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Oral Microbial Basis of Intraoral Halitosis: The Role of the Oral Microbiome

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Abstract

BACKGROUND: A respectable amount of the global population is affected by halitosis. Halitosis causes notable social and psychological distress among sufferers. It is primarily caused by the oral microbiota, which converts sulphur containing amino-acid substrate into volatile sulphur compounds. This review aims to elucidate the role of the oral microbiome in intraoral halitosis, emphasising microbial dysbiosis, volatile sulphur compound production, and the potential of microbiome-targeted therapeutic approaches.

METHODS: Relevant literatures were searched across PubMed/MEDLINE, Scopus, and Google Scholar using terms regarding the microbial etiology, biochemical mechanisms, and management of intraoral halitosis and included.

RESULTS: The primary sites for volatile sulphur compounds production are the dorsum of the tongue and diseased periodontal pockets. The main gram-negative bacteria associated with VSC production are Porphyromonas gingivalis, Treponema denticola, Fusobacterium nucleatum, Prevotella inter media, and Solobacteriummoorei. Oral dysbiosis, poor oral hygiene, periodontitis, xerostomia, and some systemic conditions, promotes the growth of these proteolytic bacteria. Microbiome-targeted treatments, such as mechanical cleaning, antiseptic agents, and probiotics, have shown significant clinical benefits in managing halitosis.

CONCLUSION: Intraoral halitosis is strongly associated with oral microbiome dysbiosis and increased volatile sulphur compound production by anaerobic bacteria. Understanding these microbial mechanisms supports targeted treatments such as antimicrobials, probiotics, and microbiome-modulating therapies to reduce oral malodour.

Keywords: Oral microbiome; Intraoral halitosis; Volatile sulphur compounds; Periodontal biofilm; Oral dysbiosis; Anaerobic bacteria;

I. INTRODUCTION

Halitosis is derived from the Latin word 'halitus' (breath) and the Greek word 'osis' (state of disease). It refers to an unpleasant odour that arises from the oral cavity or exhaled breath. Halitosis affects social interactions, self-confidence, and quality of life. According to Kapoor et al in 2016, the global prevalence ranges from 22 to 50%, making it one of the most common oral health complaints worldwide [1]. Despite this prevalence, halitosis is often underdiagnosed because sufferers are often not conscious of it [2]. The above finding prompted us to write a narrative on the association of the oral microbiome with halitosis.

Halitosis is classified into: (i) intraoral halitosis, originating within the oral cavity; (ii) extraoral halitosis, arising from pulmonary, hepatic, renal, or gastrointestinal sources; and (iii) pseudo-halitosis,

perceived by the patient. Approximately 90% of cases of halitosis arise intraorally, and they are mainly associated with oral disorders like tongue coating, periodontal conditions, impacted food debris, cavities, oral infections, and reduced saliva secretion [3]. Halitosis is mainly caused by the tongue coatings, followed by periodontal diseases and other contributing factors accounts for smaller proportions [3]. Volatile sulfur compounds (VSCs), specifically hydrogen sulfide (H₂S), methyl mercaptan (CH₃SH), and dimethyl sulfide, are the main etiological agents linked to intraoral halitosis. These compounds are formed when certain anaerobic bacteria in the oral cavity breakdown sulfur-containing substrates [4].

Human Oral Microbiome Database (HOMD) is an extensive database of more than 600 bacterium

types, including fungi, archaea, viruses, protozoa, and more, creating one of the most complex microbiomes in the human body [5]. This microbial community is in a balanced state under normal circumstances, but dysbiosis, or disturbances in microbial homeostasis, can encourage the growth of proteolytic, VSC-producing bacteria linked to halitosis.

The purpose of this review is to analyse the available data regarding the oral microbiome's involvement in intraoral halitosis, emphasizing the microbial mechanisms, important bacterial species, and possible treatment approaches that target microbial dysbiosis.

II. METHODS

This review article was developed through a comprehensive literature search of published scientific studies related to oral microbiome and intraoral halitosis. A literature search was conducted in PubMed, Scopus, and Google Scholar using keywords related to halitosis, oral microbiome, volatile sulphur compounds (VSCs), periodontal bacteria, oral dysbiosis, and probiotics. Original research papers, systematic reviews, meta-analyses, randomized control trials, and narrative reviews related to microbial etiology of halitosis, volatile sulfur compound generation, alterations in oral microbiome, and microbial interventions for treatment were considered eligible sources. Excluded sources included case studies, conference proceedings, and editorial comments. The titles and abstracts were screened to select relevant articles, which underwent further analysis. Results were grouped according to themes such as oral microbiome composition, bacteria that produce volatile sulfur compounds, pathways for the formation of VSCs, microbial dysbiosis, and treatment methods.

