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Original Article

Descriptive Assessment Of General Patterns Of Multidrug Resistance Observed In Various Dermatological Conditions Across Patient Groups

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ABSTRACT

Background: Multidrug resistance (MDR) in dermatological infections is an increasing clinical and public health concern, particularly in settings where empirical antimicrobial prescribing, self-medication, and limited routine culture testing may contribute to resistant disease. Objective: To determine the prevalence and distribution of MDR among microbiologically confirmed dermatological infections across patient groups in South Punjab. Methods: A descriptive cross-sectional study was conducted over four months in outpatient dermatology clinics and tertiary healthcare facilities across South Punjab. A total of 384 patients with confirmed microbial skin infections were enrolled. Demographic and clinical data were collected using a structured proforma, and skin swabs, scrapings, or biopsy specimens were processed using standard microbiological methods. Antimicrobial susceptibility was assessed using the Kirby-Bauer disk diffusion method, and MDR was defined as resistance to at least one agent in three or more antimicrobial classes. Data were analyzed using SPSS version 26. Results: The mean age was 38.6 ± 15.2 years, with equal male and female representation. Rural residents accounted for 62.0% of participants. Overall, MDR was identified in 196 of 384 patients (51.0%). Mixed infections showed the highest MDR proportion (58.8%), followed by bacterial (55.8%), parasitic (47.4%), and fungal infections (44.3%). Adults aged 18–40 years contributed the largest number of MDR cases (82/146; 56.2%). Staphylococcus aureus showed the highest pathogen-specific MDR rate (68/104; 65.4%), followed by Pseudomonas aeruginosa (42/68; 61.8%). Conclusion: MDR was frequent among dermatological infections in South Punjab, particularly in mixed and bacterial infections and among common bacterial pathogens. Culture-guided therapy, rational antimicrobial use, and regional resistance surveillance are essential to improve dermatological infection management. Keywords: Antimicrobial resistance, dermatological infections, multidrug resistance, skin infections, Staphylococcus aureus, Pseudomonas aeruginosa, South Punjab.

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INTRODUCTION

Multidrug resistance (MDR) has become a critical threat to the effective treatment of infectious diseases, including infections of the skin and soft tissues, where antimicrobial exposure is often repeated, prolonged, or empirically prescribed (1). Dermatological infections represent a clinically important interface between community-based antimicrobial use and microbiological resistance because they are common, recurrent, visible to patients, and frequently treated before culture confirmation. In routine dermatology practice, bacterial, fungal, parasitic, and mixed infections may initially appear uncomplicated; however, increasing resistance to commonly used antimicrobial classes has reduced therapeutic predictability, prolonged disease duration, increased recurrence, and contributed to greater healthcare burden (2). The problem is especially relevant in settings where non-prescription antimicrobial access, self-medication, delayed specialist consultation, and limited microbiological surveillance influence prescribing behavior and treatment outcomes (3).

Skin infections are caused by a broad range of pathogens, but resistance among bacterial organisms such as Staphylococcus aureus and Pseudomonas aeruginosa remains a particular concern because these organisms are frequently implicated in dermatological and soft-tissue infections and may acquire or express resistance to multiple antimicrobial classes (4). Methicillin-resistant Staphylococcus aureus has expanded beyond hospital settings into community environments, while Pseudomonas aeruginosa is clinically challenging because of intrinsic resistance mechanisms, biofilm formation, and adaptability to diverse ecological niches (5). Alongside bacterial resistance, reduced susceptibility among fungal pathogens has become increasingly important, particularly in dermatophyte and Candida infections, where inappropriate or repeated antifungal use may contribute to persistent disease and treatment failure (6). Parasitic skin infestations, including scabies, may also show poor clinical response in some populations, making it necessary to document resistance-like treatment patterns and distinguish true resistance from reinfection, inadequate treatment, or poor adherence (7).

The burden of MDR in dermatological infections is not distributed uniformly across populations. Patient age, residence, comorbid illnesses, immune status, previous antimicrobial exposure, healthcare access, hygiene practices, and local prescribing patterns can influence both infection risk and resistance emergence (8). Individuals with diabetes, immunosuppression, chronic wounds, recurrent skin disease, or frequent healthcare contact may be more vulnerable to persistent or resistant infections, whereas younger adults may experience higher antimicrobial exposure because of recurrent dermatological conditions and greater use of topical or systemic agents (9). Rural populations may face additional risks related to delayed diagnosis, informal medication use, limited access to culture-based testing, and incomplete treatment courses. These contextual factors make regional surveillance essential because resistance patterns observed in one geographic or clinical setting cannot be assumed to apply to another.

