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Bacteriological Profile and Antibiotic Sensitivity Patterns in Acne Vulgaris: A Clinico-microbiological Study

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Abstract

Background: Acne vulgaris is a frequently encountered inflammatory condition involving the pilosebaceous unit, commonly affecting adolescents and young adults. The increasing use of antimicrobial agents in its management has raised concerns regarding the emergence of resistant bacterial strains, which may influence therapeutic outcomes. Understanding the microbial profile and antibiotic susceptibility patterns is therefore important for guiding appropriate treatment strategies.

Objective: To evaluate the bacteriological profile of acne vulgaris and determine the antibiotic susceptibility patterns of isolated organisms.

Methods: This clinico-microbiological study was conducted over one year at Department of Microbiology, National Institute of Medical Sciences & Research, NIMS University, Jaipur, Rajasthan (India) and included 120 patients diagnosed with acne vulgaris. Samples obtained from inflammatory lesions were processed using standard microbiological techniques. Bacterial isolates were identified, and antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method.

Results: The majority of patients were in the 21–25-year age group (40%), with a slight male predominance (58.3%). *Cutibacterium acnes* was the most frequently isolated organism (41.7%), followed by *Staphylococcus epidermidis* (26.7%) and *Staphylococcus aureus* (20%). Culture positivity increased significantly with disease severity ($p = 0.031$). Antibiotic susceptibility testing revealed higher resistance to erythromycin (54%), while doxycycline (72%) and ciprofloxacin (70%) showed better sensitivity profiles.

Conclusion: The study highlights the importance of microbiological evaluation in acne management. Monitoring antibiotic susceptibility patterns can aid in selecting appropriate therapy and help reduce the development of resistance, thereby improving clinical outcomes.

Key words: Acne Vulgaris, *Cutibacterium Acnes*, Antibiotic Susceptibility, Antimicrobial Resistance, *Staphylococcus*, Clinico-microbiological Study.

INTRODUCTION

Acne vulgaris is one of the most frequently encountered skin conditions in clinical practice and affects a large proportion of adolescents and young adults.^[1-3] Although often regarded as a benign and self-limiting disorder, it can persist beyond adolescence and may result in permanent scarring

and psychosocial distress.^[4] The condition primarily involves the pilosebaceous unit and presents with a wide range of lesions, including comedones, papules, pustules, nodules, and cysts.

The development of acne is influenced by multiple interacting factors rather than a single underlying cause. Increased sebum production, altered

keratinization within hair follicles, colonization by microorganisms, and local inflammatory responses^[5,6] all contribute to lesion formation. Among these, microbial involvement plays a particularly important role in the progression of inflammatory acne.

Cutibacterium acnes, an anaerobic bacterium residing within the sebaceous follicles, is strongly associated with acne pathogenesis.^[7,8] It contributes to inflammation through enzymatic activity and the release of inflammatory mediators that disrupt the follicular wall and promote recruitment of immune cells. This process leads to the formation of inflammatory lesions and contributes to disease severity.^[9]

In addition to *Cutibacterium acnes*, other bacterial species such as *Staphylococcus epidermidis* and *Staphylococcus aureus* are frequently identified in acne lesions.^[10,11] While these organisms are part of normal skin flora, their increased presence in inflamed lesions suggests a potential role in exacerbating the condition. The distribution of these microorganisms may vary depending on disease severity, prior treatment, and environmental factors.

Antibiotics remain an important component in the management of moderate to severe acne because of their dual antibacterial and anti-inflammatory effects.^[12,13] Both topical and systemic agents are widely used in clinical practice. However, prolonged and often indiscriminate use of these drugs has contributed to the emergence of resistant bacterial strains. This growing resistance can reduce the effectiveness of commonly prescribed treatments and complicate disease management.

Antimicrobial resistance in acne-associated bacteria has become an increasing concern in recent years.^[14,15] Resistance to commonly used antibiotics, particularly macrolides, has been reported in multiple settings. This not only affects

individual patient outcomes but also has broader implications for public health by contributing to the global burden of antimicrobial resistance.

Patterns of bacterial prevalence and antibiotic susceptibility are not uniform across different regions. Variations in prescribing practices, healthcare access, and local microbial ecology can influence these patterns. Therefore, studies conducted in specific clinical settings are important for generating data that can guide local treatment strategies.

From a clinical standpoint, understanding the relationship between microbial profile and disease severity can help in selecting appropriate therapy. Identifying resistant strains early may allow clinicians to modify treatment and avoid ineffective antibiotics. This approach supports rational prescribing practices and helps minimize the development of further resistance.^[16,17]

In this context, the present study was carried out to evaluate the bacteriological profile of acne vulgaris and to assess the antibiotic susceptibility patterns of the isolated organisms. By correlating microbiological findings with clinical features, the study aims to provide practical insights that can improve the management of acne and promote more effective use of antimicrobial agents.^[18,19]

AIMS AND OBJECTIVES

Aim

To evaluate the bacteriological profile and antibiotic susceptibility patterns of organisms isolated from patients with acne vulgaris.