III. RESULTS

After full-text screening 43 references were included in this review. Majority of studies showed that intraoral halitosis was caused mainly due to the metabolic action of the microorganisms in the oral cavity, particularly on the dorsum of the tongue and periodontal pockets. These included *Porphyromonas gingivalis*, *Fusobacterium nucleatum*, *Treponema denticola*, *Prevotella intermedia*, and *Solobacterium moorei*. Additionally, microbiome studies revealed that the oral cavity of patient with halitosis had abundance of pathogenic anaerobic microorganisms, and fewer useful microorganisms like *Streptococcus salivarius*, *Streptococcus mitis*, and *Rothia* species. The evidence indicates that volatile sulphur compounds (VSCs), which cause halitosis, are formed mainly from degradation of amino acids

like cysteine and methionine, by these anaerobic bacteria.

Clinical trials have indicated that tongue cleansing and periodontal therapy are highly effective in reducing VSCs. Antiseptic mouth rinses, like those with chlorhexidine and cetylpyridinium chloride, were also effective. The use of probiotics like *S. salivarius* K12 was proven to reduce halitosis.

IV. DISCUSSION

I. The Human Oral Microbiome: Composition and Ecological Organisation

The microorganisms found on or in the human oral cavity till the distal oesophagus referred to as the oral microbiome. It is the second most complex microbial ecosystem within the human body and comprises bacteria, fungi, viruses, archaea, and protozoa. "Approximately 700 species of prokaryotes, which belong to 185 genera and 12 phyla, have been identified in the oral cavity. The 12 phyla are Firmicutes, Fusobacteria, Proteobacteria, Actinobacteria, Bacteroidetes, Chlamydiae, Chloroflexi, Spirochaetes, SR1, Synergistetes, Saccharibacteria (TM7), and Gracilibacteria (GN02)" [6]. The teeth, gingival sulcus, tongue dorsum, buccal mucosa, hard and soft palates, and tonsils are inhabited by specialized communities of species that together make up the highly organized oral microbiome [5]. Different sites also have different microenvironments characterised by varying levels of gradients of oxygen, pH, nutrients, mechanical stress due to chewing, and exposure to saliva and immune components. These factors shape the microbial composition, allowing certain taxa to colonise specific surfaces while preventing overgrowth of others [7].

The site-specificity is of direct relevance to intraoral halitosis. The tongue dorsum is the primary halitosis-associated habitat. In health the dorsum of tongue is covered by microbes like *Actinobacteria*, *Spirochaetes*, *Fusobacteria*, *Bacteroidetes*, *Firmicutes*, and *Proteobacteria*, whereas a shift toward an anaerobe-enriched community characterises the halitosis state [8]. 16S rRNA-based analyses of tongue coating microbiota have identified several genera associated with halitosis, including *Prevotella*, *Fusobacterium*, *Leptotrichia*, *Peptostreptococcus*, and *Stomatobaculum*, which are present in higher abundance in subjects with halitosis, whereas in healthy subjects the dorsum is enriched with *Streptococcus*, *Veillonella*, and *Rothia* species, which are associated with metabolically neutral, non-odour-producing activity is [9].

Apart from the tongue, the subgingival sulcus is another environmentally important niche associated with halitosis. Periodontal pockets serve as a suitable environment for the development of the oral microorganisms, that produce halitosis [8].

The ecological organisation of the oral microbiome can, therefore, be considered the basis for the biology behind intraoral halitosis, a condition that does not result from an individual microorganism but rather from the combined effects of proteolysis and sulfur metabolism carried out by certain microbes. This is explored in detail in the following sections.

V. PRINCIPAL VSC-PRODUCING BACTERIA

The oral bacteria that are most likely to produce hydrogen sulfide and methyl mercaptan include *Fusobacterium*, *Porphyromonas*, and *Treponemadenticola*. *Bacteroides*, *Eubacterium*, *Prevotella*, and *Solobacteriummoorei* [10].