Despite the global recognition of antimicrobial resistance as a major public health challenge, dermatology-specific MDR data remain limited in many low- and middle-income regions, including areas of Pakistan where microbiological testing is not routinely integrated into outpatient skin infection management (10). Much of the available resistance literature focuses on systemic infections, hospital-acquired pathogens, or single-organism surveillance, leaving a gap in evidence regarding the distribution of MDR across common dermatological infection categories and patient groups. This gap limits the ability of clinicians to select appropriate empirical therapy, identify populations requiring early culture testing, and develop locally relevant antimicrobial stewardship strategies. In South Punjab, where antimicrobial regulation, healthcare access, and patient treatment behaviors may vary substantially between urban and rural communities, region-specific documentation of dermatological MDR patterns is particularly needed (11).

The present study was designed to address this evidence gap by describing the frequency and distribution of multidrug resistance among patients with microbiologically confirmed dermatological infections in outpatient and tertiary healthcare settings across South Punjab. Using a descriptive cross-sectional approach, the study evaluated MDR patterns across infection types, isolated pathogens, age groups, residence, and comorbidity profiles. In PICO terms, the population comprised patients with confirmed microbial dermatological infections; the condition of interest was multidrug resistance among bacterial, fungal, parasitic, and mixed infections; the comparison involved demographic and clinical subgroups; and the outcome was the prevalence and distribution of MDR across organisms and patient categories. The objective of this study was therefore to determine the patterns and prevalence of multidrug resistance in dermatological infections across different patient groups in South Punjab, with the aim of informing culture-guided therapy, rational antimicrobial use, and future regional surveillance strategies (12).

MATERIALS AND METHODS

A descriptive cross-sectional observational study was conducted over a four-month period in outpatient dermatology clinics and tertiary healthcare facilities across South Punjab to assess the distribution and patterns of multidrug resistance among patients presenting with microbiologically confirmed dermatological infections. The cross-sectional design was selected because it allowed estimation of the frequency of multidrug resistance at a defined point within the study period and enabled comparison of resistance patterns across infection categories, demographic groups, isolated pathogens, and selected clinical characteristics.

The study population consisted of patients of all ages and both sexes who presented with clinically suspected microbial dermatological infections, including bacterial, fungal, parasitic, and mixed skin infections. Eligible participants were those who underwent microbiological evaluation through skin swabs, scrapings, or biopsy

specimens and had culture or laboratory-confirmed evidence of infection with antimicrobial susceptibility assessment. Patients with non-infectious dermatological conditions, those who had received systemic antibiotic therapy within the preceding two weeks, and those who did not provide consent were excluded to reduce potential distortion of microbiological yield and resistance profiles. Participants were enrolled after clinical evaluation in dermatology settings, and relevant demographic and clinical information was collected using a structured data collection proforma.

For each participant, data were recorded on age, sex, place of residence, clinical diagnosis, infection category, duration and type of dermatological infection, previous treatment history, and presence of comorbid conditions including diabetes mellitus and HIV infection. Dermatological infections were categorized as bacterial, fungal, parasitic, or mixed infections on the basis of clinical assessment supported by microbiological findings. Multidrug resistance was operationally defined as resistance to at least one antimicrobial agent in three or more antimicrobial classes. The primary outcome was the proportion of microbiologically confirmed dermatological infections demonstrating multidrug resistance. Secondary descriptive outcomes included MDR distribution by infection type, age group, isolated organism, residence, and comorbidity status.

Specimens were collected under aseptic conditions according to the suspected infection type. Skin swabs were obtained from infected lesions where bacterial infection was suspected, while skin scrapings or other appropriate dermatological specimens were collected for suspected fungal or parasitic infections. Samples were transported to accredited microbiology laboratories for processing. Standard culture techniques were used for pathogen isolation and identification. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method, with interpretation based on standardized laboratory susceptibility criteria. Resistance patterns were assessed for antimicrobial agents commonly used in dermatological practice, including cephalosporins, macrolides, tetracyclines, fluoroquinolones, and relevant topical or systemic antifungal agents where applicable.

