RESEARCH PAPER

Evaluation of Salivary Bacterial Load Before and After Removal of Faulty Dental Prostheses: A prospective interventional study

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ABSTRACT

Background

Faulty dental prostheses may act as plaque-retentive surfaces, promoting microbial colonization and contributing to inflammatory changes in the oral cavity.

Aim

To evaluate the change in salivary bacterial load following removal of faulty dental prostheses.

Materials and Methods

A total of 62 patients with clinically diagnosed faulty prostheses were included in the study. Unstimulated saliva samples were collected prior to removal of the prosthesis and again after 45 weeks following removal and oral prophylaxis. Microbiological analysis was performed using semi-quantitative culture techniques on 5% sheep blood agar. Bacterial identification was carried out using standard microbiological methods. Statistical analysis was performed using the Wilcoxon signed-rank test.

Results

A statistically significant reduction in bacterial counts was observed in all tested microorganisms ($p < 0.001$). Gender-based analysis showed comparable reductions in both males and females.

Conclusion

Faulty prostheses serve as reservoirs for pathogenic microorganisms. Their removal, along with maintenance of oral hygiene, significantly improves the oral microbial environment.

Keywords: Faulty prosthesis; Salivary bacterial load; Oral microbiota; Biofilm; Prosthesis removal; Oral hygiene; Microbial colonization.

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.INTRODUCTION

Dental prostheses are widely used to restore missing teeth and improve oral function, aesthetics, and phonetics. For long-term success, prosthetic restorations must maintain compatibility with surrounding oral tissues and allow effective plaque control (1,2).

However, prostheses that are improperly fabricated or poorly maintained may become plaque-retentive and compromise oral health. Such restorations are often referred to as faulty prostheses. Clinical deficiencies such as rough surfaces, over-contouring, improper marginal adaptation, and occlusal discrepancies create favourable niches for microbial colonization (2,3).

Dental plaque is a structured microbial biofilm that develops on oral surfaces and plays a critical role in the pathogenesis of oral diseases (4,8). Prosthetic surfaces with irregularities further enhance biofilm formation and facilitate colonization by opportunistic pathogens (5). Denture plaque has been shown to harbor diverse microorganisms associated with inflammatory conditions such as denture stomatitis (6,7).

In developing countries such as India, faulty prostheses are frequently encountered due to limited awareness, financial constraints, and restricted access to qualified dental care (10–12). Many patients seek treatment from unqualified practitioners, resulting in improperly fabricated prostheses and inadequate follow-up care.

Increased microbial load in the oral cavity may stimulate inflammatory responses through cytokines such as interleukin-6 and tumor necrosis factor-alpha (9).

Although the clinical complications associated with faulty prostheses are well recognized, limited studies have quantitatively evaluated the changes in microbial load following their removal. Therefore, the present study was undertaken to assess the changes in salivary bacterial load after removal of faulty dental prostheses.

MATERIALS AND METHODS

The present study was designed as a prospective interventional study and included 62 patients with clinically diagnosed faulty dental prostheses. Written informed consent was obtained from all participants before inclusion in the study.

Baseline unstimulated saliva samples were collected from all patients prior to removal of the faulty prosthesis. Following sample collection, the prostheses were removed and oral prophylaxis was performed. All patients were instructed regarding appropriate oral hygiene measures and were followed up for a period of 45 weeks, after which post-treatment saliva samples were collected for microbiological analysis.

Saliva samples were collected under sterile conditions and transported immediately to the Department of Microbiology for further processing. Semi-quantitative culture was performed using a sterile calibrated loop of 4 mm diameter capable of delivering approximately 1 µL of the sample. The specimens were inoculated onto 5% sheep blood agar plates and incubated at 37°C for 24–48 hours under aerobic conditions with 5–10% carbon dioxide.

Following incubation, colony counts were recorded and bacterial load was estimated in colony-forming units per milliliter (CFU/mL). The criteria used for CFU estimation and interpretation of bacterial growth are presented in Table 1.

