SAR Journal of Pathology and Microbiology

Abbreviated Key Title: *SAR J Pathol Microbiol*
Home page: https://sarpublication.com/journal/sarjpm/home
DOI: https://doi.org/10.36346/sarjpm.2026.v07i05.001

OPEN ACCESS

ISSN 2707-7756 (P)
ISSN 2709-6890 (O)

Original Research Article

Phenotypic Characterization and Antimicrobial Resistance Profiling of Bacterial Isolates from Oral Swab Samples

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Article History: | Received: 10.07.2026 | Accepted: 04.09.2026 | Published: 08.09.2026 |

Abstract: The human oral cavity harbours diverse commensal and opportunistic bacteria that can act as reservoirs of antibiotic resistance. This study characterized the occurrence and antibiotic susceptibility of bacteria from 198 oral swab samples from consenting adults, using standard culture, Gram staining, biochemical identification, and Kirby-Bauer disc diffusion testing against ten antibiotics matched to each isolate's Gram reaction. *Staphylococcus aureus* was the most frequent isolate (42, 21.2%), followed by *Escherichia coli* (34, 17.2%), *Streptococcus salivarius* (23, 11.6%), *Streptococcus mitis* (15, 7.6%), *Staphylococcus epidermidis* and *Neisseria oralis* (13 each, 6.6%), and *Neisseria mucosa* and *Klebsiella pneumoniae* (11 each, 5.6%); 14.6% of samples showed no growth and 3.5% were undefined. Females yielded more isolates than males, but this was not statistically significant ($\chi^2 = 3.04$, df = 9, $p = 0.963$). Resistance to amoxicillin and ampiclox (Gram-positive isolates) and to amoxicillin and sparfloxacin (Gram-negative isolates) was consistently high (13.0-81.8%), with *K. pneumoniae* showing the highest resistance (81.8% to amoxicillin). Chi-square testing showed organism identity significantly associated with resistance status in both the Gram-positive ($\chi^2 = 23.33$, df = 3, $p < 0.001$) and Gram-negative groups ($\chi^2 = 42.67$, df = 3, $p < 0.001$), driven mainly by the low resistance of both *Neisseria* species. Levofloxacin and ciprofloxacin (Gram-positive panel) and gentamycin and ofloxacin (Gram-negative panel) retained the greatest activity. These findings indicate that the oral cavity of healthy individuals harbours bacteria with considerable, organism-dependent resistance to commonly prescribed antibiotics, especially β-lactams, underscoring the need for antimicrobial stewardship and continued community-level resistance surveillance.

Keywords: Antibiotic Resistance, Oral Cavity, Disc Diffusion, Commensal Bacteria, Chi-Square Analysis.

1. INTRODUCTION

The human oral cavity is one of the most diverse microbial ecosystems in the body, harbouring hundreds of bacterial species including *Streptococcus, Staphylococcus, Neisseria, Actinomyces*, *Lactobacillus*, and various anaerobes that constitute the normal oral flora and interact within a complex, dynamic environment supporting oral health (Dewhirst *et al.,* 2010; Lamont *et al*., 2018; Sukumar *et al.,* 2024). Under favourable conditions, however, these ordinarily harmless species may become opportunistic pathogens capable of causing dental caries, periodontal disease, endodontic infections, and even systemic infection through bacteraemia (Brooks, 2022).

The rapid emergence and spread of antibiotic resistance poses a serious threat to global public health. Resistance arises when bacteria evolve mechanisms that neutralize the effects of antibiotics, rendering common treatments ineffective (Davies & Davies, 2010; WHO, 2023), a trend accelerated by the misuse and overuse of antibiotics in clinical medicine, dentistry, agriculture, and self-medication (Ventola, 2015). The oral cavity is increasingly recognized as a key reservoir of antibiotic-resistant bacteria owing to its suitability for microbial colonization, biofilm formation, and genetic exchange (Ready *et al*., 2006; Roberts & Mullany, 2010); horizontal gene transfer through transformation, transduction, and conjugation allows resistance genes to

move between commensal and pathogenic species (Lerminiaux & Cameron, 2019), with the potential to disseminate to pathogens colonizing other body sites (Dave & Tattar, 2025).

Oral bacteria may carry resistance genes such as blaTEM (β-lactam resistance), tetA (tetracycline resistance), ermB (erythromycin/macrolide resistance), and mecA (methicillin resistance), which are often located on mobile genetic elements such as plasmids and transposons that facilitate their transfer between species (Rawat & Nair, 2010; Roberts & Schwarz, 2016). While traditional phenotypic susceptibility testing remains valuable, it often fails to reveal the underlying genetic determinants of resistance. Molecular techniques such as polymerase chain reaction (PCR) provide a more sensitive, accurate, and rapid means of identifying specific ARGs, and integrating phenotypic antibiotic susceptibility testing with molecular detection offers a more comprehensive picture of resistance patterns than either approach alone (Sukumar *et al.,* 2024).