The sample size was calculated using the Raosoft sample size calculator with a 95% confidence level, 5% margin of error, and an estimated response distribution of 50%, which was appropriate for a prevalence-based descriptive study in the absence of prior local estimates. This calculation yielded a required sample of 384 participants. To minimize selection bias, eligible patients meeting the inclusion criteria during the study period were enrolled from participating dermatology settings. Standardized data collection procedures were used across participants, and laboratory-based confirmation was required to reduce misclassification of infection type and resistance status. Potential confounding by recent antimicrobial exposure was addressed by excluding patients with systemic antibiotic use during the preceding two weeks, while subgroup stratification by age, residence, infection category, pathogen type, and comorbidity status allowed descriptive assessment of variation in MDR patterns across clinically relevant patient groups.

All collected data were entered into SPSS version 26 for statistical analysis. Continuous variables were summarized using means and standard deviations when normally distributed, while categorical variables were presented as frequencies and percentages. The prevalence of multidrug resistance was calculated overall and separately for each infection category, age group, and isolated pathogen. Group comparisons for categorical variables were assessed using the chi-square test where appropriate. For continuous variables, independent-samples t-tests or one-way analysis of variance were used when comparisons involved two or more groups and distributional assumptions were satisfied. A p-value of less than 0.05 was considered statistically significant. Data integrity was maintained through structured data entry, review of completed proformas, consistency checks between clinical and laboratory records, and analysis using predefined variable categories. Ethical principles for human-subject research were followed, including informed consent, confidentiality of participant information, and use of anonymized data for analysis.

RESULTS

A total of 384 patients with microbiologically confirmed dermatological infections were included. The mean age was 38.6 ± 15.2 years, and the cohort had equal representation of males and females, with 192 males (50.0%) and 192 females (50.0%). Most participants were from rural areas, accounting for 238 patients (62.0%), while 146 patients (38.0%) were from urban settings. Diabetes mellitus was recorded in 92 patients (24.0%), HIV infection in 18 patients (4.7%), and no documented comorbidity in 274 patients (71.4%).

Bacterial infections were the most frequent dermatological infection category, affecting 172 patients (44.8%), followed by fungal infections in 140 patients (36.5%), parasitic infections in 38 patients (9.9%), and mixed infections in 34 patients (8.9%). Overall, multidrug resistance was identified in 196 of 384 patients, giving an overall MDR

prevalence of 51.0%. Mixed infections showed the highest proportional MDR burden at 58.8%, followed by bacterial infections at 55.8%, parasitic infections at 47.4%, and fungal infections at 44.3%. The difference in MDR distribution across infection categories was not statistically significant, $\chi^2 = 5.15$, $p = 0.161$.

Table 1. Demographic and Clinical Characteristics of the Study Participants

Variable	n / Value	Percentage
Mean age, years	38.6 ± 15.2	
Male	192	50.0
Female	192	50.0
Urban residence	146	38.0
Rural residence	238	62.0
Diabetes mellitus	92	24.0
HIV infection	18	4.7
No documented comorbidity	274	71.4

Table 2. Multidrug Resistance by Type of Dermatological Infection

Infection Type	Total Cases	MDR Cases	Non-MDR Cases	MDR %	95% CI for MDR %	p-value
Bacterial infections	172	96	76	55.8	48.3–63.0	0.161
Fungal infections	140	62	78	44.3	36.3–52.6	
Parasitic infections	38	18	20	47.4	32.5–62.7	
Mixed infections	34	20	14	58.8	42.2–73.6	
Overall	384	196	188	51.0	46.1–56.0	

Age-stratified analysis showed that the 18–40 years group contributed the largest number of MDR cases, with 82 MDR cases among 146 patients, corresponding to an MDR prevalence of 56.2%. Patients aged >60 years had a similarly high MDR proportion of 54.1%, followed by those aged 41–60 years at 46.6% and those aged <18 years at 41.7%. Although MDR percentages varied across age groups, the overall age-group difference was not statistically significant, $\chi^2 = 4.43$, $p = 0.219$.