Bacterial identification was carried out based on colony morphology, haemolytic characteristics, Gram staining, and standard biochemical tests.

Statistical analysis was performed using the Wilcoxon signed-rank test to compare bacterial counts before and after removal of faulty prostheses. A p-value of less than 0.05 was considered statistically significant.

Table 1- Colony Count	**Estimated CFU/mL**	**Interpretation**
1–10	$1 \times 10^3 - 1 \times 10^4$	Scanty growth
11–50	$1.1 \times 10^4 - 5 \times 10^4$	Light growth
51–100	$5.1 \times 10^4 - 1 \times 10^5$	Moderate growth
>100	$>1 \times 10^5$	Heavy growth

RESULTS

Microbiological culture findings revealed heavy bacterial growth in saliva samples collected prior to removal of faulty prostheses (Fig. 1A and 1B). Following removal of the prostheses, oral prophylaxis, and maintenance of oral hygiene, a marked reduction in colony density was observed in the post-treatment samples (Fig. 2A and 2B).

Fig. 1 A **Fig. 1B**

Fig. 1 (A and B): Semi-quantitative cultures showing microbial growth >10^5 CFU/mL on blood agar before removal of faulty prosthesis.

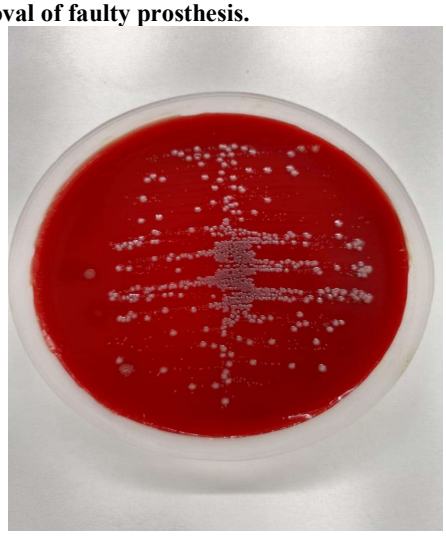

Fig: 2A **Fig: 2B**

Fig. 2 (A and B): Semi-quantitative cultures showing reduced microbial growth (<10^5 CFU/mL) on blood agar after removal of faulty prosthesis.
Representative culture plates demonstrated heavy bacterial growth prior to removal of faulty prostheses, whereas a marked reduction in colony density was observed following removal and maintenance of oral hygiene.

Analysis of the overall bacterial profile demonstrated a statistically significant reduction in all evaluated microorganisms following intervention. The mean counts of Staphylococcus, Corynebacterium, Escherichia coli, Moraxella catarrhalis, Streptococcus, and Gram-negative rods (GNR) showed a marked decrease after removal of faulty prostheses, with all reductions being statistically highly significant ($p < 0.001$) (Table 2).

Table 2: Overall Bacterial Reduction

Sl. no	Name of Bacteria		Mean	Std. deviation	Wilcoxon p value
	Staphylococcus	Before	16195.16	34983.00	< 0.001
		After	150.16	309.21	
	Corynebacterium	Before	12824.19	31547.13	< 0.001
		After	135.65	313.61	
	E. Coli	Before	34822.58	130278.83	< 0.001
		After	374.35	1302.15	
	Moraxella catarrhalis	Before	19983.87	39577.48	< 0.001
		After	169.35	347.63	
	Streptococcus	Before	13808.06	33533.67	< 0.001
		After	116.45	267.94	
	GNR	Before	85985.39	273495.95	< 0.001
		After	103.23	270.98	

Gender-Based Analysis
Gender-wise analysis revealed significant reductions in bacterial counts among both female and male patients. In female patients, Moraxella catarrhalis exhibited the highest baseline count, followed by Escherichia coli and Staphylococcus. A substantial decline in all bacterial species was observed after treatment, with statistically significant differences between pre- and post-treatment values ($p < 0.001$) (Table 3).