Porphyromonasgingivalis is the most potent VSC-producing bacterium. It is strongly associated with gum disease (periodontitis) and produces large amounts of methyl mercaptan by breaking down the amino acid methionine. It also releases enzymes called gingipains that destroy tissue proteins, creating more substrate for VSC production [11].

Fusobacteriumnucleatum is a common bacterium found on both the tongue dorsum and in periodontal pockets. It acts as a "bridge" organism by linking early, harmless bacteria with later, more harmful anaerobic bacterial species. It also produces large amounts of hydrogen sulfide and other compounds that contribute to bad breath [12].

Treponemadenticola- It is a red complex periodontal pathogen, which produces both hydrogen sulfide and methyl mercaptan. This Spirochaete is equipped with enzymes (trypsin-like proteases) that break down proteins efficiently, feeding VSC production [13].

Prevotella intermedia is found in infected pockets and on the tongue surface. It degrades sulfur-containing amino acids and produce VSC and is frequently found in patients with both periodontitis and halitosis [14].

Solobacteriummoorei is found predominantly on the dorsal tongue surface. This bacterium has been specifically and consistently linked to intraoral halitosis even in patients without gum disease. It is one of the strongest microbial predictors of tongue-coat-associated bad breath [15].

***Eubacterium* species**, particularly *Eubacterium* sulci, found in the subgingival environment, contribute to the production of VSC, primarily hydrogen sulfide and, methyl mercaptan, to a lesser extent through amino acid catabolism [16].

VI. BIOCHEMICAL PATHWAYS OF VOLATILE SULPHUR COMPOUND PRODUCTION

The degradation of sulfur-containing amino acids, such as cysteine and methionine results in formation of volatile sulfur compounds (VSCs). These sulfur-

containing amino acids are released through the breakdown of salivary glycoproteins, serum proteins, desquamated epithelial cells, and dietary substrates [17].

1. Cysteine → Hydrogen Sulfide (H₂S)

Cysteine catabolism is the principal pathway for H₂S generation. The enzyme cysteine desulphydrase (CDase) cleaves cysteine to produce pyruvate, ammonia, and H₂S in a single reaction.

Cysteine → Pyruvate + NH₃ + H₂S

Fusobacteriumnucleatum, a common periodontal pathogen, produce huge amounts of hydrogen sulfide from L-cysteine by the catalytic action of L-cysteine desulphydrase [16,17].

H₂S is the primary odorant produced on the tongue dorsum, where cysteine availability is high due to the abundance of cysteine-rich mucin glycoproteins in saliva [18].

2. Methionine → Methyl Mercaptan (CH₃SH) via Methionine γ-Lyase (MGL / METase)

Enzymatic activity of L-methionine-α-deaminomercaptomethane-lyase (METase), that catalyses the α, γ-elimination reaction of L-methionine, resulting in the release of α-ketobutyrate, methyl mercaptan, and ammonia [19].

L-Methionine → CH₃SH + α-Ketobutyrate + NH₃

This reaction is particularly active in the subgingival microenvironment, where methionine availability is enhanced by the proteolytic breakdown of serum albumin and haemoglobin. Key oral microbial species producing methanethiol are "Porphyromonasgingivalis, Prevotella intermedia, and Fusobacteriumnucleatum" [20].

3. Dimethyl Sulfide (CH₃)₂S Formation

Dimethyl sulfide is formed by S-methylation of CH₃SH via thiol S-methyltransferase.

CH₃SH → (CH₃)₂S.

While less abundant than H₂S and CH₃SH in most cases of intraoral halitosis, dimethyl sulfide can still contribute to the overall odour profile and has been reported at elevated levels in certain patients. It is a dominant VSC in systemic halitosis associated with hepatic failure and trimethylaminuria [21].

In addition to VSCs, oral bacteria produce other malodorous compounds, including volatile fatty acids (such as butyric, propionic, and valeric acids) and polyamines (including putrescine, cadaverine, indole, and skatole). These compounds further intensify oral malodour [22].

VII. ORAL MICROBIOME DYSBIOSIS AND HALITOSIS PATHOGENESIS

Dysbiosis, defined as a shift in the composition and functional activity of the microbial community from a state of health to a diseased state, plays a major role in the occurrence of intraoral halitosis [23].

Halitosis-related dysbiosis can be defined as having a reduced proportion of commensal bacteria with beneficial impacts on oral health, such as *Streptococcus salivarius*, *Streptococcus mitis*, and *Actinomyces* spp, along with an increase in the number of Gram-negative anaerobic bacteria that produce VSC [14,24].