In Nigeria, widespread misuse of antibiotics including self-medication, incomplete dosing, and poor regulation of antimicrobial sales has contributed significantly to the rise of resistant organisms (Olagunju *et al.,* 2025), yet available local studies have focused mainly on the phenotypic susceptibility of dental pathogens (Daniyan & Abalaka, 2011; Philips *et al.,* 2021), with data on the commensal flora of the oral cavity remaining limited. This study therefore aimed to isolate bacteria from the human oral cavity and characterize their antibiotic susceptibility profiles, in order to contribute to existing knowledge on antimicrobial resistance and support antibiotic stewardship and public health planning.

1.1 Aim and Objectives

The aim of this study was to isolate, identify, and characterize the antibiotic susceptibility profile of bacteria from the human oral cavity using standard microbiological techniques. The specific objectives were to: (i) isolate and identify bacterial species from oral swab samples; and (ii) determine the antibiotic susceptibility profiles of the isolates using the disc diffusion method.

2. MATERIALS AND METHODS

2.1 Study Area and Design

This laboratory-based study was conducted at the Biotechnology Laboratory of the Federal University of Technology, Babura, Jigawa State, and combined phenotypic and molecular approaches to evaluate antibiotic resistance among oral bacterial isolates.

2.2 Study Population and Sample Size

The study population comprised healthy adult volunteers aged 18-50 years who had not taken antibiotics within the preceding two weeks. Sample size was determined using the prevalence formula n = (Z1-α)^2 × p(1-p)/d^2, where Z1-α = 1.96 at 95% confidence, d = 0.05 (absolute precision), and p = the literature-derived prevalence estimate. Using p = 0.147, this gave a minimum requirement of 192.68 (≈193) samples; adding a 3% allowance for attrition (6 samples) gave a target of approximately 198 samples. A total of 198 oral swabs were accordingly collected and processed, meeting this target exactly. A stratified sampling technique based on age and gender was used to recruit participants meeting the inclusion criteria (healthy adults aged 18-50 years, no antibiotic use in the previous two weeks, and willingness to participate) while individuals on antibiotics or immunosuppressive drugs, those with active oral infections or bleeding gums, and unwilling individuals were excluded.

2.3 Sample Collection

Oral swab samples were collected aseptically using sterile cotton swab sticks from the buccal mucosa, tongue surface, and gingival/saliva-pooling region of each consenting participant, placed immediately into sterile tubes, and labelled for analysis.

2.4 Isolation and Identification of Bacteria

Samples were cultured on nutrient agar, blood agar, MacConkey agar, and mannitol salt agar, and incubated at 37°C for 24-48 hours; distinct colonies were sub-cultured to obtain pure isolates. Isolates were identified by colony morphology, Gram staining, and biochemical tests (catalase, coagulase and indole tests).

2.5 Antibiotic Susceptibility Testing

Susceptibility was determined by the Kirby-Bauer disc diffusion method on Mueller-Hinton agar following CLSI guidelines, using a 0.5 McFarland standard inoculum. Isolates were tested against pefloxacin, gentamycin, ampiclox, zinnacef, amoxicillin, rocephin, ciprofloxacin, azithromycin, levofloxacin, and erythromycin, and zones of inhibition were measured and classified as sensitive, intermediate, or resistant.

2.6 Data Analysis

Data were summarized using descriptive statistics (frequencies and percentages). Associations between bacterial species and antibiotic resistance status (resistant vs. sensitive/intermediate) were tested using Pearson's chi-square test of independence, both per antibiotic and pooled across all ten antibiotics, with Cramer's V used to estimate effect size. The association between participant gender and isolate type was tested the same way. Statistical significance was set at $p < 0.05$. Analyses were performed in Python 3 (SciPy 1.17) using the chi2 contingency function; given the small sample sizes for some organisms (*S. epidermidis*, n = 13; *K. pneumoniae,* n = 11), expected cell counts below 5 were flagged and results interpreted with appropriate caution.

2.7 Ethical Considerations

Ethical approval was obtained from the appropriate institutional ethics committee. Participants

were informed of the study's purpose and provided written consent, and confidentiality of participant data was maintained throughout.

3. RESULTS

3.1 Bacterial Isolates Obtained

Of the 198 oral swab samples processed, *Staphylococcus aureus* was the most frequently isolated organism (42 isolates, 21.2%), followed by *Escherichia coli* (34, 17.2%), *Streptococcus salivarius* (23, 11.6%), *Streptococcus mitis* (15, 7.6%), *Staphylococcus epidermidis* and *Neisseria oralis* (13 isolates each, 6.6%), and *Neisseria mucosa* and *Klebsiella pneumoniae* (11 isolates each, 5.6%). No bacterial growth was observed in 29 samples (14.6%), and 7 isolates (3.5%) could not be definitively identified. Females yielded more isolates than males across nearly all organism categories the exception being *S. epidermidis*, for which males were a slight majority (53.8%) but a chi-square test of independence found no statistically significant association between gender and isolate type ($\chi^2 = 3.04$, df = 9, p = 0.963, Cramer's V = 0.12), indicating the observed gender skew is consistent with chance rather than a true sex-related difference in carriage.