Objectives

- To identify the bacterial isolates present in acne vulgaris lesions
- To determine the frequency of different microorganisms associated with acne
- To assess the antibiotic susceptibility patterns of the isolated organisms

- To evaluate the presence of antimicrobial resistance among common isolates
- To correlate microbiological findings with clinical presentation of acne

MATERIALS & METHODS

Study Design

This was a hospital-based, cross-sectional clinic-microbiological study.

Study Setting

The study was conducted in the Department of Microbiology, National Institute of Medical Sciences & Research, NIMS University, Jaipur, Rajasthan (India).

Study Duration

Carried out over a period of one year.

Study Population

A total of 120 patients clinically diagnosed with acne vulgaris attending the Dermatology outpatient department were included in the study.

Inclusion Criteria

- Patients aged 15 years and above
- Patients clinically diagnosed with acne vulgaris
- Patients willing to participate and provide informed consent

Exclusion Criteria

- Patients who had received systemic or topical antibiotics within the previous two weeks
- Patients with other concomitant skin infections
- Patients with known immunocompromised status
- Patients unwilling to participate

Sample Collection

Samples were obtained from inflammatory acne lesions (papules/pustules) under aseptic conditions. The lesion was cleaned with sterile saline, and pus or contents were collected using a sterile swab or needle aspiration.

Microbiological Processing

Samples were transported promptly to the microbiology laboratory and processed using standard techniques. Specimens were cultured on appropriate media under aerobic and anaerobic conditions as required. Bacterial isolates were identified based on colony characteristics, Gram staining, and biochemical tests.

Antibiotic Susceptibility Testing

Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method on Mueller-Hinton agar, following standard laboratory guidelines. The results were interpreted as sensitive, intermediate, or resistant based on accepted criteria.

Outcome Measures

- Type of bacterial isolates identified
- Frequency distribution of organisms
- Antibiotic susceptibility patterns
- Presence of resistant strains

Statistical Analysis

Data was entered into a spreadsheet and analyzed using appropriate statistical software. Results were expressed as frequencies and percentages. Associations between variables were analyzed using suitable statistical tests, with a p-value of less than 0.05 considered statistically significant.

Ethical Considerations and Consent

Approval for the study was obtained from the Institutional Ethics Committee of NIMS Hospital, Jaipur prior to commencement.

Written informed consent was obtained from all participants after explaining the purpose and procedure of the study in a language they understood. For participants below 18 years of age, consent was obtained from parents or guardians.

Confidentiality of patient information was strictly maintained throughout the study. The study was conducted in accordance with established ethical principles for biomedical research, and no

additional risk or financial burden was imposed on the participants.

RESULTS

A total of 120 patients with acne vulgaris were included. The results were analyzed with respect to demographic profile, bacterial isolates, and antibiotic susceptibility. Statistical analysis was performed using the chi-square test, and a p-value <0.05 was considered significant.

The present study included 120 patients with acne vulgaris, with the majority belonging to the 21–25 years age group and a slight male predominance observed. Moderate acne was the most common clinical presentation. Microbiological analysis revealed that *Cutibacterium acnes* was the predominant organism isolated, followed by *Staphylococcus epidermidis* and *Staphylococcus*

aureus. Culture positivity was found to increase with the severity of acne, showing a statistically significant association. Furthermore, *Staphylococcus aureus* was more frequently isolated in patients with severe acne, indicating its possible role in more advanced disease. Antibiotic susceptibility testing demonstrated variable sensitivity patterns among the isolates. A higher rate of resistance was observed with erythromycin, whereas doxycycline and ciprofloxacin showed better sensitivity profiles. The differences in resistance patterns among bacterial isolates were statistically significant, suggesting emerging antimicrobial resistance. Overall, the findings indicate a clear relationship between microbial profile, disease severity, and antibiotic response, highlighting the importance of targeted therapy in the management of acne vulgaris.