Factors like diet, smoking, alcohol consumption, lifestyle choices, and medical conditions can lead to dysbiosis. Xerostomia is major factor leading to dysbiosis, as saliva is essential for maintaining oral homeostasis through its mechanical cleansing action, buffering capacity, and antimicrobial components. The reduced production of saliva, which can be caused by various drugs or conditions like Sjogren's syndrome, or occurs physiologically while sleeping, enables anaerobic and proteolytic bacteria to thrive [25]. Poor oral hygiene also encourages plaque and tongue coating build-up, leading to increased bacteria and thus enhanced formation of volatile sulfur compounds. A diet rich in protein provides abundant substrate for bacterial metabolism and thus increases the production of odorous compounds. An association between oral dysbiosis and bad breath is characterised by a self-reinforcing cycle. Hydrogen sulfide (H_2S) and methyl mercaptan (CH_3SH), generated by pathogenic, anaerobic bacteria, not only cause the odour but also cause gingival epithelial cell and periodontal fibroblast injuries. This weakens the epithelial barrier, promotes inflammation, and creates an environment that encourages bacterial colonisation and perpetuates dysbiosis and halitosis [26].

VIII. THERAPEUTIC STRATEGIES TARGETING THE ORAL MICROBIOME

Management of intraoral halitosis increasingly focuses on modulating the oral microbiome rather than simply masking odour. Therapeutic strategies aim to reduce anaerobic, proteolytic bacterial populations or shift them toward a healthier balance as VSC are mainly produced by these organisms residing in oral niches [27].

1. Mechanical Cleaning — Removing the Bacteria Physically

The first and most important step in treating bad breath is simply removing the bacteria and the material they feed on.

Tongue cleaning is highly effective, as the tongue dorsum harbours a large bacterial load. A Cochrane systematic review (Outhouse et al., 2016) showed that tongue scraping reduces volatile sulfur compound (VSC) levels by 42%–75% [28]. A systematic review by Slot et al. (2015) further confirmed that regular tongue cleaning significantly lowers both tongue coat scores and breath Odor measurements, though evidence for long-term benefits remains limited [29]. Patients should be

advised to scrape from the back of the tongue to the front, doing 4–5 strokes, twice a day.

Scaling and root planing (SRP) is required when periodontitis is the underlying cause of halitosis. Subgingival microbiota significantly contribute to halitosis, and their mechanical elimination through periodontal therapy leads to a measurable reduction in oral malodour [30].

Flossing and interdental brushing remove bacteria that ferment food debris in tight interdental spaces, thereby significantly reducing halitosis [31].

2. Antiseptic Mouthwashes — Killing the Odour-Causing Bacteria

Antiseptic mouthrinses, particularly those containing chlorhexidine (CHX), zinc salts, and cetylpyridinium chloride (CPC), are among the most commonly used chemical agents in the management of halitosis.

Chlorhexidine is a potent antiseptic mouthwash with high substantivity, allowing prolonged antibacterial activity for up to 12 hours after use. It was identified as the gold-standard antimicrobial agent in periodontology and halitosis management. However, prolonged use may cause tooth staining, taste alteration, and disturbance of the oral microbiota, limiting its use to short-term therapy (typically 2–4 weeks) [32].

Cetylpyridinium chloride (CPC) Cetylpyridinium chloride (CPC) is a mild antiseptic commonly used in over-the-counter mouthwashes. It disrupts bacterial cell membranes, reducing microbial load. Unlike chlorhexidine, CPC is generally considered suitable for long-term daily use. Shiina et al. (2025) evaluated the effects of 0.05% cetylpyridinium chloride (CPC) mouthwash on halitosis in orthodontic patients [33]. The study found that regular use of CPC significantly reduced halitosis. Microbiome analysis showed a shift toward a healthier oral microbial profile, with a reduction in halitosis-associated bacteria [33].

Zinc compounds (zinc chloride, zinc acetate, zinc lactate) work through two mechanisms: i) eliminate bad breath by neutralising VSCs via formation of non-volatile odourless complexes and ii) by preventing the proliferation of VSC-forming bacteria, thus offering both immediate and long-term protection against bad breath [34].

Essential oil mouthwashes, which contains eucalyptol, menthol, and methyl salicylate (for example, Listerine®), inhibit the growth of odour-producing bacteria. Essential oil-containing mouthrinses are therefore considered effective adjuncts to mechanical oral hygiene in the management of halitosis [35].