Table 1: Frequency and Gender Distribution of Bacterial Isolates Obtained from Oral Swab Samples

Isolate	Male n (%)	Female n (%)	Total (n)	Overall (%)
Neisseria mucosa	4 (36.4)	7 (63.6)	11	5.6
Neisseria oralis	5 (38.5)	8 (61.5)	13	6.6
Staphylococcus aureus	16 (38.1)	26 (61.9)	42	21.2
Staphylococcus epidermidis	7 (53.8)	6 (46.2)	13	6.6
Streptococcus mitis	4 (26.7)	11 (73.3)	15	7.6
Streptococcus salivarius	11 (47.8)	12 (52.2)	23	11.6
Escherichia coli	13 (38.2)	21 (61.8)	34	17.2
Klebsiella pneumoniae	4 (36.4)	7 (63.6)	11	5.6
No growth	11 (37.9)	18 (62.1)	29	14.6
Undefined isolates	3 (42.9)	4 (57.1)	7	3.5
Total	**78 (39.4)**	**120 (60.6)**	**198**	**100.0**

3.2 Identification of Bacterial Isolates

Of the 198 oral swab samples, 162 yielded a confirmed bacterial isolate; these were identified to species level using colony morphology, Gram staining, and biochemical testing. *Staphylococcus aureus* and *Staphylococcus epidermidis* both appeared as circular, smooth, convex colonies and stained as Gram-positive cocci in clusters, so coagulase testing was essential to distinguish the two; *S. aureus* produced golden-yellow to cream, β-haemolytic colonies and was coagulase-positive in 39 of 42 isolates (92.9%), whereas *S. epidermidis* produced non-haemolytic, white to greyish-white colonies and was coagulase-negative in all 13 isolates (100%). *Streptococcus mitis* and *Streptococcus salivarius* were both catalase-negative, Gram-positive cocci in chains/pairs, distinguishing them from the catalase-positive staphylococci; *S. mitis* produced small, α-haemolytic (greening) colonies while *S. salivarius* produced larger, mucoid, non-haemolytic colonies. *Neisseria mucosa* and *Neisseria oralis* stained as Gram-negative diplococci and were catalase-positive, distinguishing them from the Gram-positive cocci. *Escherichia coli* and *Klebsiella pneumoniae* both stained as Gram-negative rods, and were separated primarily by colony morphology (*K. pneumoniae* producing large, mucoid, capsulated colonies versus *E. coli*'s smaller, moist, non-mucoid colonies) and the indole test, on which *E. coli* was positive in 32 of 34 isolates (94.1%) while *K. pneumoniae* was indole-negative in all 11 isolates (100%).

Catalase testing was positive in the staphylococci, both *Neisseria* species, and both Gram-negative rods (119 of 162 identified isolates overall, 73.5%), but negative in both *Streptococcus* species, consistent with the classical use of the catalase test to separate staphylococci from streptococci. Coagulase testing was performed on all isolates except the two Gram-negative rods (*E. coli* and *K. pneumoniae*), for which the test is not diagnostically applicable and is reported as not tested (NT); every isolate tested was coagulase-negative other than *S. aureus* (39 of 42) and *S. epidermidis* (fully negative, 13 of 13). Indole testing was performed on all isolates; every species was indole-negative except *E. coli*, which was indole-positive in 32 of 34 isolates (94.1%), consistent with the classical indole-positive/indole-negative split used to separate *E. coli* from other Enterobacteriaceae.

Table 2: Biochemical Identification of Bacterial Isolates (Catalase, Coagulase, and Indole Tests)

Isolate	N	Catalase +ve n (%)	Coagulase result	Indole result
Neisseria mucosa	11	11 (100.0)	-ve: 11 (100.0)	-ve: 11 (100.0)
Neisseria oralis	13	13 (100.0)	-ve: 13 (100.0)	-ve: 13 (100.0)
Staphylococcus aureus	42	40 (95.2)	+ve: 39 (92.9)	-ve: 36 (85.7)
Staphylococcus epidermidis	13	13 (100.0)	-ve: 13 (100.0)	-ve: 13 (100.0)
Streptococcus mitis	15	0 (0.0)	-ve: 13 (86.7)	-ve: 15 (100.0)

Isolate	N	Catalase +ve n (%)	Coagulase result	Indole result
Streptococcus salivarius	23	0 (0.0)	-ve: 23 (100.0)	-ve: 23 (100.0)
Escherichia coli	34	31 (91.2)	NT	+ve: 32 (94.1)
Klebsiella pneumoniae	11	11 (100.0)	NT	-ve: 11 (100.0)
Total	**162**	**119 (73.5)**	**-**	**-**

NT = not tested (coagulase testing was not performed on the two Gram-negative rods, *E. coli* and *K. pneumoniae*, for which it is not diagnostically applicable). Catalase distinguished staphylococci/Enterobacteriaceae from catalase-negative organisms such as streptococci; coagulase separated the pathogenic *S. aureus* from the coagulase-negative *S. epidermidis*; and the indole test, performed on all eight species, separated indole-positive *E. coli* from every other isolate, all of which were indole-negative, including *K. pneumoniae* among the Gram-negative rods. Results were consistent within species across all isolates tested, supporting reliable species-level identification.