Table 3. Multidrug Resistance by Age Group

Age Group	Total Cases	MDR Cases	Non-MDR Cases	MDR %	95% CI for MDR %	p-value
<18 years	48	20	28	41.7	28.8–55.7	0.219
18–40 years	146	82	64	56.2	48.1–64.0	
41–60 years	116	54	62	46.6	37.7–55.6	
>60 years	74	40	34	54.1	42.8–64.9	
Overall comparison	384	196	188	51.0	46.1–56.0	

Pathogen-specific analysis demonstrated the highest MDR proportion among Staphylococcus aureus, with 68 MDR isolates among 104 isolates, corresponding to 65.4%. Pseudomonas aeruginosa also showed a high MDR burden, with 42 of 68 isolates (61.8%) demonstrating multidrug resistance. Among fungal pathogens, Candida spp. showed MDR in 20 of 44 isolates (45.5%), while Trichophyton spp. showed MDR in 38 of 96 isolates (39.6%). Sarcoptes scabiei showed MDR or treatment-resistance classification in 16 of 38 cases (42.1%). MDR distribution differed significantly across pathogen groups, $\chi^2 = 18.21$, $p = 0.001$, with bacterial pathogens showing the highest resistance proportions.

Table 4. Multidrug Resistance by Isolated Pathogen

Pathogen	Isolates / Cases	MDR Isolates / Cases	Non-MDR Isolates / Cases	MDR %	95% CI for MDR %	p-value
Staphylococcus aureus	104	68	36	65.4	55.8–73.8	0.001
Pseudomonas aeruginosa	68	42	26	61.8	49.9–72.4	
Candida spp.	44	20	24	45.5	31.7–59.9	
Trichophyton spp.	96	38	58	39.6	30.4–49.6	
Sarcoptes scabiei	38	16	22	42.1	27.9–57.8	
Overall comparison	350	184	166	52.6		

Taken together, the results indicate that multidrug resistance was present in approximately one-half of dermatological infections in the study population. The highest proportional resistance by infection category was observed in mixed infections, while the most pronounced pathogen-specific resistance was observed among Staphylococcus aureus and Pseudomonas aeruginosa. Age-wise, MDR was numerically most frequent in adults aged 18–40 years, although age-group variation did not reach statistical significance. The statistically significant pathogen-level variation suggests that the burden of MDR was concentrated more strongly in specific organisms than in broad demographic age categories.

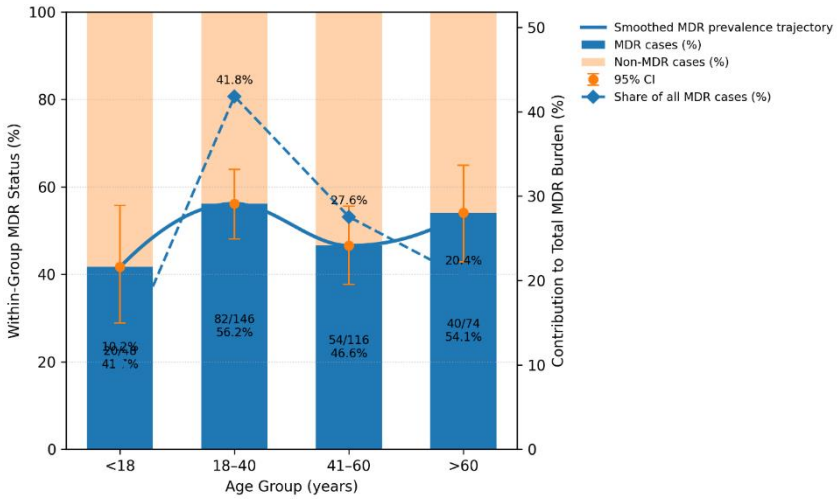

Figure 1. Age-Stratified Multidrug Resistance Burden and Prevalence Gradient

The age-stratified visualization shows that multidrug resistance was not evenly distributed across the cohort: adults aged 18–40 years had the highest within-group MDR prevalence at 56.2% and contributed the largest share of all MDR cases at 41.8%. Patients aged >60 years had a similarly elevated MDR prevalence of 54.1%, but because this group was smaller, it contributed 20.4% of the total MDR burden. The 41–60 years group showed an intermediate MDR prevalence of 46.6% and accounted for 27.6% of all MDR cases, while patients aged <18 years had the lowest MDR prevalence at 41.7% and contributed only 10.2% of total MDR cases. This pattern indicates that the clinical burden of MDR was driven primarily by the combination of high prevalence and larger sample size in younger adults, whereas older adults showed a high proportional resistance signal despite representing a smaller subgroup.