3. Oxidising Agents — Destroying the odour Gases

As the bacteria that cause halitosis are anaerobic, substances that release oxygen into the oral cavity, referred to as oxidising agents, can eliminate these bacteria and break down the gases they produce. [36]

Chlorine dioxide (ClO₂) oxidises the sulfur gases, converting them into odourless compounds, and simultaneously disrupts the bacterial cell membrane [37].

Hydrogen peroxide (H₂O₂) in low concentrations of 1–3% releases reactive oxygen molecules that inhibit bacterial growth and degrade VSCs. However, higher concentrations are avoided as it causes mucosal irritation [38].

Sodium bicarbonate increases oral PH and creates an unfavourable environment for the bacteria that produce VSCs and reduces their metabolism [39].

IX. BLOCKING BACTERIAL ENZYMES — STOPPING VSC PRODUCTION AT THE SOURCE

Inhibition of bacterial enzymes involved in proteolysis and VSC formation effectively reduces oral malodour at its source. Natural agents such as green tea catechins and polyphenols, along with salivary substitutes, further support this approach by suppressing enzyme activity and limiting anaerobic conditions [40].

5. Probiotics — Replacing Bad Bacteria with Good Bacteria

Using probiotics to reshape the oral microbiome and suppress volatile sulfur compound-producing bacteria is an increasingly promising therapeutic approach [41]. Probiotics reduce bad breath primarily through **competitive inhibition**, where helpful bacteria attach to the tongue's mucosal layer and block harmful, odour-causing bacteria from colonizing the tongue dorsum. Additionally, certain probiotic strains produce **bacteriocins**, which are natural antimicrobial proteins that actively target and eliminate undesirable oral bacteria [42].

Streptococcus salivarius K12, which produces the bacteriocins salivaricin A2 and B, is a well-studied oral probiotic for halitosis and has shown markable reductions in organoleptic scores as well as VSC levels, and the effects lasts for several weeks in some cases [42,43].

Lactobacillus salivarius WB21, taken as a lozenge two to three times daily, works through competitive exclusion — occupying binding sites on the tongue and mucosal surfaces so that harmful bacteria cannot colonise them. WB21 is particularly beneficial in patients where halitosis is linked to periodontal disease, as it targets both halitosis and periodontal inflammation [44].

Lactobacillus reuteri, produces an antimicrobial substance called reuterin that restricts harmful bacteria while simultaneously reducing the gum inflammation and bleeding that frequently triggers chronic halitosis [42]

Weissellacibaria, a oral probiotic strain that produces hydrogen peroxide, creates an oxidative environment that adversely affects strict anaerobes such as *Fusobacterium nucleatum* and *Porphyromonas gingivalis*. [42]

The key advantage of probiotics over antiseptics is that they guide the microbiome toward a healthier balance rather than disrupting it entirely. Standard gut probiotics that are swallowed whole are ineffective against halitosis because they bypass the mouth entirely. Oral-retention formats like lozenges, or chewable tablets must be used. These dissolve slowly in the mouth, allowing the helpful bacteria to directly colonize the tongue and mucosal surfaces where odor-causing pathogens reside. [44]

X. CONCLUSION

Intraoral Halitosis is a multi-factorial problem where an important role is played by the microbial composition of the oral cavity plays an important part. The selective enrichment of microorganisms like "*Porphyromonas gingivalis*, *Treponema denticola*, *Fusobacterium nucleatum*, *Prevotella intermedia*, and *Solobacterium moorei*" in the tongue coating and periodontal pockets causes the breakdown of sulfur-rich amino acids to form volatile sulfur compounds, which is the main source of bad breath. Poor oral hygiene, periodontal diseases, xerostomia and systemic factors leads to dysbiosis of the oral microbiota and increases VSC production thereby intensifying halitosis.

Halitosis should be effectively managed by addressing its underlying microbial cause via mechanical removal of biofilm from both teeth and tongue surface, professional periodontal treatment, and the application of antimicrobial agents and VSC scavengers. Probiotics that competitively exclude VSC-producing bacteria offer a novel and encouraging approach. Future advances in microbiome science, including metagenomic profiling and personalised therapeutic targeting, hold considerable promise for improving the precision and efficacy of halitosis management.