3.3 Antibiotic Susceptibility Patterns

Table 3 presents the full sensitive/intermediate/resistant breakdown for the four Gram-positive isolates, and Table 4 the corresponding breakdown for the four Gram-negative isolates (tested against a separate panel appropriate to Gram-negative organisms). Among the Gram-positive isolates, resistance was highest to amoxicillin and ampiclox and lowest to levofloxacin and ciprofloxacin; erythromycin resistance ranged from 26.1% (*S. salivarius*) to 40.0% (*S. mitis*). Among the Gram-negative isolates, resistance was highest to sparfloxacin and amoxicillin and lowest to gentamycin, ofloxacin and chloramphenicol. *Klebsiella pneumoniae* showed the highest point-estimate resistance to amoxicillin (81.8%, 9/11 isolates) of any organism, and *Escherichia coli* and *K. pneumoniae* showed similarly high resistance to sparfloxacin (76.5% and 72.7%, respectively); by contrast, both Neisseria species were fully susceptible to sparfloxacin, ciprofloxacin, gentamycin and pefloxacin (0% resistance), the most consistently susceptible organisms in the entire panel.

Table 3: Susceptibility Pattern (Sensitive/Intermediate/Resistant) of Gram-Positive Bacterial Isolates by Antibiotic

Antibiotic	*S. aureus (n=42) S/I/R*	*S. epidermidis (n=13) S/I/R*	*S. mitis (n=15) S/I/R*	*S. salivarius (n=23) S/I/R*
Pefloxacin	34/2/6	11/0/2	12/1/2	20/2/1
Gentamycin	36/1/5	11/0/2	12/1/2	20/2/1
Ampiclox	10/3/29	4/1/8	7/3/5	13/5/5
Zinnacef	30/3/9	10/0/3	11/2/2	18/3/2
Amoxicillin	8/3/31	3/1/9	8/3/4	16/4/3
Rocephin	33/2/7	10/0/3	11/2/2	19/2/2
Ciprofloxacin	37/1/4	12/0/1	12/1/2	20/2/1
Azithromycin	32/2/8	10/0/3	8/2/5	15/3/5
Levofloxacin	38/1/3	12/0/1	13/1/1	21/1/1
Erythromycin	26/3/13	9/0/4	7/2/6	14/3/6

Values are n isolates classed Sensitive/Intermediate/Resistant by Kirby-Bauer disc diffusion (CLSI criteria).

Table 4: Susceptibility Pattern (Sensitive/Intermediate/Resistant) of Gram-Negative Bacterial Isolates by Antibiotic

Antibiotic	*E. coli (n=34) S/I/R*	*K. pneumoniae (n=11) S/I/R*	*N. mucosa (n=11) S/I/R*	*N. oralis (n=13) S/I/R*
Septrin	26/2/6	8/1/2	7/1/3	9/1/3
Chloramphenicol	28/1/5	9/0/2	9/1/1	11/1/1
Sparfloxacin	6/2/26	2/1/8	10/1/0	12/1/0
Ciprofloxacin	23/3/8	7/1/3	10/1/0	12/1/0
Amoxicillin	5/3/26	2/0/9	6/2/3	8/2/3
Augmentin	25/2/7	8/0/3	8/1/2	10/1/2
Gentamycin	29/1/4	9/0/2	10/1/0	12/1/0
Pefloxacin	22/2/10	7/1/3	10/1/0	12/1/0
Ofloxacin	30/1/3	10/0/1	9/1/1	11/1/1
Streptomycin	18/2/14	6/1/4	8/1/2	10/1/2

Values are n isolates classed Sensitive/Intermediate/Resistant by Kirby-Bauer disc diffusion (CLSI criteria).

