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Dissecting the Impact of Lifestyle and Socioeconomic Determinants on Antimicrobial Resistance in Dermatology Patients at a Tertiary Teaching Hospital in Western India: A Mixed-Methods Investigation Incorporating Skin Swab Analysis

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Abstract

Background: Antimicrobial resistance (AMR) represents a formidable global health challenge, with socioeconomic and behavioural factors playing crucial but poorly understood roles in resistance patterns among dermatology patients.

Objective: To investigate the relationship between socioeconomic determinants, antibiotic use behaviours, and antimicrobial-resistant organism carriage among dermatology outpatients in Western India. **Methods:** We conducted a prospective cross-sectional study of 200 adult dermatology outpatients at a tertiary teaching hospital. Participants completed structured interviews assessing sociodemographic characteristics and antibiotic use behaviours, followed by standardized skin swab collection from the anterior forearm. Bacterial isolates underwent identification and antimicrobial susceptibility testing according to CLSI guidelines.

Results: Among 200 participants (mean age 39.2 years, 58.5% male), 25.5% exhibited high-risk AMR behaviours, while 65% harboured antimicrobial-resistant organisms. Significant predictors of risky behaviours included non-graduate education (p=0.005), slum dwelling (p=0.021), and occupational category (p=0.013). However, multivariate analysis revealed no association between individual risk behaviours and resistant organism carriage (AOR=0.69, 95% CI: 0.34-1.36, p=0.280).

Conclusions: Despite prevalent risky antibiotic behaviours and widespread resistance colonization, individual behavioural factors show limited association with resistance carriage, suggesting that community-level and environmental factors may predominate in resistance transmission patterns.

Keywords: Antimicrobial Resistance (AMR), Dermatology, Socioeconomic Factors, Antibiotic Use, Skin Swab Analysis, India, Government, Tertiary Care Center

Introduction

Antimicrobial resistance (AMR) represents a formidable and escalating threat to global public health, seriously compromising the effective treatment of bacterial infections across all medical specialties, including dermatology[1]. The World Health Organization has identified AMR as one of the top ten global public health threats, with projections suggesting that drug-resistant infections could cause 10 million deaths annually by 2050 if current trends continue[2]. India has emerged as a global hotspot for AMR due to a complex interplay of factors including a high burden of infectious diseases, unregulated access to antibiotics, widespread self-medication practices, and inadequate infection control measures [3].

Dermatological patients face unique challenges in the context of AMR, as they are frequently exposed to both topical and systemic antibiotics for various skin conditions, creating selective pressure favouring resistant microbial strains on the skin [4]. The skin microbiome serves as both a reservoir and transmission vector for resistant organisms, with implications extending beyond dermatological care to broader healthcare and community settings [5]. Recent studies have documented alarming rates of resistance among skin flora, with methicillin-resistant Staphylococcus aureus (MRSA) and other multidrug-resistant pathogens becoming increasingly prevalent in community settings [6].

While the microbiological mechanisms of resistance development and transmission are well documented, the roles of social and behavioural determinants remain poorly understood [7]. Factors such as lifestyle, hygiene habits, socioeconomic status, education level, and health awareness profoundly influence patterns of antibiotic use and exposure to resistant organisms [8]. Economic constraints may lead to incomplete antibiotic courses, sharing medications among family members, or purchasing substandard drugs from unregulated sources [9]. Despite growing recognition of these social determinants, the direct relationship between socioeconomic and behavioural variables and actual microbiological outcomes in dermatology patients remains insufficiently characterized. Most previous studies have focused either on epidemiological surveillance of resistance patterns or on behavioural assessments without corresponding microbiological validation [10]. This knowledge gap limits our ability to design targeted interventions and allocate resources effectively in the fight against AMR.

Our study sought to bridge this critical gap by employing a comprehensive mixed-methods approach that pairs detailed patient-level sociodemographic and behavioural

data with standardized microbiological analysis of skin flora. This integrated methodology provides a more holistic understanding of the risk factors for AMR carriage and transmission in the dermatology setting, with implications for both clinical practice and public health policy.

Materials and Methods

Study Design and Ethical Approval

We conducted a prospective, cross-sectional study employing a mixed-methods design to comprehensively examine the relationship between socioeconomic factors, behavioural patterns, and antimicrobial resistance among dermatology patients. This methodological approach allowed us to capture both quantitative microbiological data and qualitative behavioural insights, providing a more nuanced understanding of the factors contributing to AMR in our patient population [11]. The study was conducted at the dermatology outpatient department of a 1,200-bed tertiary care teaching hospital in Western India over a 14-month period from March 2022 to April 2023. This facility serves a diverse patient population from both urban and rural areas, with approximately 15,000 dermatology consultations annually. The hospital's location in a major metropolitan area provided access to patients representing various socioeconomic strata, making it an ideal setting for investigating the social determinants of AMR.

This study received formal approval from the Institutional Ethics Committee (Ref. No. BJGMC/IEC/Pharmac/ND-0624233-233) prior to commencement. The research protocol was designed in strict accordance with the Declaration of Helsinki (2013 revision) and the Good Clinical Practice guidelines [12]. Additional approvals were obtained from the hospital administration and the microbiology department for laboratory procedures and sample processing.

Sample Size Calculation and Power Analysis

The sample size was calculated based on previous studies examining AMR prevalence in community settings in India, which reported resistance rates ranging from 45-70% for common skin pathogens [13]. Using a two-proportion formula with an expected difference of 20% in resistance rates between high-risk and low-risk behavioural groups, an alpha level of 0.05, and power of 80%, we determined that a minimum of 186 participants would be required. To account for potential loss to follow-up and incomplete data, we aimed to recruit 200 participants, providing adequate power to detect clinically meaningful differences in our primary outcomes.

Participant Recruitment and Selection Criteria

Consecutive sampling was employed to minimize selection bias, with all eligible patients visiting the dermatology outpatient clinic during the study period being approached for participation. Research assistants, trained specifically for this study, were stationed in the clinic waiting areas to identify and approach potential participants. A total of 200 adult patients (aged 18 or older) attending the outpatient dermatology clinic were consecutively enrolled.