REFERENCES

1. Kapoor, U., Sharma, G., Juneja, M., & Nagpal, A. (2016). Halitosis: Current concepts on etiology, diagnosis, and management. *European Journal of Dentistry*, 10(02), 292-300. <https://doi.org/10.4103/1305-7456.178294>.
2. Settineri, S., Mento, C., Gugliotta, S.C., Saitta, A., Terranova, A., Trimarchi, G., & Mallamace, D. (2010). Self-reported halitosis and

- emotional state: impact on oral conditions and treatments. *Health and Quality of Life Outcomes*, 8(1), 34-34. <https://doi.org/10.1186/1477-7525-8-34>.
3. Cortelli, J.R., Barbosa, M.D.S., & Westphal, M.A. (2008). Halitosis: a review of associated factors and therapeutic approach. *Brazilian Oral Research*, 22(suppl 1), 44-54. <https://doi.org/10.1590/s1806-83242008000500007>.
4. Tangerman, A., & Winkel, E.G. (2012). Volatile Sulfur Compounds as The Cause of Bad Breath: A Review. Phosphorus, sulfur, and silicon and the related elements, 188(4), 396-402. <https://doi.org/10.1080/10426507.2012.736894>.
5. Dewhirst, F.E., Chen, T., Izard, J., Paster, B.J., Tanner, A.C.R., Yu, W., 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>.
6. Deo, P., & Deshmukh, R. (2019). Oral microbiome: Unveiling the fundamentals. *Journal of Oral and Maxillofacial Pathology*, 23(1), 122-122. https://doi.org/10.4103/jomfp.jomfp_304_18.
7. Willis, J.R., & Gabaldón, T. (2020). The Human Oral Microbiome in Health and Disease: From Sequences to Ecosystems. *Microorganisms*, 8(2), 308-308. <https://doi.org/10.3390/microorganisms8020308>.
8. Lee, Y., & Hong, J. (2023). Oral microbiome as a co-mediator of halitosis and periodontitis: a narrative review. *Frontiers in Oral Health*, 4, 1229145-1229145. <https://doi.org/10.3389/froh.2023.1229145>.
9. Oshiro, A., Zaitzu, T., Ueno, M., & Kawaguchi, Y. (2020). Characterization of oral bacteria in the tongue coating of patients with halitosis using 16S rRNA analysis. *Acta Odontologica Scandinavica*, 78(7), 541-546. <https://doi.org/10.1080/00016357.2020.1754459>.
10. Hampelska, K., Jaworska, M.M., Babalska, Z., & Karpiński, T.M. (2020). The Role of Oral Microbiota in Intra-Oral Halitosis. *Journal of Clinical Medicine*, 9(8), 2484-2484. <https://doi.org/10.3390/jcm9082484>.
11. Myšák, J.,těpánPodzimek, Sommerova, P., Lyuya-Mi, Y., Bártová, J., Janatova, T., Procházková, J., & Dušková, J. (2014). Porphyromonas gingivalis: Major Periodontopathic Pathogen Overview. *Journal of Immunology Research*, 2014, 1-8. <https://doi.org/10.1155/2014/476068>.
12. Choe, I. (2024). Association Of Fusobacterium Nucleatum With Halitosis. Zenodo (CERN European Organization for Nuclear Research). <https://doi.org/10.5281/zenodo.15608651>.
13. Fenno, J.C. (2012). Treponemadenticolainteractions with host proteins. *Journal of Oral Microbiology*, 4(1), 9929-9929. <https://doi.org/10.3402/jom.v4i0.9929>.
14. Kazor, C., Mitchell, P.M., Lee, A.M., Stokes, L.N., Loesche, W.J., Dewhirst, F.E., & Paster, B.J. (2003). Diversity of Bacterial Populations on the Tongue Dorsa of Patients with Halitosis and Healthy Patients. *Journal of Clinical Microbiology*, 41(2), 558-563. <https://doi.org/10.1128/jcm.41.2.558-563.2003>.
15. Barrak, I., Stájer, A., Gajdács, M., & Urbán, E. (2020). Small, but smelly: the importance of Solobacteriummoorei in halitosis and other human infections. *Heliyon*, 6(10), e05371-e05371. <https://doi.org/10.1016/j.heliyon.2020.e05371>.
16. Yoshida, A., Yoshimura, M., Ohara, N., Yoshimura, S., Nagashima, S., Takehara, T., & Nakayama, K. (2009). Hydrogen Sulfide Production From Cysteine and Homocysteine by Periodontal and Oral Bacteria. *Journal of Periodontology*, 80(11), 1845-1851. <https://doi.org/10.1902/jop.2009.090012>.
17. Basic, A., Blomqvist, M., Dahlén, G., & Svensäter, G. (2017). The proteins of Fusobacterium spp. involved in hydrogen sulfide production from L-cysteine. *BMC Microbiology*, 17(1), 61-61. <https://doi.org/10.1186/s12866-017-0967-9>.
18. Lee, W., Jo, J.H., Park, Y., & Park, J.W. (2025). Clinical and measurement variables affecting halitosis intensity following cysteine challenge test. *Scientific Reports*, 15(1), 4467-4467. <https://doi.org/10.1038/s41598-024-83177-x>.
19. Yoshimura, M., Nakano, Y., Yamashita, Y., Oho, T., Saito, T., & Koga, T. (2000). Formation of Methyl Mercaptan from l - Methionine by Porphyromonas gingivalis. *Infection and Immunity*, 68(12), 6912-6916. <https://doi.org/10.1128/iai.68.12.6912-6916.2000>.
20. Nakano, Y., Yoshimura, M., & Koga, T. (2002). Correlation between oral malodor and periodontal bacteria. *Microbes and Infection*, 4(6), 679-683.