DISCUSSION

The present study demonstrated a substantial burden of multidrug resistance among microbiologically confirmed dermatological infections, with approximately one-half of all cases showing resistance to multiple antimicrobial classes. This finding supports the growing concern that skin and soft-tissue infections are no longer reliably manageable through empirical antimicrobial therapy alone, particularly in settings where recurrent infection, delayed culture testing, over-the-counter antimicrobial access, and repeated exposure to topical or systemic agents may influence resistance emergence. The observed overall MDR burden emphasizes that dermatological infections should be considered an important component of antimicrobial resistance surveillance, rather than a minor or isolated clinical problem. Similar concerns have been reported in dermatology-focused resistance studies, where resistant bacterial pathogens, especially Staphylococcus aureus, have increasingly complicated treatment outcomes and narrowed effective therapeutic options (13).

Bacterial infections represented the largest infection category and showed a high MDR proportion, while mixed infections had the highest proportional resistance burden. This pattern is clinically meaningful because mixed infections may reflect more complex microbial ecology, prior treatment exposure, chronicity, or compromised local skin barriers, all of which can increase the likelihood of resistant organisms being present. The high MDR rate among bacterial infections is consistent with broader evidence that bacterial skin pathogens are under strong antimicrobial selection pressure, particularly where broad-spectrum antibiotics are used before microbiological confirmation. Among the isolated pathogens, Staphylococcus aureus demonstrated the highest MDR proportion, followed closely by Pseudomonas aeruginosa. This finding is important because S. aureus remains a leading cause of dermatological and soft-tissue infections, and resistant strains may circulate in both hospital and community environments. Similarly, P. aeruginosa is clinically challenging because of its intrinsic resistance mechanisms, environmental persistence, and capacity to acquire additional resistance determinants, making infections difficult to treat when empirical regimens are not guided by susceptibility data (14).

The resistance observed among fungal pathogens also deserves attention. Although fungal infections had a lower MDR proportion than bacterial and mixed infections, resistance among Candida spp. and Trichophyton spp. indicates that antimicrobial resistance in dermatology is not confined to bacterial disease. Chronic dermatophytosis, recurrent candidiasis, incomplete treatment courses, and inappropriate use of topical combinations containing antifungals, corticosteroids, and antibiotics may contribute to reduced treatment

responsiveness. Emerging literature has increasingly recognized the clinical relevance of antifungal resistance and difficult-to-treat fungal skin infections, particularly in regions where self-medication and non-prescription topical therapy are common (15). The presence of resistance or poor therapeutic response among parasitic infections, particularly scabies-related cases, further highlights the need to distinguish pharmacological resistance from reinfection, inadequate contact treatment, poor adherence, and environmental persistence, all of which can influence apparent treatment failure.

Age-stratified findings showed that adults aged 18–40 years contributed the largest number and share of MDR cases, while patients older than 60 years also showed a high proportional MDR burden. The predominance of MDR among younger adults may be related to higher healthcare-seeking frequency for visible dermatological conditions, greater exposure to topical and systemic antimicrobial therapy, occupational or social contact patterns, and recurrent skin conditions requiring repeated treatment. In contrast, the elevated MDR proportion among older adults may reflect age-associated immune changes, comorbid illness, chronic wounds, polypharmacy, and repeated healthcare exposure. Although the youngest group had the lowest MDR proportion, the presence of resistance in children remains clinically relevant because early antimicrobial exposure may shape future microbial susceptibility patterns and increase the risk of recurrent resistant infection over time. Similar population-level variability has been described in antimicrobial resistance research, where host factors, healthcare exposure, and immune status influence both infection persistence and resistance selection (16).

The pathogen-specific distribution showed that resistance was more strongly concentrated by organism type than by broad demographic category. This is an important clinical observation because treatment decisions in dermatology are often initially based on lesion morphology and clinical suspicion rather than confirmed microbiology. The high MDR rates in S. aureus and P. aeruginosa suggest that recurrent, severe, non-healing, or previously treated skin infections should be prioritized for culture and susceptibility testing. Gram-positive cocci and gram-negative rods have distinct resistance mechanisms, and their clinical behavior differs according to tissue involvement, prior antimicrobial exposure, and host factors (17). P. aeruginosa, in particular, is associated with intrinsic resistance, efflux pump activity, reduced outer membrane permeability, and biofilm-related persistence, all of which can reduce susceptibility to commonly used antimicrobial agents and complicate empirical treatment (18).