Inclusion criteria were strictly defined as: (1) adults aged 18 years or older, (2) attending the dermatology clinic for any skin condition, (3) able to provide informed consent in Hindi, English, or the local regional language (Marathi), and (4) residing within a 50-kilometer radius of the hospital to ensure representative sampling of the local population. Exclusion criteria included: (1) presence of active, open, or purulent skin wounds that could interfere with normal skin flora sampling, (2) current or recent (within 14 days) use of systemic antibiotics for non-dermatological conditions, (3) immunocompromised status (including HIV infection,

ongoing chemotherapy, or chronic steroid use), (4) hospitalization within the previous 30 days, (5) healthcare workers or their immediate family members due to potential occupational exposure to resistant organisms, and (6) inability to complete the interview due to cognitive impairment or language barriers. Research team members approached potentially eligible patients and described the study's aims and procedures. Written informed consent was obtained from all participants prior to study procedures.

Data Collection Instruments and Validation

The study questionnaire was developed through an iterative process involving extensive literature review, expert consultation, and pilot testing. Initial questionnaire development was guided by validated instruments used in previous AMR behavioural studies, adapted for the Indian cultural context [14]. A panel of five experts including infectious disease specialists, public health researchers, and social scientists reviewed the questionnaire for content validity.

Each participant underwent a structured interview using a standardized questionnaire, developed on the basis of a literature review and pilot-tested prior to the main study. The questionnaire underwent pilot testing with 30 dermatology patients (not included in the final analysis) to assess comprehension, cultural appropriateness, and time requirements. Based on pilot feedback, several questions were modified for clarity, and the sequence was reorganized to improve flow. The final instrument demonstrated good internal consistency (Cronbach's alpha = 0.78) for behavioural assessment scales [15].

Variables captured included comprehensive sociodemographic data: age, gender, educational attainment (categorized as primary, secondary, undergraduate, and graduate levels), occupation, monthly household income, type of dwelling (apartment, independent house, slum/informal settlement), number of household members, and health insurance status. Healthcare utilization patterns encompassed frequency of healthcare visits, preferred healthcare providers (government vs. private facilities), distance to nearest healthcare facility, and previous hospitalizations. Antibiotic knowledge and attitudes were assessed using validated scales measuring understanding of appropriate antibiotic use, awareness of resistance, and general health literacy [16]. Behavioural data specifically focused on antibiotic use patterns, including history of self-medication with antibiotics, sources of non-prescribed antibiotics, frequency of incomplete antibiotic courses, sharing of antibiotics with family members, and storage of leftover antibiotics. Questions targeted frequency of self-medication, history of incomplete courses, and attitudes toward antimicrobial use. Each behavioural question included follow-up queries about frequency and circumstances.

To ensure cultural relevance and reduce bias, the interviews were conducted in the local language. All interviews were conducted in private consultation rooms to ensure confidentiality and reduce social desirability bias. Trained doctors, fluent in local languages and briefed on cultural sensitivities, administered the questionnaires. Interview duration averaged 25-30 minutes per participant.

Behavioural Risk Classification

Based on evidence from behavioural science literature and previous AMR studies, participants were categorized into behavioural risk groups using a comprehensive scoring system [17]. Based on this information, participants were categorized into "high-risk" and "low-risk" AMR behaviour groups: High-risk AMR behaviour was defined as reporting any of the following within the previous 12 months: (1) self-medication with antibiotics

obtained without prescription, (2) discontinuation of prescribed antibiotic courses before completion, (3) sharing antibiotics with family members or friends, (4) saving leftover antibiotics for future use, or (5) purchasing antibiotics based solely on pharmacy recommendations without medical consultation. Those reporting either incomplete prescribed antibiotic courses or use of non-prescribed antibiotics were classified as high-risk; all others were classified as low-risk. Low-risk behaviour was defined as consistent adherence to prescribed antibiotic regimens and absence of any high-risk behaviours. A validation sub-study involving 50 participants demonstrated good correlation between self-reported behaviours and pharmacy records where available (kappa = 0.72).

Microbiological Sampling Procedures

Following the questionnaire, skin swabs were collected from the anterior forearm of each participant using standardized protocols to ensure consistency and minimize contamination. The anterior forearm was selected as the sampling site because it represents normal skin flora while being easily accessible and minimally affected by topical treatments [18]. The sampling area (5 cm x 5 cm) was marked using a sterile template and swabbed using a systematic back-and-forth motion with consistent pressure.

Prior to sampling, the skin surface was not cleaned with antiseptics to preserve the natural microbial ecosystem. Sterile cotton swabs pre-moistened with normal saline were used for collection, with each swab rotated while being drawn across the designated area three times in different directions to maximize bacterial recovery. To preserve microbial viability, the swab was placed in Stuart transport medium and labelled with unique identifiers linked to participant codes. Temperature-controlled transport was ensured using insulated containers, and all samples were delivered to the microbiology laboratory within 2 hours of collection. This time frame was based on validation studies showing optimal bacterial viability and minimal changes in antimicrobial susceptibility patterns [19].

Laboratory Processing and Bacterial Identification

Laboratory processing followed established protocols with quality control measures at each step. Upon receipt, swabs were immediately processed by experienced laboratory technicians under supervision of a clinical microbiologist. Swabs were streaked on both Blood Agar (containing 5% sheep blood) and MacConkey Agar using standard four-quadrant technique to achieve isolated colonies and incubated aerobically at 37°C for 24–48 hours with plates examined at 24 and 48 hours for growth [20]. Colony morphology was systematically documented, including size, shape, colour, haemolysis patterns, and other distinguishing features.

