.

Antimicrobial resistance to penicillin was observed in 74% of the tested isolates (n = 26/35), a figure that – despite the small sample size – aligns with broadly global data. In Southwest China, a penicillin resistance rate of 54.0% among gram-positive isolates was found.[20] In the UK an increasing trend of resistance against penicillin has been observed,[17] and in New Zealand 49% of gram-positive isolates and 92% of gram-negative isolates were penicillin resistant.[42] Collectively, these observations seem to indicate that penicillin offers unreliable coverage for MK worldwide.

Gentamicin and tobramycin resistance in our study was 11.0% for each drug, (n = 23/216; n = 20/177, respectively). A 2022 meta-analysis by Zhang et al. reported aminoglycoside susceptibility of 86.0% in gram-positive cocci and 92.0% in gram-negative bacilli, i.e. global antimicrobial resistance rates of 14.0% and 8.0%, respectively.[2] South African surveillance by Anderson et al.[8] documented a gentamicin resistance rate of 5.8% across isolates; unchanged since the 2008 Koetsie cohort.[25] UK data showed universal susceptibility of *Pseudomonas* spp. to both agents.[15] In contrast, an Indian study by Palmer et al.[43] describes 63.6% resistance to gentamicin among *Pseudomonas* isolates. *Staphylococcus* spp. were 80% susceptible, and *Streptococcus* spp. 100% susceptible.[43] Aminoglycosides retain high, although not universal, efficacy: recent studies still show a greater than 90.0% susceptibility of *Pseudomonas* spp. and other gram-negative organisms to gentamicin and tobramycin,[2,8,15,25,44,45] yet discrete foci of resistance have been reported.[43,46]

Among 107 isolates tested for vancomycin susceptibility in this study, no resistance was detected (0.0%). This finding is consistent with regional and international reports. South African studies by Anderson et al.[8] and Koetsie et al.[25] both documented a 0.0% vancomycin resistance, while Guo et al. reported >98.0% susceptibility among gram-positive keratitis isolated in Southwest China.[20] In an Iranian cohort, Soleimani et al. reported 100.0% vancomycin susceptibility among CoNS.[44] Similarly, a United States based study reported 100.0% susceptibility to vancomycin among common corneal pathogens.[47] In contrast, a Saudi Arabian single centre series found 7.0% vancomycin resistance in CoNS, highlighting regional variability.[48] Collectively, the evidence indicates that vancomycin is a robust option in the treatment of MK.

Limitations

The retrospective design imposed several methodological constraints, including reliance on pre-existing laboratory

records of variable completeness and the absence of clinical correlates such as ulcer size, contact-lens wear or prior antimicrobial exposure. All specimens were processed by a single private laboratory company, potentially introducing selection bias and limiting external validity to other private facilities or the public sector. Specimen collection and transport were not standardised but reflected real-world practice, which may have reduced culture yield. Furthermore, resistance estimates for certain drug – organism combinations were derived from small denominators, generating wide CIs and necessitating cautious interpretation of those specific rates.

Conclusion

This 8 year review provides the first nationwide overview of MK in South Africa's private sector, revealing a predominance of *P. aeruginosa*, a substantial burden of chloramphenicol and penicillin resistance, and stable but non-negligible fluoroquinolone and aminoglycoside resistance. Although current empiric regimens of a fluoroquinolone or fortified aminoglycoside–cephalosporin combination remain broadly appropriate, this study emphasises the importance of regular, regional surveillance and targeted antibiotic stewardship to preserve therapeutic efficacy.

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Competing interests

The authors declare that they have no financial or personal relationships that may have inappropriately influenced them in writing this article.

CRediT authorship contribution

Amy Lombard: Conceptualisation, Data curation, Formal analysis, Investigation, Methodology, Project administration, Resources, Visualisation, Writing – original draft, Writing – review & editing. Bongi Sithole: Conceptualisation, Methodology, Resources, Supervision, Writing – review & editing. Justyna Wojno: Data curation, Resources, Supervision, Writing – review & editing. Roland Höllhumer: Conceptualisation, Methodology, Resources, Supervision, Writing – review & editing. All authors reviewed the article, contributed to the discussion of results, approved the final version for submission and publication, and take responsibility for the integrity of its findings.

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Data availability

Raw data were provided by Lancet Laboratories through their publications committee and can only be obtained through application. Summary data is available from the corresponding author, Amy Lombard, on reasonable request, in consultation with Lancet Laboratories.

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Appendix 1

TABLE 1-A1: Cultured organisms of the cornea among patients accessing private healthcare in South Africa (N = 267).