Table 3: Comparison of bacterial counts in female patients before and after removal of faulty prosthesis.

Sl. no	Name of Bacteria	Mean	Std. deviation	Wilcoxon

					p value
	Staphylococcus	Before	175555.56	352946.46	< 0.001
		After	148.52	310.37	
	Corynebacterium	Before	133704.07	314883.59	< 0.001
		After	137.41	313.81	
	E. Coli	Before	193333.33	392707.12	< 0.001
		After	200.00	390.27	
	Moraxella catarrhalis	Before	264007.41	444008.30	< 0.001
		After	207.41	387.22	
	Streptococcus	Before	114111.11	319200.72	< 0.001
		After	107.78	261.39	
	GNR	Before	4300.00	192216.16	< 0.001
		After	62.96	192.45	

Similarly, male patients demonstrated significant reductions in all evaluated bacterial species. Escherichia coli showed the highest baseline count among males, followed by Streptococcus and Staphylococcus. Post-treatment values showed a marked reduction in bacterial load, indicating improvement in the oral microbial environment after removal of faulty prostheses and oral prophylaxis (Table 4).

Table 4: Comparison of bacterial counts in male patients before and after removal of faulty prosthesis.

Sl. no	Name of Bacteria		Mean	Std. deviation	Wilcoxon p value
	Staphylococcus	Before	151455.71	35222.514	< 0.001
		After	151.43	312.835	
	Corynebacterium	Before	124000.00	32048.86	< 0.01
		After	134.29	318.03	
	E. Coli	Before	467711.43	170098.775	< 0.01
		After	508.86	1697.9	
	Moraxella catarrhalis	Before	150285.57	35272.457	< 0.01
		After	140.00	316.414	
	Streptococcus	Before	156557.14	35074.662	< 0.01
		After	123.14	276.499	
	GNR	Before	119104.29	32147.98	< 0.01
		After	134.29	318.03	

Comparison of mean bacterial counts between male and female patients before removal of faulty prostheses demonstrated variations in baseline microbial load, with males showing higher counts of Escherichia coli, Streptococcus, and Gram-negative rods, whereas females exhibited higher counts of Moraxella catarrhalis and Staphylococcus (Fig. 3).

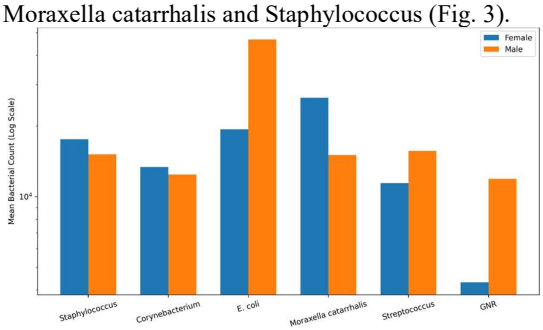

Fig. 3: Comparison of mean bacterial counts between male and female patients before removal of faulty prosthesis.

Following treatment, both genders showed a considerable reduction in bacterial counts. However, male patients continued to demonstrate comparatively higher post-treatment counts of Escherichia coli and Gram-negative rods, while females showed lower residual bacterial counts overall, indicating a more favorable microbial response following intervention (Fig. 4).

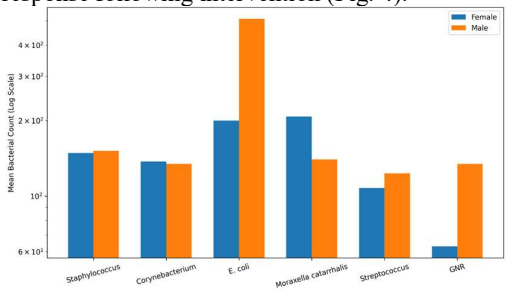

Fig. 4: Comparison of mean bacterial counts between male and female patients after removal of faulty prosthesis.