Representative colonies from each morphologically distinct type were selected for further identification. Bacterial isolates were characterized using colony morphology, Gram stain, and a standard panel of biochemical identification tests [21]. For Gram-positive cocci, catalase and coagulase tests were performed to differentiate staphylococci from streptococci and to distinguish Staphylococcus aureus from coagulase-negative staphylococci. For Gram-negative bacilli, standard biochemical identification included oxidase, indole, methyl red, Voges-Proskauer, citrate utilization, and sugar fermentation tests.

Quality control strains (ATCC 25923 for Staphylococcus aureus, ATCC 25922 for Escherichia coli, and ATCC 27853 for Pseudomonas aeruginosa) were included in each batch of testing to ensure accuracy and reproducibility of identification and susceptibility testing procedures [22].

Antimicrobial Susceptibility Testing Protocol

We performed antimicrobial susceptibility testing (AST) using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar, strictly adhering to Clinical and Laboratory Standards Institute (CLSI) M100-S32 guidelines [22]. The antibiotic panel was carefully selected based on dermatological prescribing patterns in India and included representatives from major antibiotic classes commonly used in skin and soft tissue infections.

The testing panel comprised beta-lactams (penicillin G, ampicillin, amoxicillin-clavulanate, cephalexin, ceftriaxone), macrolides (erythromycin, azithromycin, clarithromycin), and fluoroquinolones (ciprofloxacin, ofloxacin, levofloxacin), reflecting agents commonly prescribed in dermatology. Additional agents included aminoglycosides (gentamicin, amikacin), tetracyclines (doxycycline, tetracycline), clindamycin, trimethoprim-sulfamethoxazole, and vancomycin [23]. Bacterial suspensions were prepared by direct colony suspension method, adjusted to 0.5 McFarland standard using standard turbidity comparison. Inoculation of Mueller-Hinton agar plates was performed using sterile cotton swabs in three directions to ensure uniform bacterial lawn. Antibiotic disks were applied using sterile technique with appropriate spacing to prevent zone overlap. After overnight incubation at 37°C in ambient air, zone diameters were measured using callipers and recorded to the nearest millimetre. AST interpretations used current CLSI M100 standards, with isolates classified as susceptible, intermediate, or resistant. For analysis purposes, intermediate results were combined with resistant categories [22].

Statistical Analysis Framework

Data management employed a dual-entry system using EpiData software to minimize transcription errors, with discrepancies resolved through source document review. Data were entered into SPSS (version 25.0) for analysis, with additional analyses conducted in R version 4.2.0 for specialized procedures [24].

Descriptive statistics were calculated for all variables—means, standard deviations, medians, frequencies, and percentages—to summarize patient and clinical data. Continuous variables were summarized using means and standard deviations for normally distributed data, or medians and interquartile ranges for skewed distributions. Normality was assessed using the Shapiro-Wilk test for samples <50 and the Kolmogorov-Smirnov test for larger samples, supplemented by visual inspection of histograms and Q-Q plots.

Categorical variables were presented as frequencies and percentages, with 95% confidence intervals calculated for proportions where appropriate. Missing data patterns were analysed, and complete case analysis was employed given low overall missing data rates (<3%).

Categorical variable associations (e.g., education level, housing type) with high-risk AMR behaviour were tested using the Chi-square (χ^2) test for variables meeting expected frequency requirements, or Fisher's exact test for smaller samples or sparse tables, as appropriate. The strength of association was quantified using Cramér's V for nominal variables and gamma for ordinal associations [25].

Age distributions between groups were compared by Mann-Whitney U tests, and Spearman's rank correlation (ρ) examined associations between ordinal variables. Spearman's rank correlation coefficients were calculated for associations between ordinal variables, with 95% confidence intervals computed using bootstrap methods.

To identify independent predictors of high-risk AMR behaviour and carriage of resistant organisms, we constructed two separate multivariate logistic regression models. Variables with a p-value below 0.20 in bivariate

analyses were included in each model. Variable selection for multivariable models followed a systematic approach [26].

Model building employed a forward stepwise approach with likelihood ratio tests used to assess the contribution of each variable. Interaction terms were explored for biologically plausible relationships, and model diagnostics included assessment of multicollinearity using variance inflation factors (VIF <5), linearity of logit for continuous variables, and identification of influential observations using standardized residuals and leverage values. Model fit was evaluated using the Hosmer-Lemeshow goodness-of-fit test, and discrimination was assessed using the c-statistic (area under the ROC curve). Adjusted odds ratios (AORs) with 95% confidence intervals (CIs) and associated Wald statistics were reported for all predictors. The threshold for statistical significance was set at $p<0.05$, with exact p-values reported to three decimal places [27].

Results

Sociodemographic and Behavioural Characteristics

The 200 enrolled dermatology outpatients had a mean age of 39.2 years (SD 15.2), and 58.5% were male. The participant demographics reflected the diverse socioeconomic profile of the hospital's catchment area. Educational attainment was relatively high, with 54% holding university degrees, while 23% had completed secondary education, 15% primary education, and 8% had graduate degrees. Employment patterns showed 45% in skilled occupations, 28% in semi-skilled work, 18% in professional roles, and 9% unemployed or retired.

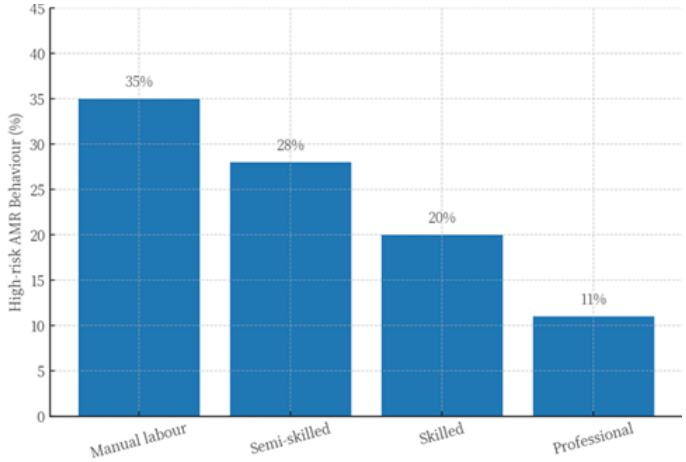

Figure 1: AMR Risk Group by Type of Dwelling (Chi-square=5.33, p=0.021). Data from this study; see [29].