- https://doi.org/10.1016/s1286-4579(02)01586-1.
21. Tangerman, A., &Winkel, E.G. (2007). Intra- and extra-oral halitosis: finding of a new form of extra-oral blood-borne halitosis caused by dimethyl sulphide. *Journal Of Clinical Periodontology*, 34(9), 748-755. https://doi.org/10.1111/j.1600-051x.2007.01116.x.
22. Bollen, C., &Beikler, T. (2012). Halitosis: the multidisciplinary approach. *International Journal of Oral Science*, 4(2), 55-63. https://doi.org/10.1038/ijos.2012.39.
23. Zarco, M., Vess, T., & Ginsburg, G. (2011). The oral microbiome in health and disease and the potential impact on personalized dental medicine. *Oral Diseases*, 18(2), 109-120. https://doi.org/10.1111/j.1601-0825.2011.01851.x.
24. Takeshita, T., Suzuki, N., Nakano, Y., Shimazaki, Y., Yoneda, M., Hirofujii, T., & Yamashita, Y. (2010). Relationship between Oral Malodor and the Global Composition of Indigenous Bacterial Populations in Saliva. *Applied and Environmental Microbiology*, 76(9), 2806-2814. https://doi.org/10.1128/aem.02304-09.
25. Kleinberg, I., Wolff, M.S., &Codipilly, D.M. (2002). Role of saliva in oral dryness, oral feel and oral malodour. *International Dental Journal*, 52(5), 236-240. https://doi.org/10.1002/j.1875-595x.2002.tb00932.x.
26. Lee, Y., Shin, S., & Hong, J. (2023). Investigation of volatile sulfur compound level and halitosis in patients with gingivitis and periodontitis. *Scientific Reports*, 13(1), 13175-13175. https://doi.org/10.1038/s41598-023-40391-3.
27. Hampelska, K.,Jaworska, M.M.,Babalska, Z., &Karpiński, T.M. (2020). The Role of Oral Microbiota in Intra-Oral Halitosis. *Journal of Clinical Medicine*, 9(8), 2484-2484. https://doi.org/10.3390/jcm9082484.
28. Outhouse, T.L., Al-Alawi, R.,Fedorowicz, Z., & Keenan, J.V. (2016). Tongue scraping for treating halitosis. *Cochrane Database of Systematic Reviews*, 2016(5), CD005519-CD005519. https://doi.org/10.1002/14651858.cd005519.pub3.
29. der Sleen, M.V., Slot, D., vanTrijffel, E.,Winkel, E., & der Weijden, G.V. (2010). Effectiveness of mechanical tongue cleaning on breath odour and tongue coating: a systematic review. *International Journal of Dental Hygiene*, 8(4), 258-268. https://doi.org/10.1111/j.1601-5037.2010.00479.x.
30. Eid, H.A. (2014). Non-surgical management of periodontitis related halitosis among adults. *Saudi Journal for Health Sciences*, 3(2), 80-80. https://doi.org/10.4103/2278-0521.134855.
31. Izidoro, C.,Botelho, J., Machado, V., Reis, A.M.,Proença, L., Alves, R., & Mendes, J.J. (2022). Revisiting Standard and Novel Therapeutic Approaches in Halitosis: A Review. *International Journal of Environmental Research and Public Health*, 19(18), 11303-11303. https://doi.org/10.3390/ijerph191811303.
32. Marsh, P. (2010). Controlling the oral biofilm with antimicrobials. *Journal of Dentistry*, 38, S11-S15. https://doi.org/10.1016/s0300-5712(10)70005-1
33. Shiina, N., Shimpo, Y., Kikuchi, K., Sekiya, T., &Tomonari, H. (2025). Effects of 0.05% Cetylpyridinium Chloride Mouthwash on Halitosis and Tongue Microbiota in Patients Undergoing Orthodontic Treatment: A Double-Blind Randomized Clinical Trial. *Journal of Clinical Medicine*, 14(13), 4576-4576. https://doi.org/10.3390/jcm14134576.
34. Suzuki N, Nakano Y, Watanabe T, Yoneda M, Hirofujii T, Hanioka T. Two mechanisms of oral malodor inhibition by zinc ions. *Journal of Applied Oral Science*. 2018;26:e20170161.https://doi.org/10.1590/1678-7757-2017-0161.
35. Dobler, D., Runkel, F., &Schmidts, T. (2020). Effect of essential oils on oral halitosis treatment: a review. *European Journal of Oral Sciences*, 128(6), 476-486. https://doi.org/10.1111/eos.12745.
36. Khounganian, R.M., Alasmari, O.N., Aldosari, M., &Alghanemi, N.M. (2023). Causes and Management of Halitosis: A Narrative Review. *Cureus*, 15(8), e43742-e43742. https://doi.org/10.7759/cureus.43742.
37. gnesSzalai, E., Tajti, P., Szabó, B., Hegyi, P., Czumbel, L.M., Shojazadeh, S., Varga, G., Németh, O., &Kerémi, B. (2023). Daily use of chlorine dioxide effectively treats halitosis: A meta-analysis of randomised controlled trials. *PLoS ONE*, 18(1), e0280377-e0280377. https://doi.org/10.1371/journal.pone.0280377.
38. Rashed, H.T. (2016). Evaluation of the effect of hydrogen peroxide as a mouthwash in comparison with chlorhexidine in chronic periodontitis patients: A clinical study. *Journal of International Society of Preventive and Community Dentistry*, 6(3), 206-206. https://doi.org/10.4103/2231-0762.183114.