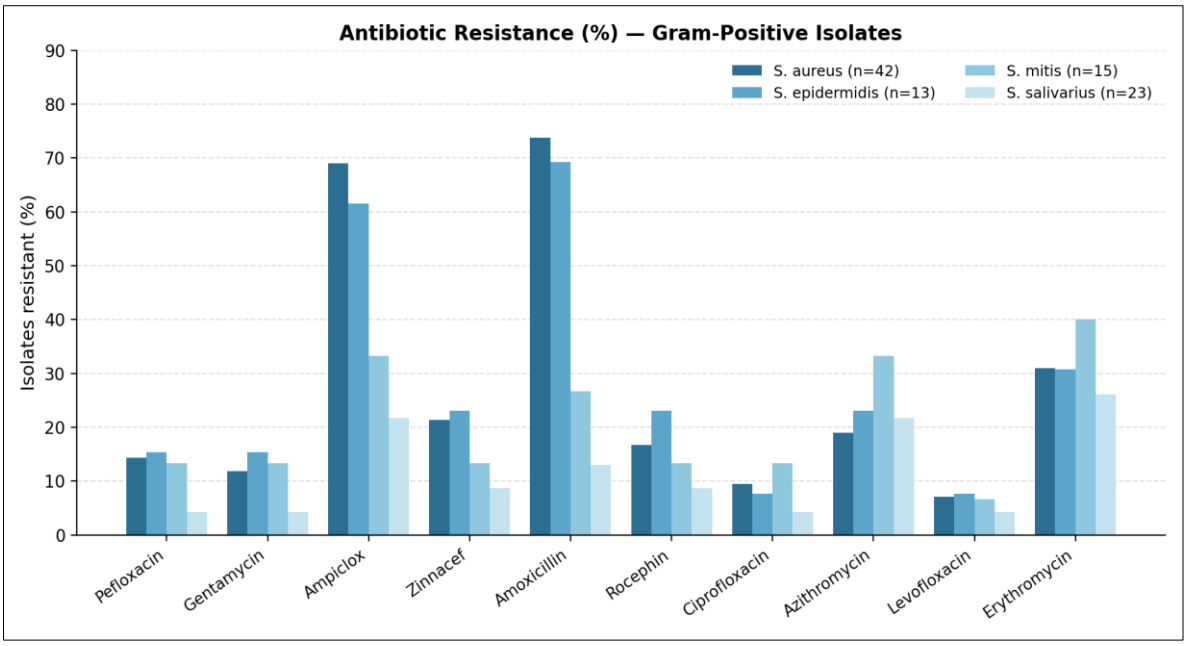

Figure 1a: Percentage of isolates classified as resistant to each of the ten antibiotics tested, among the four Gram-positive bacterial species

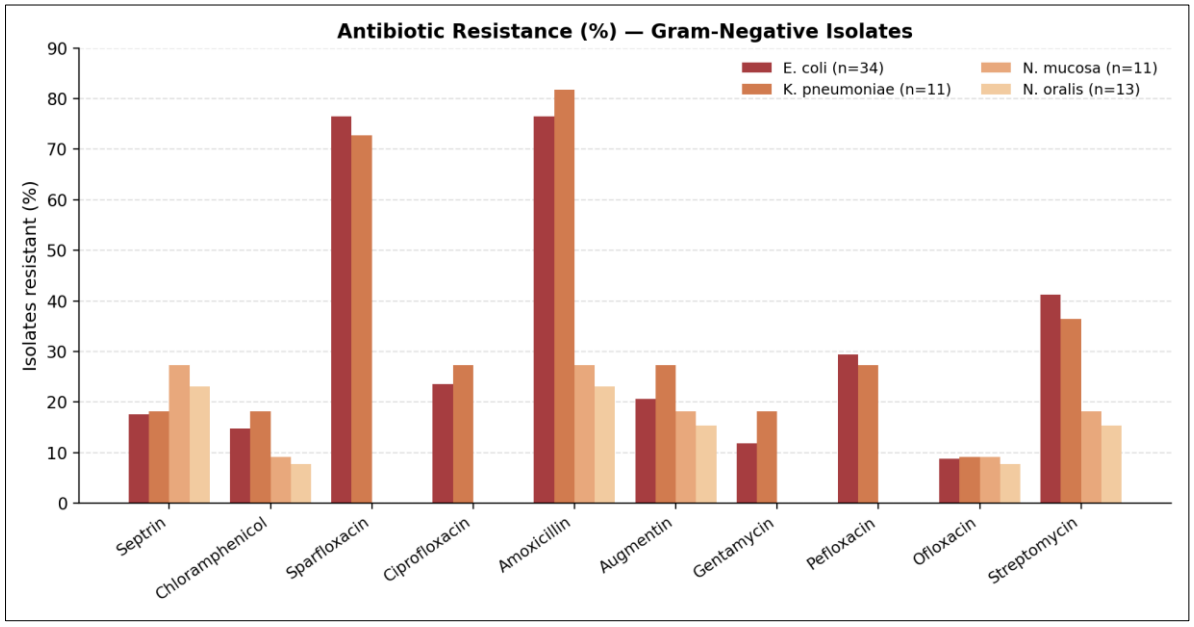

Figure 1b: Percentage of isolates classified as resistant to each of the ten antibiotics tested, among the four Gram-negative bacterial species

3.4 Mean Zone of Inhibition

Tables 5 and 6 present the mean zone of inhibition (mm ± standard deviation) for each antibiotic against the Gram-positive and Gram-negative isolates respectively, corroborating the categorical susceptibility patterns in Tables 3 and 4: agents with higher resistance rates produced correspondingly smaller mean zones (e.g., ampiclox and amoxicillin against the Gram-positive isolates; sparfloxacin and amoxicillin against *E. coli* and *K. pneumoniae*), while agents with high sensitivity rates produced larger zones. Some agent-organism combinations show a standard deviation that is large relative to the mean for example pefloxacin against *N. mucosa* (14 ± 10.86 mm) and ofloxacin against *N. oralis* (16.5 ± 11.14 mm) which reflects genuine bimodal variability in the raw zone measurements (some isolates fully resistant with near-zero zones, others clearly susceptible with much larger zones) within these small isolate groups, rather than a data-recording error.