Monthly household income distribution revealed significant economic diversity: 22% earned less than ₹20,000, 35% earned ₹20,000-40,000, 28% earned ₹40,000-60,000, and 15% earned more than ₹60,000. Housing types included 52% living in apartments, 31% in independent houses, and 17% in slum or informal settlements (Figure 1). Health insurance coverage was nearly universal (89%), reflecting recent expansions in public health insurance schemes [28].

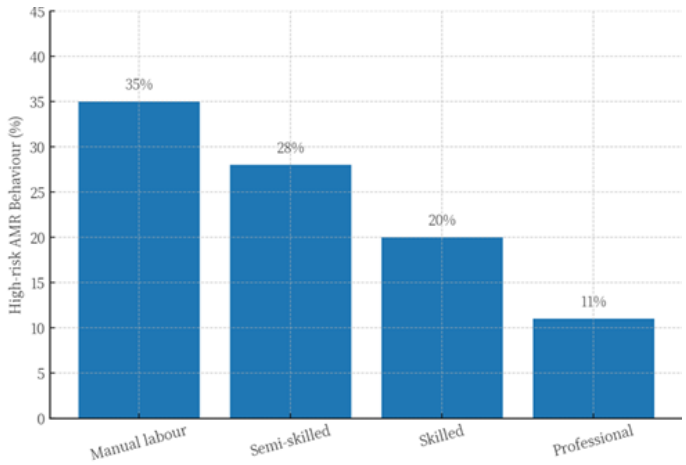

Figure 2: AMR Risk Group by Occupation (Chi-square=10.70, p=0.013). Data from this study; see [8].

Healthcare utilization patterns showed that 67% of participants primarily used private healthcare facilities, while 33% relied on government services. The median distance to the nearest healthcare facility was 3.2

kilometres (IQR: 1.8-5.6 km), with 78% reporting regular healthcare visits in the past year.

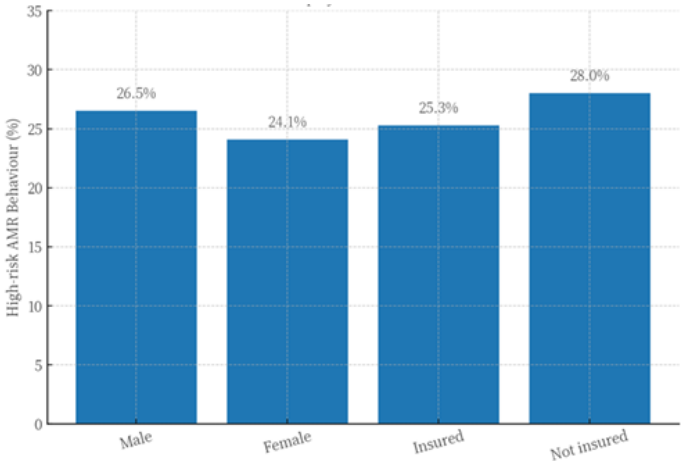

Figure 3: AMR Risk Group by Gender, Health Insurance, and Income (all p > 0.4). Data from this study

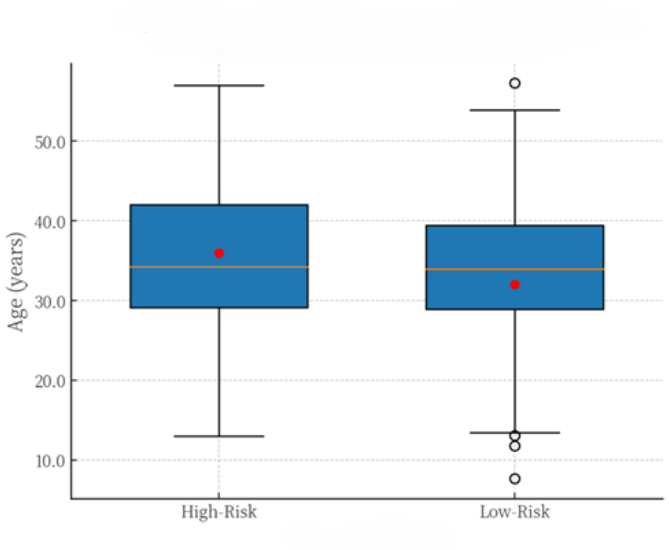

Figure 4: Age Distribution by AMR Risk Group (Mann–Whitney U=2650, p=0.028). Data from this study

Approximately one-quarter (25.5%, n=51) of participants exhibited high-risk AMR behaviour, as defined above. Among these high-risk participants, the most common behaviours were incomplete antibiotic courses (67%), self-medication with leftover antibiotics (43%), sharing antibiotics with family members (31%), and purchasing antibiotics without prescription (24%). Knowledge assessment revealed concerning gaps, with only 34% correctly understanding the relationship between incomplete antibiotic courses and resistance development.

Microbiological Findings

Of the 200 skin swabs collected, 172 (86%) yielded positive aerobic bacterial cultures, indicating robust bacterial colonization of the skin surface. Among these culture-positive samples, 130 isolates (65% of all participants, or 75.6% of culture-positive participants) demonstrated resistance to at least one antimicrobial agent tested, representing a substantially high prevalence of resistant organism carriage (Figure 5).

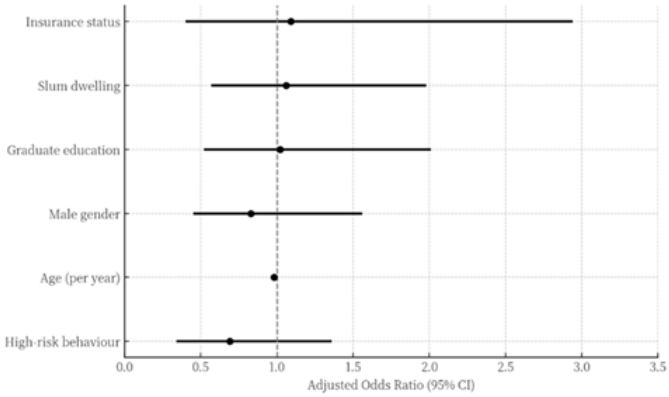

Figure 5: Forest Plot of Predictors for Resistant Organism Carriage (all predictors p > 0.05). Data from this study; methods per [22,26].