DISCUSSION

A clear reduction in bacterial load was observed after removal of the faulty prosthesis, indicating improvement in the oral microbial environment. This finding highlights the role of faulty prostheses as plaque-retentive surfaces that promote microbial colonization and biofilm formation.

High baseline counts of organisms such as *Staphylococcus* and *Streptococcus* indicate active plaque accumulation associated with poorly designed prostheses. Their marked reduction after removal suggests that elimination of plaque-retentive niches, along with oral prophylaxis, plays an important role in restoring oral hygiene.

The presence of *Escherichia coli* in higher quantities prior to treatment is clinically important, as it is not considered a normal oral inhabitant. Its presence may reflect poor oral hygiene or contamination associated with long-standing faulty prostheses. Similarly, the significant reduction in *Moraxella catarrhalis* and Gram-negative rods following treatment indicates improvement in the oral microbial environment and reduction of potentially pathogenic flora.

Gender-based analysis showed significant bacterial reduction in both males and females. Female patients demonstrated comparatively higher baseline counts of *Moraxella catarrhalis* but also showed marked reduction after treatment, suggesting effective improvement following oral prophylaxis and prosthesis removal. Male patients exhibited relatively higher counts of *E. coli* and Gram-negative rods, which may indicate greater microbial contamination and variability in oral hygiene maintenance.

From a clinical perspective, the presence of pathogenic microorganisms associated with faulty prostheses may contribute not only to local oral inflammation but also to systemic complications in susceptible individuals. The findings emphasize the importance of proper prosthetic design, regular follow-up, and maintenance of oral hygiene in preventing microbial colonization and maintaining oral health.

CONCLUSION

Faulty dental prostheses act as reservoirs for pathogenic microorganisms and contribute to increased bacterial colonization in the oral cavity. Their removal, along with maintenance of proper oral hygiene, results in a significant reduction in microbial load. Early diagnosis and correction of faulty prostheses are essential for maintaining oral health.

REFERENCES :

1. Zarb GA, Hobkirk JA, Eckert SE, Jacob RF. Prosthodontic treatment for edentulous patients: complete dentures and implant-supported prostheses. 13th ed. St. Louis: Mosby; 2013.
2. Carr AB, Brown DT. McCracken's removable partial prosthodontics. 13th ed. St. Louis: Elsevier; 2016.
3. Anusavice KJ, Shen C, Rawls HR. Phillips' science of dental materials. 12th ed. St. Louis: Elsevier; 2013.
4. Marsh PD, Martin MV. Oral microbiology. 5th ed. Edinburgh: Churchill Livingstone; 2009.
5. Coulthwaite L, Verran J. Potential pathogenic aspects of denture plaque. Br J Biomed Sci. 2007;64(4):180–189.
6. Pereira-Cenci T, Del Bel Cury AA, Crielaard W, Ten Cate JM. Development of Candida-associated denture stomatitis: new insights. J Appl Oral Sci. 2008;16(2):86–94.
7. Gendreau L, Loewy ZG. Epidemiology and etiology of denture stomatitis. J Prosthodont. 2011;20(4):251–260.
8. Marsh PD. Dental plaque as a biofilm and a microbial community – implications for health and disease. BMC Oral Health. 2006;6(Suppl 1):S14.
9. Takahashi N, Nyvad B. The role of bacteria in the caries process: ecological perspectives. J Dent Res. 2011;90(3):294–303.
10. Bhatia G, Bhatia SK. Dentistry in rural India: public health perspective. Int J Health Sci (Qassim). 2014;8(3):301–305.
11. Gambhir RS, Singh G, Talwar PS. Primary health care in dentistry: an untapped potential. Indian J Public Health. 2011;55(4):244–247.
12. Kumar S, Tadakamadla J, Kroon J, Johnson NW. Impact of socioeconomic status on oral health: a systematic review. J Int Soc Prev Community Dent. 2015;5(3):168–175