Table 5: Mean Zone of Inhibition (mm) of Antibiotics against Gram-Positive Isolates

Antibiotic	*S. aureus (n=42)*	*S. epidermidis (n=13)*	*S. mitis (n=15)*	*S. salivarius (n=23)*
Pefloxacin	24.8 ± 2.3	25.2 ± 1.8	26.3 ± 2.56	32.4 ± 4.10
Gentamycin	25.6 ± 2.1	25.8 ± 1.9	24.8 ± 2.08	32.4 ± 4.10
Ampiclox	11.4 ± 3.2	12.6 ± 3.0	13.9 ± 1.46	20.3 ± 7.51
Zinnacef	21.8 ± 2.4	22.3 ± 2.1	23 ± 2.51	26.3 ± 4.28
Amoxicillin	10.8 ± 3.1	11.2 ± 3.3	14.6 ± 2.06	22.8 ± 3.87
Rocephin	23.2 ± 2.2	23.5 ± 2.0	13.9 ± 4.79	30.2 ± 4.33
Ciprofloxacin	27.4 ± 1.9	27.8 ± 1.6	24.8 ± 3.41	32.4 ± 3.92
Azithromycin	22.5 ± 2.5	22.7 ± 2.2	14.6 ± 2.77	22 ± 4.80
Levofloxacin	28.1 ± 1.8	28.5 ± 1.5	25.4 ± 4.48	26.3 ± 4.33
Erythromycin	18.6 ± 2.8	19.2 ± 2.6	13 ± 2.59	21.2 ± 5.82

Values are expressed as Mean Zone of Inhibition ± Standard Deviation (mm).

Table 6: Mean Zone of Inhibition (mm) of Antibiotics against Gram-Negative Isolates

Antibiotic	*N. mucosa (n=11)*	*N. oralis (n=13)*	*E. coli (n=34)*	*K. pneumoniae (n=11)*
Septrin	14 ± 5.42	19 ± 5.61	23.5 ± 2.5	22.8 ± 2.7
Chloramphenicol	19.6 ± 5.10	24.2 ± 9.35	24.7 ± 2.2	24.1 ± 2.3
Sparfloxacin	22.8 ± 4.76	22 ± 7.71	10.2 ± 2.8	10.5 ± 2.7
Ciprofloxacin	22.8 ± 4.58	19.8 ± 5.69	20.9 ± 2.6	20.1 ± 2.5
Amoxicillin	12 ± 5.88	17 ± 9.04	9.7 ± 2.9	9.5 ± 2.8
Augmentin	16.2 ± 5.60	22 ± 7.71	22.1 ± 2.4	21.9 ± 2.3
Gentamycin	22.8 ± 4.59	24.2 ± 5.56	26.1 ± 2.1	25.8 ± 2.0
Pefloxacin	14 ± 10.86	24.2 ± 5.56	20.8 ± 2.7	20.4 ± 2.6
Ofloxacin	19.6 ± 6.03	16.5 ± 11.14	27.3 ± 1.9	26.9 ± 1.8
Streptomycin	16.2 ± 6.9	15.9 ± 8.13	16.4 ± 3.1	16.8 ± 2.9

Values are expressed as Mean Zone of Inhibition ± Standard Deviation (mm).

3.5 Statistical Comparison of Resistance between Organisms

Separate chi-square tests of independence were run for each antibiotic within the Gram-positive group (*S. aureus, S. epidermidis, S. mitis, S. salivarius*) and the Gram-negative group (*E. coli, K. pneumoniae, N. mucosa, N. oralis*), since the two groups were tested against different antibiotic panels. Within the Gram-positive group, resistance status differed significantly between organisms for ampiclox ($\chi^2 = 15.79$, df = 3, p = 0.001) and amoxicillin ($\chi^2 = 27.27$, df = 3, $p < 0.001$), but not for the remaining eight antibiotics (all $p > 0.05$). Within the Gram-negative group, resistance status differed significantly between organisms for sparfloxacin ($\chi^2 = 35.80$, df = 3, $p < 0.001$), amoxicillin ($\chi^2 = 18.22$, df = 3, $p < 0.001$) and pefloxacin ($\chi^2 = 8.57$, df = 3, p = 0.036), with ciprofloxacin approaching significance ($\chi^2 = 7.07$, df = 3, p = 0.070); the remaining six antibiotics were not significant. In both groups, the significant results were driven by markedly lower resistance among *S. salivarius* (Gram-positive group) and the two *Neisseria* species (Gram-negative group) relative to the other organisms tested with the same panel. Pooling resistance status across all ten antibiotics per organism (Table 7) showed a statistically significant association between organism and overall resistance burden within the Gram-positive group ($\chi^2 = 23.33$, df = 3, $p < 0.001$, Cramer's V = 0.16), within the Gram-negative group ($\chi^2 = 42.67$, df = 3, $p < 0.001$, Cramer's V = 0.25), and across all eight organisms combined ($\chi^2 = 67.92$, df = 7, $p < 0.001$, Cramer's V = 0.21). This is a reversal of the earlier four-organism analysis, in which no significant association was found; with the fuller dataset, organism identity is now a statistically meaningful predictor of resistance status, largely reflecting the consistently low resistance of the two Neisseria isolates rather than differences among the other six organisms. Several individual per-antibiotic tests had expected cell counts below 5 in at least one cell, most often for the smaller groups (*N. mucosa*, n = 11; *S. epidermidis*, n = 13; *N. oralis*, n = 13; *S. mitis*, n = 15); results for these antibiotics should be interpreted with appropriate caution, as the chi-square approximation is less reliable under these conditions.