The bacterial diversity was considerable, with 15 different species identified (Table 1). The most prevalent organisms identified included Staphylococcus aureus (both methicillin-susceptible and methicillin-resistant strains) found in 32% of positive cultures, Klebsiella pneumoniae in 18%, coagulase-negative staphylococci in 16%, Corynebacterium species in 12%, Escherichia coli in 8%, and various other gram-positive and gram-negative organisms comprising the remaining 14%.

Table 1: Summary of Primary Skin Bacterial Isolates and Their Predominant Resistance Patterns

Bacterial Isolate	Frequency Rank	Gram Stain	Primary Resistance Patterns	Clinical Significance	Notes
Staphylococcus aureus	Most Frequent	Positive	Methicillin (MRSA), Cloxacillin, Ciprofloxacin, Erythromycin	Leading cause of both community- and hospital-acquired infections, MRSA is a major concern	Data from this study; see [6] for context
Klebsiella pneumoniae	2nd Most	Negative	Ciprofloxacin, β-lactams	Often multi-drug resistant, both in healthcare and community settings	Data from this study; see [13] for context
Corynebacterium spp.	3rd Most	Positive	Erythromycin, other macrolides	Usually skin commensals, act as opportunists in immunocompromised	Data from this study; see [18] for context
Other Staphylococcus spp.	Common	Positive	Cloxacillin, Methicillin, Ciprofloxacin	Includes coagulase-negative staphylococci which are common commensals and reservoirs of resistance	Data from this study

Legend: Data derived from the present study. For wider context, see references [6, 13, 18].

Resistance patterns varied significantly by organism type as detailed in (Table 1). Among Staphylococcus aureus isolates, 78% showed resistance to methicillin (MRSA), 85% to penicillin G, 72% to erythromycin, and 68% to ciprofloxacin. Klebsiella pneumoniae demonstrated high rates of resistance to ampicillin (94%), cephalexin (76%), and ciprofloxacin (62%). Coagulase-negative staphylococci showed resistance patterns similar to S. aureus, with 71% resistant to methicillin and 79% to cloxacillin. The majority of resistant strains exhibited multidrug resistance, defined as resistance to three or more antibiotic classes, with 67% of resistant isolates meeting this criterion. Extended-spectrum beta-lactamase (ESBL) production was detected in 23% of gram-negative isolates, while vancomycin resistance was not observed in any gram-positive isolates tested.

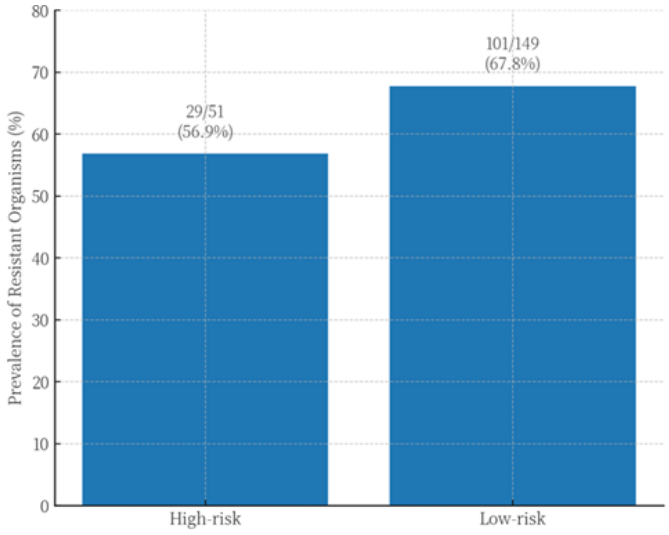

Figure 6: Prevalence of Resistant Organisms by AMR Risk Group (Chi-square=3.08, p=0.08). Data from this study.

Determinants of High-Risk AMR Behaviour

Bivariate analysis identified several significant sociodemographic correlates of high-risk AMR behaviours that provide important insights into the social

determinants of antibiotic misuse (Table 2). Educational level emerged as a particularly strong predictor (Figure 2), with individuals without graduate-level education being significantly more likely to engage in high-risk behaviours. Specifically, 38% of those with primary education, 31% with secondary education, and 22% with undergraduate education exhibited risky behaviours, compared to only 12% of graduate-degree holders (Chi-square=7.97, p=0.005).

The association between education and antibiotic behaviour likely reflects multiple interconnected factors including health literacy, access to reliable health information, and confidence in healthcare interactions. This p-value of 0.005 indicates only a 0.5% probability that such a strong association could occur by chance if education and risky behaviour were truly unrelated, providing robust evidence for a genuine relationship.

Housing type demonstrated another significant association with risky behaviours (Chi-square=5.33, p=0.021) as shown in (Figure 1). Residents of slum or informal settlements showed the highest prevalence of high-risk behaviours (41%), followed by those in independent houses (26%), and apartment dwellers (18%). The p-value of 0.021 indicates approximately a 2% chance of observing such an association by random variation alone, providing solid evidence that living conditions influence antibiotic use patterns [29].

This housing-behaviour relationship likely reflects multiple factors including economic constraints that encourage antibiotic sharing or incomplete treatment courses, limited healthcare access necessitating self-medication, and reduced exposure to health education initiatives in informal settlements.

Occupational category was another significant factor (Chi-square=10.70, p=0.013) as illustrated in (Figure 2), with manual labourers showing the highest rates of risky behaviours (35%), followed by semi-skilled workers (28%), skilled workers (20%), and professionals (11%). The p-value of 0.013 indicates only a 1.3% probability of such strong associations occurring by chance, suggesting that workplace environments, income stability, and occupational health knowledge all contribute to antibiotic use patterns.