The findings also have implications for routine dermatology practice. Empirical treatment may remain appropriate for uncomplicated first-episode infections, but the high MDR burden observed in this cohort supports a more selective and evidence-guided approach in persistent, recurrent, mixed, comorbid, or treatment-resistant cases. Culture-guided therapy can improve antimicrobial targeting, reduce unnecessary broad-spectrum prescribing, and help prevent further resistance selection. This is particularly relevant in regions where antimicrobial access is insufficiently regulated and patients may begin treatment before clinical consultation. Incorporating microbiological testing into dermatological care pathways would also support local resistance mapping, allowing clinicians to update empirical treatment choices according to regional susceptibility patterns rather than relying on generalized recommendations from other populations (19).

A major strength of this study is its inclusion of multiple dermatological infection categories rather than restricting analysis to a single organism or infection type. The study also incorporated microbiological confirmation and susceptibility testing, which strengthens the validity of the reported resistance patterns compared with purely clinical diagnosis. Stratification by age group, infection category, and pathogen type provides a useful descriptive framework for identifying where MDR burden is most concentrated. The use of standardized susceptibility testing methods further supports consistency in laboratory assessment and allows the findings to contribute to regional surveillance efforts (20).

Several limitations should be considered when interpreting these results. The descriptive cross-sectional design allows estimation of MDR frequency and distribution but does not establish causality or determine independent predictors of resistance. The study was conducted within a defined regional setting, so resistance proportions may differ in other provinces, rural-urban healthcare systems, or tertiary-care populations with different prescribing practices. The absence of molecular characterization limits interpretation of specific resistance mechanisms, clonal spread, and distinction between community-associated and healthcare-associated resistant strains. Follow-up outcomes were also not assessed, so the relationship between MDR status, treatment response, recurrence, complications, and healthcare utilization could not be evaluated. These limitations are common in baseline surveillance studies but are important for framing the findings as descriptive evidence rather than causal inference (21,22).

Despite these limitations, the study provides clinically relevant baseline evidence showing that multidrug resistance is frequent across dermatological infections in South Punjab and is especially pronounced among bacterial and mixed infections. The findings support the need for stronger antimicrobial stewardship in dermatology, improved access to culture and susceptibility testing, and patient education regarding incomplete or unsupervised antimicrobial use. Future analytical studies should examine prior antimicrobial exposure, duration of disease, recurrence, socioeconomic factors, topical steroid-antibiotic combination use, hygiene practices, healthcare contact, and treatment adherence as potential determinants of MDR. Molecular studies would further clarify resistance mechanisms and transmission patterns, while longitudinal designs could determine whether MDR status predicts delayed healing, relapse, or treatment failure (23,24). Overall, the results indicate that dermatological MDR should be addressed through an integrated strategy combining clinical vigilance, laboratory confirmation, rational prescribing, regional surveillance, and public health measures aimed at preserving the effectiveness of available antimicrobial agents.

CONCLUSION

This study demonstrated a substantial burden of multidrug resistance among microbiologically confirmed dermatological infections in South Punjab, with MDR identified in approximately half of the study population and the highest proportional resistance observed among mixed and bacterial infections. Staphylococcus aureus and Pseudomonas aeruginosa showed the most prominent pathogen-specific MDR patterns, while adults aged 18–40 years contributed the largest share of resistant cases and older adults also showed a high proportional resistance burden. These findings emphasize the clinical importance of integrating culture and susceptibility testing into the management of recurrent, persistent, mixed, or previously treated skin infections, particularly in settings where empirical antimicrobial use and non-prescription treatment practices may contribute to resistance selection. Strengthening dermatology-focused antimicrobial stewardship, promoting rational prescribing, improving access to microbiological diagnostics, and establishing regional resistance surveillance are essential to preserve therapeutic effectiveness and improve patient outcomes in dermatological care.