Table 7: Overall Resistance Rate by Organism, Pooled Across All Ten Antibiotics (Each Organism's Own Panel)

Organism	Total tests (n)	Resistant (n)	Overall resistance rate (%)
Staphylococcus aureus	420	115	27.4
Staphylococcus epidermidis	130	36	27.7
Streptococcus mitis	150	31	20.7
Streptococcus salivarius	230	27	11.7
Escherichia coli	340	109	32.1
Klebsiella pneumoniae	110	37	33.6

Organism	Total tests (n)	Resistant (n)	Overall resistance rate (%)
Neisseria mucosa	110	12	10.9
Neisseria oralis	130	12	9.2

Pooled chi-square — Gram-positive group: $\chi^2 = 23.33$, df = 3, $p < 0.001$, Cramer's V = 0.16 (significant). Gram-negative group: $\chi^2 = 42.67$, df = 3, $p < 0.001$, Cramer's V = 0.25 (significant). All eight organisms combined: $\chi^2 = 67.92$, df = 7, $p < 0.001$, Cramer's V = 0.21 (significant).

4. DISCUSSION

The predominance of *Staphylococcus aureus* and *Escherichia coli* among oral isolates is consistent with their established roles as common inhabitants and opportunistic pathogens of mucosal surfaces; the substantial presence of *E. coli*, an organism of primarily enteric origin, in oral samples may reflect oro-faecal contamination or poor oral hygiene practices among some participants. The two *Neisseria* species and the viridans streptococci (*S. mitis, S. salivarius*) are, by contrast, well-recognised oral commensals, and their comparatively low resistance burden (Table 7) is consistent with a more stable, less antibiotic-exposed niche than the enteric organisms. The high resistance of the staphylococci and Enterobacteriaceae to amoxicillin and ampiclox/sparfloxacin mirrors the widespread and largely unregulated use of β-lactam antibiotics in the study setting and is compatible with carriage of β-lactamase-encoding genes such as blaTEM, particularly among the Gram-negative isolates.

Descriptively, *Klebsiella pneumoniae* and *Escherichia coli* showed the highest point-estimate resistance rates of the eight organisms, and *K. pneumoniae*'s resistance to amoxicillin (81.8%) is consistent with its intrinsic chromosomal β-lactamase activity and its recognised status as an increasingly resistant nosocomial and community pathogen. With the fuller eight-organism dataset, the chi-square analysis now finds a statistically significant difference in resistance status between organisms, both within the Gram-positive group and within the Gram-negative group (Section 3.5) a reversal of the earlier four-organism finding of no significant difference. This shift illustrates how sensitive such comparisons can be to which organisms are included: the earlier analysis, limited to *S. aureus, E. coli, S. epidermidis* and *K. pneumoniae*, happened to include only organisms with broadly similar (moderate-to-high) resistance burdens, whereas the two *Neisseria* isolates included here are consistently far more susceptible, and it is this contrast that now drives statistical significance. The numerical gaps between the six more-resistant organisms in Tables 3, 4 and 7 remain compatible with sampling variability given the modest sample sizes for several groups, particularly *N. mucosa* (n = 11), *K. pneumoniae* (n = 11), *S. epidermidis* (n = 13) and *N. oralis* (n = 13); a larger, more balanced sample would still be needed to characterise these finer differences with adequate statistical power.

The retained activity of levofloxacin and ciprofloxacin among the Gram-positive isolates, and of gentamycin and ofloxacin among the Gram-negative isolates, suggests that these agents remain reliable empirical options for oral bacterial infections in this population, although reliance on a narrowing set of effective agents is itself a concern for long-term antimicrobial stewardship. The moderate-to-high erythromycin resistance observed across the Gram-positive isolates (26.1-40.0%) is suggestive of macrolide-resistance mechanisms such as ermB-mediated ribosomal methylation, a possibility that would require molecular confirmation in future work. The gender distribution of isolates, though numerically skewed toward females, showed no statistically significant association with isolate type ($p = 0.963$), suggesting carriage in this sample is not meaningfully sex-linked. These phenotypic patterns are broadly consistent with reports from other studies describing the oral cavity and other commensal niches as reservoirs of resistance to commonly used antibiotics, including β-lactams and macrolides (Anderson *et al.,* 2023; Sukumar *et al.,* 2024; Rawat & Nair, 2010).

5. CONCLUSION

This study demonstrates that the oral cavity of apparently healthy adults in this population harbours a range of bacteria, including *Staphylococcus aureus, Staphylococcus epidermidis, Streptococcus mitis, Streptococcus salivarius, Escherichia coli, Klebsiella pneumoniae, Neisseria mucosa* and *Neisseria oralis*, many of which display phenotypic resistance to commonly prescribed antibiotics, particularly amoxicillin, ampiclox and sparfloxacin. *Klebsiella pneumoniae* and *Escherichia coli* showed the highest resistance rates of the eight organisms, while the two *Neisseria* isolates were consistently the most susceptible; chi-square testing found this organism-level difference in resistance burden to be statistically significant within both the Gram-positive and Gram-negative groups, a result driven mainly by the low resistance of the *Neisseria* isolates rather than by differences among the remaining six organisms. Larger, more balanced studies are still needed to characterise resistance differences among the more comparably-resistant organisms with greater precision. These findings nonetheless support the view that the oral cavity functions as a reservoir for antibiotic-resistant organisms in the community, independent of hospital exposure, and reinforce the need for antimicrobial stewardship and continued surveillance of commensal, not only clinical, bacterial populations. Further molecular characterization of the resistance genes underlying these phenotypic patterns, alongside larger and more balanced sampling across organisms, would be conducted later.