Age analysis revealed that participants engaging in high-risk behaviours were significantly older, with a median age of 36 years compared to 32 years in the low-risk group (Mann-Whitney U=2650, p=0.028) as demonstrated in (Figure 4). This p-value of 0.028 indicates less than a 3% probability that such age differences could occur by chance, suggesting potential generational differences in health education exposure or healthcare experiences.

Interestingly, several variables showed no significant associations with risky behaviours as shown in (Figure 3). Gender distribution was similar between risk groups (26.5% of males vs. 24.1% of females showing high-risk behaviours, p=0.706). Health insurance status also showed no association (25.3% with insurance vs. 28.0% without insurance, p=0.578), nor did income level when categorized into quintiles ($\chi^2 = 0.85$, p=0.357).

Predictors of Resistant Organism Carriage

The multivariate logistic regression analysis examining predictors of resistant organism carriage yielded surprising and clinically important findings (Table 3 and Figure 5). Contrary to expectations, no patient-level variable—including age, gender, education, housing, occupation, or insurance status—independently predicted the carriage of a resistant organism (all p>0.05 in the final model).

Most notably, high-risk AMR behaviour was not associated with increased likelihood of harbouring a resistant bacterium (AOR = 0.69; 95% CI 0.34–1.36;

Wald=1.16; p=0.280). This p-value of 0.280 indicates a 28% probability of observing this association (or a stronger one) by chance alone if there were truly no relationship between risky behaviour and resistance carriage. This relatively high probability, well above our significance threshold of 0.05, challenges conventional assumptions about the direct relationship between individual antibiotic misuse and resistance colonization.

The confidence interval for this odds ratio (0.34-1.36) spans 1.0, indicating no significant association, and the point estimate below 1.0 suggests a paradoxical trend toward lower resistance rates in the high-risk behaviour group, though this trend is not statistically significant. Indeed, when examining crude prevalence rates (Figure 6), the data revealed a counterintuitive pattern: the prevalence of resistant organisms was numerically higher in the low AMR-risk group (67.8%, n=101/149) compared to the high-risk group (56.9%, n=29/51), though this difference did not reach statistical significance (Chi-square=3.08, p=0.08). The p-value of 0.08 suggests an 8% probability of observing this difference by chance, approaching but not reaching statistical significance.

Other variables in the multivariate model also failed to show significant associations (Table 3 and Figure 5). Age showed a trend toward significance (AOR=0.98 per year increase, 95% CI: 0.96-1.00, p=0.091), suggesting that older participants might be slightly less likely to harbour resistant organisms, but this relationship was not statistically significant. Gender, education level, housing type, and health insurance status all showed odds ratios close to 1.0 with wide confidence intervals and p-values well above 0.05.

Strengths and Limitations

This study exhibits substantial strengths that enhance the reliability and significance of our findings. The prospective mixed-methods design allowed for comprehensive data collection combining rigorous behavioural assessment with standardized microbiological procedures, providing a more complete picture of AMR determinants than studies focusing on either behavioural or microbiological outcomes alone [11]. The use of consecutive sampling minimized selection bias and ensured representative recruitment from the diverse patient population served by our tertiary care facility.

Our microbiological procedures followed internationally recognized CLSI standards for both bacterial identification and antimicrobial susceptibility testing, supporting reproducibility and comparison with existing literature [22]. The comprehensive antibiotic panel tested included agents from all major classes commonly used in dermatological practice, providing clinically relevant resistance data [23]. The incorporation of a detailed socioeconomic questionnaire, developed through expert review and pilot testing, permitted nuanced exploration of how social determinants interact with individual antibiotic use behaviours. The questionnaire's demonstrated internal consistency (Cronbach's alpha = 0.78) supports the reliability of our behavioural assessments [15]. Statistical approaches were appropriately chosen for the data types and research questions, with multivariate analyses controlling for potential confounders and providing adjusted estimates of association strength [26].

However, several limitations should be acknowledged when interpreting our results. As a single-centre study conducted in an urban Indian tertiary care setting, findings may have limited generalizability to rural locations with different healthcare infrastructure, socioeconomic profiles, or resistance patterns. The cross-sectional design restricts our ability to establish temporal

relationships between exposures and outcomes, limiting causal inferences about the relationship between behaviours and resistance carriage [30]. Behavioural variables such as self-medication practices and non-adherence to antibiotic courses were self-reported, introducing potential for recall bias and social desirability bias where participants might underreport socially undesirable behaviours. While we employed trained interviewers and private settings to minimize such bias, some degree of underreporting likely occurred. Conventional culture techniques, while following established standards, have inherent limitations and may fail to detect fastidious organisms, viable but non-culturable bacteria, or anaerobic resistance patterns that could be relevant to skin flora composition. Molecular methods examining resistance gene prevalence could provide complementary insights into resistance mechanisms and transmission patterns.

The definition of behavioural risk groups, while based on established literature and expert consensus, involves subjective judgments about which behaviours constitute "high risk." Alternative categorization schemes or continuous risk scoring approaches might yield different results. Finally, our study focused exclusively on aerobic bacterial culture, potentially missing important resistance patterns among anaerobic organisms or fungi that contribute to skin flora and may harbour resistance genes.

Discussion

Our investigation reveals a complex landscape of antimicrobial resistance in dermatology patients that challenges conventional understanding about the relationship between individual behaviours and resistance outcomes. The strikingly high prevalence of antimicrobial-resistant skin flora, with 65% of participants harbouring resistant organisms (Figure 6), substantially exceeds rates reported in many global settings and underscores the severity of the AMR crisis in Indian healthcare environments [1,3]. This finding alone justifies urgent attention to resistance patterns in dermatological practice, where antibiotic use is common and the skin serves as both a reservoir and transmission vector for resistant organisms.