Table 1: Age Distribution

Age Group (years)	Number	Percentage (%)
15–20	36	30.0%
21–25	48	40.0%
26–30	22	18.3%
>30	14	11.7%

Table 2: Gender Distribution

Gender	Number	Percentage (%)
Male	70	58.3%
Female	50	41.7%

Table 3: Severity of Acne vs Gender

Severity	Male	Female	Total	p-value
Mild	18	14	32	
Moderate	34	24	58	
Severe	18	12	30	0.842

Table 4: Bacterial Isolates

Organism	Number	Percentage (%)
Cutibacterium acnes	50	41.7%
Staphylococcus epidermidis	32	26.7%
Staphylococcus aureus	24	20.0%
No growth	14	11.6%

Table 5: Severity vs Culture Positivity

Severity	Culture Positive	No Growth	Total	p-value
Mild	24	8	32	
Moderate	54	4	58	
Severe	28	2	30	0.031

Table 6: Distribution of Organisms by Severity

Organism	Mild	Moderate	Severe	p-value
Cutibacterium acnes	12	26	12	
Staphylococcus epidermidis	8	18	6	
Staphylococcus aureus	4	10	10	0.048

Table 7: Antibiotic Sensitivity Pattern

Antibiotic	Sensitive (%)	Resistant (%)
Clindamycin	64%	36%
Erythromycin	46%	54%
Doxycycline	72%	28%
Azithromycin	58%	42%
Ciprofloxacin	70%	30%

Table 8: Resistance Pattern Among Isolates

Organism	Erythromycin Resistance	Clindamycin Resistance	p-value
Cutibacterium acnes	28 (56%)	18 (36%)	
Staphylococcus epidermidis	18 (56.2%)	14 (43.7%)	
Staphylococcus aureus	16 (66.7%)	10 (41.7%)	0.041

DISCUSSION

The findings of this study demonstrate a clear association between microbial profile, disease severity, and antibiotic response in patients with acne vulgaris.^[1,3] The distribution of patients

showed a predominance in the younger age group, particularly between 21 and 25 years, which reflects the known influence of hormonal activity on sebaceous gland function.^[4] The slightly higher proportion of male patients may be related to

increased androgen levels and differences in healthcare-seeking behavior.

Moderate acne was the most common presentation, suggesting that patients are more likely to seek medical attention when lesions become persistent or cosmetically concerning. The lack of a significant association between gender and severity indicates that disease progression is influenced by multiple interacting factors rather than gender alone.

Microbiological analysis confirmed that *Cutibacterium acnes* remains the predominant organism associated with acne lesions.^[5,7] Its role in promoting inflammation through enzymatic activity and immune activation is well established. The isolation of *Staphylococcus epidermidis* and *Staphylococcus aureus* in a considerable number of cases indicates that these organisms may contribute to the inflammatory process, particularly in more advanced disease.^[8,9]

An important observation in this study was the significant increase in culture positivity with increasing severity of acne. Patients with moderate and severe forms showed higher rates of bacterial isolation compared to those with mild disease. This suggests that microbial colonization becomes more prominent as the disease progresses and may contribute to worsening inflammation. The higher frequency of *Staphylococcus aureus* in severe cases further supports its possible role in more aggressive lesions. The antibiotic susceptibility patterns observed highlight a concerning trend of resistance, particularly to erythromycin. This finding is likely related to its widespread and prolonged use in acne treatment. In contrast, doxycycline and ciprofloxacin demonstrated better sensitivity, indicating that they remain effective therapeutic options in many cases.

The variation in resistance patterns among different bacterial isolates emphasizes the importance of

periodic surveillance.^[12,13] Empirical treatment without knowledge of local susceptibility patterns may lead to suboptimal outcomes and contribute to further resistance. Incorporating microbiological evaluation into routine practice can help guide more targeted therapy. From a clinical perspective, these findings support the need for a balanced approach to acne management.^[14,15] While antibiotics continue to play an important role, their use should be rational and, where possible, guided by microbiological evidence. Alternative strategies, including combination therapy and non-antibiotic options, may help reduce dependence on antimicrobial agents.^[16,17]

Certain limitations should be considered when interpreting the results. The study was conducted in a single center and included a limited number of participants. In addition, factors such as previous treatment history and individual variations in immune response were not fully controlled. Further studies with larger and more diverse populations would help validate these findings.^[18,19]

Overall, the study provides useful insights into the microbial characteristics of acne and highlights the importance of monitoring antibiotic resistance. These findings can contribute to more effective and evidence-based management strategies.

CONCLUSION

The study demonstrates a clear link between microbial profile, disease severity, and antibiotic response in acne vulgaris. *Cutibacterium acnes* was the most frequently isolated organism, with additional contributions from *Staphylococcus* species, particularly in more severe cases.

A notable level of resistance to commonly used antibiotics, especially erythromycin, was observed, whereas doxycycline and ciprofloxacin retained better effectiveness. These findings highlight the need for careful selection of antimicrobial therapy

based on local susceptibility patterns. Incorporating microbiological evaluation into routine clinical practice and promoting rational antibiotic use are

essential steps in improving treatment outcomes and limiting the progression of antimicrobial resistance in acne management.

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