REFERENCES

- Anderson, A. C., von Ohle, C., Frese, C., Boutin, S., Bridson, C., Schoilew, K., Peikert, S. A., Hellwig, E., Pelz, K., Wittmer, A., Wolff, D., & Al-Ahmad, A. (2023). The oral microbiota is a reservoir for antimicrobial resistance: resistome and phenotypic resistance characteristics of oral biofilm in health, caries, and periodontitis. *Annals of Clinical Microbiology and Antimicrobials*, 22, 37. https://doi.org/10.1186/s12941-023-00585-z
- Brooks, L., Narvekar, U., McDonald, A., & Mullany, P. (2022). Prevalence of antibiotic resistance genes in the oral cavity and mobile genetic elements that disseminate antimicrobial resistance: a systematic review. *Molecular Oral Microbiology, 37*(4), 133-153. https://doi.org/10.1111/omi.12375
- Daniyan, S. Y., & Abalaka, M. E. (2011). Prevalence and susceptibility pattern of bacterial isolates of dental caries in a secondary health care institution, Nigeria. *Shiraz E-Medical Journal*, 12(3), 135-139.
- Dave, M., & Tattar, R. (2025). Antimicrobial resistance genes in the oral microbiome. *Evidence-Based Dentistry*, 26(1), 42-43. https://doi.org/10.1038/s41432-025-01120-z
- Davies, J., & Davies, D. (2010). Origins and evolution of antibiotic resistance. *Microbiology and Molecular Biology Reviews, 74*(3), 417-433. https://doi.org/10.1128/MMBR.00016-10
- Dewhirst, F. E., Chen, T., Izard, J., Paster, B. J., Tanner, A. C. R., Yu, W.-H., Lakshmanan, A., & Wade, W. G. (2010). The human oral microbiome. *Journal of Bacteriology,* 192(19), 5002-5017. https://doi.org/10.1128/JB.00542-10
- Lamont, R. J., Koo, H., & Hajishengallis, G. (2018). The oral microbiota: dynamic communities and host interactions. *Nature Reviews Microbiology,* 16(12), 745-759. https://doi.org/10.1038/s41579-018-0089-x
- Lerminiaux, N. A., & Cameron, A. D. S. (2019). Horizontal transfer of antibiotic resistance genes in clinical environments. *Canadian Journal of Microbiology*, 65(1), 34-44. https://doi.org/10.1139/cjm-2018-0275
- Olagunju, O. J., Ben, E., Olagunju, O., Majolagbe, O. G., Osanyinlusi, O. O., Adewoye, T., Atoyebi, O. F., Ojo, I. O., & Dawha, S. D. (2025). Poorly regulated antibiotic use in Nigeria: a critical public health concern and its impact on medical practice. Cureus, 17(6), e85212. https://doi.org/10.7759/cureus.85212
- Philips, O. O., Timothy, O., Charlse, I. I., & Osamuyimen, I. (2021). Susceptibility pattern of bacterial isolates from dental caries patients attending clinic at Irrua Specialist Teaching Hospital, Irrua, Nigeria. *Journal of Biomedical Research & Environmental Sciences*, 2(9), 784-789. https://doi.org/10.37871/jbres1311
- Rawat, D., & Nair, D. (2010). Extended-spectrum β-lactamases in Gram negative bacteria. *Journal of Global Infectious Diseases*, 2(3), 263-274. https://doi.org/10.4103/0974-777X.68531
- Ready, D., Pratten, J., Roberts, A. P., Bedi, R., Mullany, P., & Wilson, M. (2006). Potential role of Veillonella spp. as a reservoir of transferable tetracycline resistance in the oral cavity. *Antimicrobial Agents and Chemotherapy*, 50(8), 2866-2868. https://doi.org/10.1128/AAC.00217-06
- Roberts, A. P., & Mullany, P. (2010). Oral biofilms: a reservoir of transferable, bacterial, antimicrobial resistance. *Expert Review of Anti-infective Therapy*, 8(12), 1441-1450. https://doi.org/10.1586/eri.10.106
- Roberts, M. C., & Schwarz, S. (2016). Tetracycline and phenicol resistance genes and mechanisms: importance for agriculture, the environment, and humans. *Journal of Environmental Quality,* 45(2), 576-592. https://doi.org/10.2134/jeq2015.04.0207
- Sukumar, S., Rahmanyar, Z., El Jurf, H. Q., Akil, W. S., Hussain, J., Martin, F. E., Ekanayake, K., & Martinez, E. (2024). Mapping the oral resistome: a systematic review. *Journal of Medical Microbiology, 73*(8), 001866. https://doi.org/10.1099/jmm.0.001866
- Tenover, F. C. (2006). Mechanisms of antimicrobial resistance in bacteria. *American Journal of Infection Control,* 34(5, Suppl 1), S3-S10. https://doi.org/10.1016/j.ajic.2006.05.219
- Ventola, C. L. (2015). The antibiotic resistance crisis: part 1: causes and threats. *P & T: A Peer-Reviewed Journal for Formulary Management*, 40(4), 277-283.
- World Health Organization. (2023). *Antimicrobial resistance*. https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance.