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TOPICAL REVIEW

Tongue coating: its characteristics and role in intra-oral halitosis and general health—a review

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Keywords: tongue coating (TC), halitosis, intra-oral halitosis (IOH), volatile sulfur compound (VSC), tongue microbiome

Abstract

Tongue coating (TC), a grayish-white deposit on the tongue, is the main cause of intra-oral halitosis (IOH), a socially unacceptable condition. This review covers the general features of TC, including its formation and the factors that influence it. Volatile sulfur compounds (VSCs) are the principal elements of IOH, and TC and periodontal diseases are the two main sources of VSCs. This review covers the relationship between VSCs, TC, and periodontal disease. We comprehensively discuss the methods employed to quantify TC, its microbial composition, its influence on general health and its importance in general medicine.

List of abbreviations

BANA	Benzoyl-DL-arginine-2 napthylamide
CFU	Colony Forming Units
CH_3SH	Methyl mercaptan
$(CH_3)_2S$	Dimethyl sulfide
DNA	Deoxyribonucleic acid
CORE	16S rDNA database of the core oral microbiome
EOH	Extra-oral halitosis
H_2S	Hydrogen sulfide
IOH	Intra-oral halitosis
PCR	Polymerase Chain Reaction
16S rDNA	16S ribosomal Deoxyribonucleic Acid
16S rRNA	16S ribosomal Ribonucleic Acid
TC	tongue coating
WTCI	Winkel Tongue Coating Index
mWTCI	modified Winkel Tongue Coating Index

1. Introduction

Halitosis is commonly referred to as bad breath. It has a long history, dating back to 1500 BC, when Hippocrates, the ancient Greeks, and the Romans all mentioned it in their writings. In the modern world, halitosis has enormous impact on individual social and psychological well-being. It has no gender-specificity [1] and has been classified into four types: genuine halitosis (extra- and intra-oral halitosis); temporary or transient halitosis; pseudo-halitosis; and halitophobia [2]. Extra-oral halitosis (EOH) has a source outside the oral cavity, and intra-oral halitosis (IOH) has a source inside the oral cavity. Pseudo-halitosis is the case where no malodor is present, but the patient stubbornly believes that he or she has halitosis. With halitophobia, the patient has been treated for genuine halitosis or counseled for pseudo-halitosis, but believes that his or her halitosis persists [2]. Among the different types of halitosis, nearly 90 percent are caused by IOH. The exact prevalence of IOH is not currently known, but according to previous studies, IOH affects 10%–30% of the total population in the United States [3] and China [4]. IOH is caused

by pathological conditions (periodontitis and gingivitis) and physiological traits, particularly tongue coating [TC]. Among other causes of IOH, TC is a major causative factor [5]. In general, TC is much more common than other tongue conditions, such as fissured tongue (associated with hyposalivation, candidiasis, diabetes mellitus, vitamin B deficiency, lichenoid reactions, and Sjögren syndrome) and depapillated tongue (indicative of nutritional deficiencies, xerostomia, local trauma, or candidiasis) [6]. The tongue is the mirror of the body, because it often provides information on systemic changes that can be used for diagnostic purposes [7]. For example, in the case of HIV, symptoms such as the presence of white patches that are corrugated, or hairy leukoplakia, which is a hairy appearance on the lateral tongue margin, help in the early diagnosis of HIV [8]. However, the tongue receives little attention in the literature, and health care professionals have rather limited knowledge of TC and IOH [9]. This review provides an overview of the current knowledge of TC and its role in IOH.

2. The formation of tongue coating

There is no substantial evidence to explain the precise cause of TC formation. The TC consists of dead epithelial cells, bacteria, blood metabolites, secretions from the postnasal area and the gingiva, and saliva [10]. The tongue papillae, particularly the filiform papillae, comprise the specific structure involved in TC formation. Light and transmission electron microscopic studies on the TC revealed the presence of bacteria and exfoliated (desquamated) keratinized epithelium that originated from filiform papillae. Moreover, this exfoliated epithelium had degenerated [11]. The entrapment of food particles, saliva, and bacteria in between these filiform papillae can result in the formation of a thick coating [7]. The tongue is covered with keratinized and non-keratinized epithelial cells, and the balance between retaining and removing these cells influences TC formation [7]. A microscopic study on the ultrastructure of the tongue showed that the rates of epithelial cell multiplication and membrane-coating granule production were associated with TC formation [12].

3. The characteristics of tongue coating

Before studying TCs, it is of paramount importance to understand that the light source and the position of the patient during the examination [13] might influence the appearance and color of the TC.