REFERENCES

1. Ugoala EJ. Antimicrobial drug resistance: a systematic review and assessment of resistant pathogen infection prevention and control. 2023.
2. El-Saadony MT, Saad AM, Mohammed DM, Korma SA, Alshahrani MY, Ahmed AE, et al. Medicinal plants: bioactive compounds, biological activities, combating multidrug-resistant microorganisms, and human health benefits: a comprehensive review. 2025;16:1491777.
3. Cosio T, Pica F, Fontana C, Pistoia ES, Favaro M, Valsecchi I, et al. Stephanoascus ciferrii complex: the current state of infections and drug resistance in humans. 2024;10(4):294.
4. Hardefeldt L, Thomas K, Page S, Norris J, Browning G, El-Hage C, et al. Antimicrobial prescribing guidelines for horses in Australia. 2025.
5. Open Resources for Nursing, Ernstmeyer K, Christman E. Antimicrobials. In: Nursing Pharmacology. 2nd ed. Chippewa Valley Technical College; 2023.
6. Agarwal D. Clinicopathological study of skin tumors. 2023.
7. Huia Haira T. The chemical biology of antimicrobial bioactivity derived from kānuka (Kunzea robusta). Wellington: Te Herenga Waka—Victoria University of Wellington; 2024.
8. Duhaniuc A, Păduraru D, Nastase EV, Trofin F, Iancu LS, Sima CM, et al. Multidrug-resistant bacteria in immunocompromised patients. 2024;17(9):1151.
9. Iancu AV, Maftei NM, Dumitru C, Baroiu L, Gurau G, Elisei AM, et al. Prevalence of multidrug resistance pathogens in dermatology: a retrospective study in Romania, 2018–2022. 2024;21(3).
10. Lawal H, Saeed S, Gaddafi M, Mansor N, Yang Q, Hossain D, et al. Nanoparticle-based therapeutics for the treatment of skin infections in animals: a comprehensive literature review. Ger. 2025;5(1):4-19.
11. Marzaman ANF, Roska TP, Sartini S, Utami RN, Sulistiawati S, Enggi CK, et al. Recent advances in pharmaceutical approaches of antimicrobial agents for selective delivery in various administration routes. 2023;12(5):822.
12. Jiang S, Wei Y, Ke H, Song C, Liao W, Meng L, et al. Shengming Jiang, Yangyan Wei, Hu Ke, Chao Song, Wenbiao Liao, Lingchao Meng, Chang Sun, Jiawei Zhou, Chuan Wang, Xiaozhe Su, Caitao Dong, Yunhe Xiong and Sixing Yang. 2023.

13. Khan A, Ali N, Fatima S, Jamshaid A, Saeed A, Zahid MA. Prevalence and antibiotic resistance patterns of Staphylococcus aureus in dermatological infections: a 5-year retrospective study. Int J Biol Res. 2025;3(2):386-393.
14. Hameed S. Human fungal diseases: diagnostics, pathogenesis, drug resistance and therapeutics. Boca Raton: CRC Press; 2024.
15. Chambial P, Thakur N, Bhukya PL, Subbaiyan A, Kumar U. Frontiers in superbug management: innovating approaches to combat antimicrobial resistance. Arch Microbiol. 2025;207(3):60.
16. Labes A. Marine resources offer new compounds and strategies for the treatment of skin and soft tissue infections. Mar Drugs. 2023;21(7):387.
17. Chakrabarti A, Balaji V, Bansal N, Gopalakrishnan R, Gupta P, Jain A, et al. NAMS task force report on antimicrobial resistance. 2025:1-40.
18. Loeffler A, Cain CL, Ferrer L, Nishifuji K, Varjonen K, Papich MG, et al. Antimicrobial use guidelines for canine pyoderma by the International Society for Companion Animal Infectious Diseases. Vet Dermatol. 2025;36(3):234-282.
19. Kelkar R. Microbiology in oncology. In: Tata Memorial Centre Textbook of Oncology. Singapore: Springer; 2024. p. 89-97.
20. Safdar M, ur Rehman S, Hussain M, Nawaz MN, Mueen MA, e Subhani F, et al. Antimicrobial resistance: a global challenge in disease prevention and control. 2023;2.
21. Anderson E, Nair B, Nizet V, Kumar G. Man vs microbes: the race of the century. J Med Microbiol. 2023;72(1):001646.
22. Alqahtani M, Alshehri R, Albarnawi F, Almalki H, Alhalwani A, Alobaidallah M, et al. The correlation between blood antioxidant levels and Klebsiella pneumoniae urinary tract infection. 2023.
23. Bamgbose T, Abdullahi IO, Inabo HI, Bello M, Anvikar AR, editors. Probiotics for the control of malaria and other infectious diseases. 44th Annual Conference of the Nigerian Society for Microbiology; 2023.
24. Lee H, Park SY, Yoon YK. Infection & chemotherapy. 2024;56(1):S1-S98.