Organism name	Overall		2016		2017		2018		2019		2020		2021		2022		2023		2024	
	n	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%
Total	**267**	-	**20**	-	**11**	-	**21**	-	**12**	-	**14**	-	**13**	-	**18**	-	**12**	-	**11**	-
Gram-positive	**132**	**49**	**20**	**54**	**11**	**55**	**21**	**47**	**12**	**63**	**14**	**48**	**13**	**48**	**18**	**58**	**12**	**35**	**11**	**44**
Staphylococcus epidermidis	38	29	4	20	3	27	2	9.5	7	58	4	29	6	46	8	44	2	17	2	18
Staphylococcus aureus	35	27	4	20	3	27	8	38	0	0	6	43	3	23	5	28	4	33	2	18
Streptococcus pneumoniae	10	7.6	2	10	0	0	4	19	0	0	1	7.1	1	7.7	0	0	2	17	0	0
Enterococcus faecalis	7	5.3	0	0	0	0	1	4.8	1	8.3	0	0	2	15	1	5.6	0	0	2	18
Bacillus spp.	6	4.5	2	10	1	9.1	0	0	1	8.3	0	0	1	7.7	0	0	0	0	1	9.1
Streptococcus viridans	6	4.5	3	15	0	0	0	0	1	8.3	0	0	0	0	2	11	0	0	0	0
Staphylococcus warneri	4	3.0	0	0	2	18	1	4.8	0	0	1	7.1	0	0	0	0	0	0	0	0
Streptococcus mitis/ Streptococcus oralis	4	3.0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	25	1	9.1
Coagulase Negative Staphylococcus	3	2.3	2	10	0	0	1	4.8	0	0	0	0	0	0	0	0	0	0	0	0
Enterococcus faecium	2	1.5	1	5.0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9.1
Staphylococcus capitis	2	1.5	0	0	1	9.1	0	0	0	0	0	0	0	0	0	0	0	0	1	9.1
Staphylococcus haemolyticus	2	1.5	0	0	0	0	0	0	0	0	1	7.1	0	0	1	5.6	0	0	0	0
Staphylococcus hominis	2	1.5	1	5.0	0	0	0	0	1	8.3	0	0	0	0	0	0	0	0	0	0
Staphylococcus lentus	2	1.5	0	0	0	0	2	9.5	0	0	0	0	0	0	0	0	0	0	0	0
Bacillus cereus	1	0.8	0	0	0	0	0	0	1	8.3	0	0	0	0	0	0	0	0	0	0
Corynebacterium amycolatum	1	0.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9.1
Nocardia spp.	1	0.8	0	0	0	0	1	4.8	0	0	0	0	0	0	0	0	0	0	0	0
Staphylococcus caprae	1	0.8	0	0	0	0	1	4.8	0	0	0	0	0	0	0	0	0	0	0	0
Staphylococcus chromogenes	1	0.8	0	0	1	9.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Staphylococcus saprophyticus	1	0.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8.3	0	0
Stephanoascus ciferrii	1	0.8	1	5.0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Streptococcus Group B	1	0.8	0	0	0	0	0	0	0	0	1	7.1	0	0	0	0	0	0	0	0
Streptococcus sanguinis	1	0.8	0	0	0	0	0	0	0	0	0	0	0	0	1	5.6	0	0	0	0
Gram-negative	**125**	**47**	**16**	**43**	**8**	**40**	**20**	**44**	**7**	**37**	**15**	**52**	**14**	**52**	**12**	**39**	**20**	**59**	**13**	**52**
Pseudomonas aeruginosa	77	62	8	50	7	88	9	45	6	86	10	67	8	57	11	92	10	50	8	62
Serratia marcescens	14	11	2	13	1	13	2	10	1	14	0	0	3	21	0	0	5	25	0	0
Escherichia coli	4	3.2	0	0	0	0	1	5.0	0	0	3	20	0	0	0	0	0	0	0	0
Klebsiella pneumoniae	4	3.2	0	0	0	0	2	10	0	0	0	0	0	0	0	0	0	0	2	15
Acinetobacter baumannii	3	2.4	0	0	0	0	0	0	0	0	1	6.7	0	0	1	8.3	1	5.0	0	0
Enterobacter cloacae	3	2.4	1	6.3	0	0	0	0	0	0	0	0	1	7.1	0	0	0	0	1	7.7
Klebsiella oxytoca	3	2.4	1	6.3	0	0	0	0	0	0	0	0	1	7.1	0	0	1	5.0	0	0
Proteus mirabilis	3	2.4	2	13	0	0	1	5.0	0	0	0	0	0	0	0	0	0	0	0	0
Haemophilus influenzae	2	1.6	1	6.3	0	0	0	0	0	0	1	6.7	0	0	0	0	0	0	0	0
	2	1.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5.0	1	7.7
Klebsiella spp.	2	1.6	0	0	0	0	0	0	0	0	0	0	1	7.1	0	0	1	5.0	0	0
Moraxella lacunata	2	1.6	0	0	0	0	2	10	0	0	0	0	0	0	0	0	0	0	0	0
Pseudomonas putida	2	1.6	0	0	0	0	1	5.0	0	0	0	0	0	0	0	0	1	5.0	0	0
Enterobacter spp.	1	0.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7.7
Haemophilus spp.	1	0.8	0	0	0	0	1	5.0	0	0	0	0	0	0	0	0	0	0	0	0
Serratia liquefaciens	1	0.8	0	0	0	0	1	5.0	0	0	0	0	0	0	0	0	0	0	0	0
Stenotrophomonas maltophilia	1	0.8	1	6.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

TABLE 1-A1 continues on the next page→

TABLE 1-A1 (Continues...): Cultured organisms of the cornea among patients accessing private healthcare in South Africa (N = 267).

Organism name	Overall		2016		2017		2018		2019		2020		2021		2022		2023		2024	
	n	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%
Fungal	**10**	**3.7**	**1**	**2.7**	**1**	**5.0**	**4**	**8.9**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**3.2**	**2**	**5.9**	**1**	**4.0**
Candida albicans	8	80	1	100	1	100	3	75	0	0	2	100	1	100	0	0	0	0	0	0
Candida parapsilosis	1	10	0	0	0	0	1	25	0	0	0	0	0	0	0	0	0	0	0	0
Candida tropicalis	1	10	0	0	0	0	0	0	1	100	0	0	0	0	0	0	0	0	0	0

Note: N = 267 as some patients had co-infections.