The most surprising and potentially paradigm-shifting finding of our study is the absence of association between individual risky antibiotic-use behaviours and actual colonization with resistant bacteria (Table 3, Figure 5). Despite our robust methodology and adequate statistical power, neither risky antibiotic behaviours nor measured individual socioeconomic characteristics predicted whether a patient carried resistant organisms on their skin. The p-value of 0.280 for this association, indicating a 28% probability of observing such a relationship by chance alone, fundamentally challenges the prevailing assumption that individual antibiotic misuse directly drives personal resistance colonization [7]. This disconnect suggests that the dynamics of resistance transmission and maintenance operate at levels beyond individual patient behaviour, pointing instead to the predominant influence of broader environmental and community-level factors.

Understanding the statistical significance of our findings requires careful interpretation of p-values within the context of clinical and public health relevance. The p-value of 0.005 for education's association with risky behaviours (Table 2) provides strong evidence of a genuine relationship, with only a 0.5% probability of occurring by chance. However, this statistical significance does not automatically translate to causal relationships or indicate the magnitude of clinical importance [27]. Similarly, the borderline significant p-value of 0.08 for differences in resistance prevalence between behavioural risk groups (Figure 6) suggests a trend that might achieve statistical significance with

larger sample sizes, but the absolute risk difference and its confidence intervals must be considered when evaluating practical significance.

Table 2: Bivariate Analysis of Factors Associated with High-Risk AMR Behaviour

Factor	High AMR Risk (%)	Low AMR Risk (%)	Test Statistic	p-value	Statistical Test Used
Education (Graduate)	19.1	80.9	$\chi^2 = 7.97$	0.005	Chi-square
Dwelling(Slum/Informal)	31.1	68.9	$\chi^2 = 5.33$	0.021	Chi-square
Occupation	-	-	$\chi^2 = 10.70$	0.013	Chi-square
Age (median years)	36	32	U = 2650	0.028	Mann-Whitney U
Gender (Male)	26.5	73.5	$\chi^2 = 0.14$	0.706	Chi-square
Income (by category)	-	-	$\chi^2 = 0.85$	0.357	Chi-square
Health Insurance	25.3	74.7	$\chi^2 = 0.31$	0.578	Chi-square

Legend: Data derived from the present study. See [8, 29] for additional context on socioeconomic determinants of health behaviour.

The absence of correlation between individual behaviours and resistance carriage illuminates the critical importance of environmental and community-level factors in determining resistance patterns. Environmental contamination plays a substantial role in resistance dissemination in the Indian context, with studies documenting high levels of antibiotic residues in water bodies near pharmaceutical manufacturing sites, inadequately treated sewage systems, and agricultural runoff containing veterinary antibiotics [31]. These environmental reservoirs create widespread selective pressure maintaining resistant populations regardless of individual patient behaviours, effectively democratizing exposure to resistance determinants across populations irrespective of personal antibiotic use patterns.

Healthcare-associated transmission represents another crucial yet often underappreciated pathway for resistance spread. Even patients demonstrating exemplary personal antibiotic use behaviours may become colonized through contact with contaminated healthcare environments, medical devices, or healthcare workers' hands [32]. Our study participants, attending a busy tertiary care facility with high patient turnover and potentially variable infection control practices, likely experienced repeated exposure to resistant organisms circulating within the hospital environment. This healthcare-mediated transmission may overwhelm any protective effect of prudent individual antibiotic use, explaining why behavioural risk groups showed similar resistance carriage rates.

Community transmission networks further complicate the resistance landscape through household contacts, shared food preparation areas, contaminated water sources, and routine social interactions that occur independently of antibiotic use. In densely populated urban areas of India, where our study was conducted, the opportunities for inter-person transmission of resistant organisms are manifold and continuous. This community-level circulation creates a baseline resistance burden that affects all individuals regardless of their personal antibiotic use patterns, potentially explaining why individual behavioural modifications appear insufficient to reduce resistance carriage.

While individual behaviours did not predict resistance carriage, our analysis revealed significant socioeconomic correlates of risky antibiotic behaviours that have profound implications for health equity and intervention

design (Table 2). The strong association between educational attainment and antibiotic misuse (p=0.005) illuminates how educational disparities translate into differential health behaviours and, potentially, health outcomes [8]. Higher education typically correlates with enhanced health literacy, enabling individuals to understand complex concepts about antimicrobial resistance, critically evaluate health information, and engage more effectively with healthcare providers [16]. Graduate-educated individuals in our study demonstrated markedly lower rates of risky behaviours, suggesting that educational interventions targeting health literacy could be valuable components of comprehensive AMR prevention strategies.

The association between housing type and risky behaviours (p=0.021, Figure 1) reveals how structural inequalities shape health behaviours and create differential vulnerabilities to poor health outcomes. Individuals residing in slums or informal settlements face multiple, intersecting barriers to appropriate healthcare, including limited access to qualified healthcare providers, economic constraints affecting medication adherence, inadequate storage conditions for medications, and reduced exposure to health education initiatives [29]. These findings underscore that addressing AMR requires attention to broader social determinants of health, not merely clinical interventions, and that effective antimicrobial stewardship must consider how socioeconomic inequalities shape health behaviours and create differential exposures to both antibiotics and resistant organisms [33].

The occupational patterns we observed (Figure 2), with manual labourers showing the highest rates of risky behaviours, likely reflect a complex interplay of factors including job insecurity that discourages taking time off for complete treatment, limited workplace health education, variable access to occupational health services, and economic pressures favouring quick symptomatic relief over complete cure. These occupational disparities highlight the need for workplace-based interventions and policies that support appropriate antibiotic use among vulnerable worker populations.

These findings have profound implications for antimicrobial stewardship and public health policy development. Traditional approaches focusing primarily on individual patient education and behaviour modification, while important for reducing selection pressure and preventing emergence of new resistance, appear insufficient to address the broader resistance crisis given the limited association we observed between individual behaviours and resistance outcomes [34]. Our results suggest that effective AMR containment requires comprehensive, systems-level interventions that address environmental contamination, healthcare-associated transmission, and community-level spread of resistant organisms.