39. Pindobilowo, P., Ariani, D., Herawati, M., Dwiyono, S., &Byungchan, A. (2023). Effects of Sodium Bicarbonate Mouthwash on Saliva pH and Oral Microflora. *Formosa Journal of Applied Sciences*, 2(9), 2133-2140. <https://doi.org/10.55927/fjas.v2i9.6095>.
40. Ajith S, Sanjeev R, Devi S, Palathingal P, Varghese M, Musthafa N. Recent advances in management of halitosis. *International Journal of Applied Dental Sciences*. 2019;5(4):33-7.
41. Huang, N.K., Li, J., Qiao, X., Wu, Y., Liu, Y., Wu, C., & Li, L. (2022). Efficacy of probiotics in the management of halitosis: a systematic review and meta-analysis. *BMJ Open*, 12(12), e060753-e060753. <https://doi.org/10.1136/bmjopen-2022-060753>.
42. Karbalaee M, Keikha M, Kobylak NM, Zadeh ZK, Yousefi B, Eslami M. Alleviation of halitosis by use of probiotics and their protective mechanisms in the oral cavity. *New microbes and new infections*. 2021 Jul 1;42:100887.<https://doi.org/10.1016/j.nmni.2021.100887>.
43. He, L., Hong-Jiang, Y., Chen, Z., & Ouyang, X. (2020). The Effect of *Streptococcus salivarius* K12 on Halitosis: a Double-Blind, Randomized, Placebo-Controlled Trial. *Probiotics and Antimicrobial Proteins*, 12(4), 1321-1329. <https://doi.org/10.1007/s12602-020-09646-7>.
44. Iwamoto, T., Suzuki, N., Tanabe, K., Takeshita, T., &Hirofuji, T. (2010). Effects of probiotic *Lactobacillus salivarius* WB21 on halitosis and oral health: an open-label pilot trial. *Oral Surgery Oral Medicine Oral Pathology Oral Radiology and Endodontology*, 110(2), 201-208. <https://doi.org/10.1016/j.tripleo.2010.03.032>.