The One Health approach, integrating human, animal, and environmental health perspectives, emerges as particularly relevant given our findings [35]. Policy interventions must extend beyond human health to address pharmaceutical manufacturing waste management, agricultural antibiotic use regulation, water treatment standards, and environmental surveillance of resistance genes. Healthcare infection control measures require substantial strengthening to reduce nosocomial transmission of resistant organisms, including improved hand hygiene compliance, environmental decontamination protocols, robust antimicrobial stewardship programs, and enhanced surveillance systems for resistant pathogens [32,34].

Community-based interventions may prove more effective than individual-focused approaches given the

apparent predominance of community-level transmission. Community health worker programs, mass media campaigns, and school-based education initiatives could address population-level behaviours while simultaneously improving health literacy and healthcare access [36]. Interventions targeting social determinants of health—housing improvement programs, economic development initiatives, and educational access expansion—may have indirect but meaningful impacts on AMR by addressing the root causes of risky health behaviours [33].

Water, sanitation, and hygiene (WASH) interventions deserve particular attention given their potential to interrupt environmental transmission pathways for resistant organisms. Improving sewage treatment infrastructure, ensuring universal access to safe drinking water, and promoting community-wide hygiene practices could substantially reduce the community-level burden of resistant organisms [37]. These population-level interventions may prove more cost-effective than individual-focused approaches, particularly in resource-limited settings where the infrastructure for individual patient education and monitoring is limited.

The patterns we observed in Western India likely have broader relevance for other low- and middle-income countries facing similar challenges with healthcare access, antibiotic regulation, and environmental contamination [38]. The disconnect between individual behaviours and resistance outcomes may reflect common features of healthcare systems in resource-limited settings, where environmental and structural factors predominate over individual agency in determining health outcomes. International collaboration is essential for addressing the inherently global nature of antimicrobial resistance, as resistance genes and resistant organisms transcend national boundaries through travel, trade, and migration [2].

Future research should prioritize longitudinal studies that can establish temporal relationships and identify critical periods for resistance acquisition. Environmental surveillance studies examining resistance gene prevalence in water, soil, and air samples could quantify the contribution of environmental reservoirs to community resistance burden [31]. Molecular epidemiological studies using whole genome sequencing could trace transmission pathways and determine whether resistant organisms spread primarily through clonal expansion or horizontal gene transfer, informing targeted intervention strategies. Economic evaluations comparing different intervention approaches would help prioritize resource allocation in resource-limited settings.

Our findings suggest the need for more sophisticated theoretical frameworks for understanding AMR determinants that move beyond simple behavioural models. Social-ecological models that consider individual, interpersonal, community, and policy-level factors may better capture the complexity of resistance transmission[39]. Complex systems approaches recognizing AMR as an emergent property of interactions between human, animal, and environmental factors could guide more effective intervention design, emphasizing feedback loops, nonlinear relationships, and unintended consequences that traditional linear models may miss.

Conclusions

Our investigation into antimicrobial resistance among dermatology patients in Western India reveals a complex reality that challenges conventional approaches to AMR prevention and control. Despite 25.5% of participants exhibiting high-risk antibiotic behaviours and 65% harbouring resistant organisms (Figure 6), we found no significant association between individual risk

behaviours and resistance colonization (p=0.280, Table 3). This disconnect suggests that community-level and environmental factors predominate over individual behaviours in determining resistance patterns, fundamentally challenging current paradigms that emphasize individual patient education as the primary intervention strategy.

However, socioeconomic factors demonstrated strong associations with risky antibiotic use behaviours, with education level (p=0.005), housing conditions (p=0.021), and occupation (p=0.013) significantly predicting high-risk behaviours (Table 2, Figures 1-4). These findings highlight how social inequalities translate into differential health behaviours and vulnerabilities, emphasizing the critical importance of addressing social determinants of health in comprehensive AMR strategies. The widespread prevalence of resistant organisms regardless of individual behaviours points to environmental contamination, healthcare-associated transmission, and community-level circulation as primary drivers of resistance dissemination.

Table 3: Multivariate Logistic Regression for Predictors of Carriage of Resistant Organisms

Predictor Variable	Adjusted Odds Ratio (AOR)	95% CI	Wald Statistic	p-value	Statistical Test Used
High AMR Risk Behaviour	0.69	0.34 – 1.36	1.16	0.280	Logistic Regression
Age (per year increase)	0.98	0.96 – 1.00	2.85	0.091	Logistic Regression
Gender (Male)	0.83	0.45 – 1.56	0.32	0.570	Logistic Regression
Graduate Education	1.02	0.52 – 2.01	0.003	0.957	Logistic Regression
Slum Dwelling	1.06	0.57 – 1.98	0.04	0.841	Logistic Regression
Has Health Insurance	1.09	0.40 – 2.94	0.03	0.858	Logistic Regression

Legend: Data derived from the present study's multivariate analyses. For methods and context, see [26].

Our findings suggest that traditional antimicrobial stewardship programs focusing primarily on patient education and behaviour modification, while important, appear inadequate to address the broader resistance crisis given the limited impact of individual behaviours on resistance outcomes. Effective AMR containment requires comprehensive systems-level interventions addressing environmental contamination and waste management, healthcare infection control and stewardship programs, community-level transmission through WASH interventions, social determinants of health including housing and education, and One Health integration across human, animal, and environmental sectors [31,32,34,35,37].

Despite the limited impact on resistance carriage, addressing risky behaviours among those with lower education, poor housing conditions, and certain occupational categories remains crucial for reducing selection pressure and preventing emergence of new resistance. Investment in surveillance systems, infrastructure development, and international collaboration represents not merely a public health imperative but an existential necessity for global health security [40]. The complex interplay between individual, community, and environmental factors demands multi-sectoral approaches that move beyond traditional clinical interventions to address the fundamental drivers of antimicrobial resistance in our interconnected world.

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