A TC is normally present in healthy people [14]. The normal TC is characterized by a thin, slightly moist, whitish substance, which is associated with the dorsal surface of the tongue. The normal TC may vary in color, thickness, moisture, and distribution, depending on the patient's health [15]. Studies have indicated that there are wide variations in TC thickness and extent, depending on oral parameters such as periodontal status and IOH. For instance, among subjects with good periodontal health, those with IOH were reported to have thicker TCs than those without IOH [16–18]. Subjects with periodontal disease had four times as much TC (estimated in terms of wet weight) compared to subjects with healthy periodontal tissues [10, 19]. With periodontal disease, the TC thickness increases, due to the migration of leukocytes from periodontal pockets into the saliva, and subsequently, these cells are deposited onto the tongue surface [10].

4. Factors that affect tongue coating

4.1. The importance of age

The age of the individual influences the thickness of the TC [14]. In the elderly, TCs tend to be thicker and more discolored than the TCs of younger people. These age-related TC features might be related to a physical inability to cope with oral hygiene, increased intake of soft food, and a reduction in the natural cleansing of the tongue by saliva. Age might be related to changes in the nature of saliva or reduced salivary flow [20]. Furthermore, filiform papillae, which assist in TC formation, were found to increase with age, and fungiform papillae decreased with age [12].

4.2. The effect of diet on tongue coating

The thickness and color of the TC are affected by dietary conditions. Depending on the type of foods ingested, the appearance of the TC ranges from a water-like, clear solution to a viscous, pigmented, and mucous-like paste. Greasy foods that are rich in fat contribute to TC formation [21]. The TC may also become discolored after consuming colored or pigmented substances, including: (1) foods such as chocolate and watermelon [21]; (2) drinks such as coffee [22] and red wine; (3) mouth rinses, such as chlorhexidine [23]; (4) materials related to lifestyle choices such as smoking [22], and; (5) drugs [24]. Coffee and smoking often lead to a false impression of the quantity of TC [22].

In daily life, tongue movements involved in chewing and swallowing, saliva production, and dietary elements (e.g., fibrous foods) are involved in the cleansing of the tongue, which results in a normal, thin layer of TC. A soft diet, which we mostly consume when ill, might result in reduced tongue movements and less saliva secretion. Consequently, the thickness of the TC might increase [7].

4.3. Oral hygiene

Oral hygiene is the strongest influential factor in the formation of TC [22]. Natural mechanisms for cleansing the tongue might not necessarily remove the TC,

when the coating is thick. In this scenario, mechanical tongue cleaning can remove debris, but often, tongue cleaning is not considered a routine oral hygienic procedure [21].

5. The importance of tongue coating in western medicine

In earlier times, the TC received considerable attention. For instance, in 1828, Dr Robert Froriep, a German physician-scientist and anatomist, described the importance of the quantity and color of the TC in diagnosing diseases. As scientific knowledge has grown, and improvements have been made in modern laboratory techniques and sophisticated instrumentation, the tongue and its coating have lost importance in the diagnosis of diseases [25]. In Western biomedicine, research on the TC has been scarce. In older individuals who are edentulous, aspiration pneumonia is a serious health problem. The presence of a TC has been considered a risk factor for aspiration pneumonia in people of 65 years or older. Hence, TC removal has been recommended in older individuals who are edentulous [26]. Moreover, thicker TCs were observed in patients with gastrointestinal and liver diseases, compared to healthy subjects [27]. Thus, more research on the TC is demanded in the field of biomedicine.

6. Tongue coating and volatile sulfur compounds in the oral cavity

IOH is mainly attributed to VSCs, particularly hydrogen sulfide (H_2S) and methyl mercaptan (CH_3SH), and to a lesser extent, dimethyl sulfide $(CH_3)_2S$. Together, H_2S and CH_3SH contribute up to 90 percent of VSC content in the oral cavity [28]; $(CH_3)_2S$ is mainly related to EOH, but in subjects with IOH, CH_3SH can be converted to $(CH_3)_2S$ in the oral cavity [29]. The periodontal pockets and the TC are the two main sources of VSCs. The relationship between VSCs, TC, and periodontal diseases has been studied by several research groups [10, 19, 28, 30, 31]. According to Tonzetich, the VSC concentration increases with the severity of periodontal disease [28]. Miyazaki *et al* (1995) found a significant correlation between VSCs and the TC in all age groups, but found an association between VSCs and periodontal status only in older age groups. The study concluded that IOH was caused by the TC in young people and by periodontal disease in older people [30]. In contrast to that study, Bosy *et al* (1994) showed that VSCs and periodontal status were not associated; they demonstrated that the tongue was the major site of VSC production [31]. Subsequently, another study reported that VSC levels, particularly the methyl mercaptan (CH_3SH) concentration and the $(CH_3SH)/H_2S$ ratio, were higher in patients with periodontal disease (pocket depth $\geqslant$ 4 mm) than in the control group (pocket depth $<$ 4 mm). Similar results were observed in an analysis of the bleeding index, which indicated that blood components in periodontal pockets may accelerate VSC production. Moreover, in those subjects (patients and controls), TC removal resulted in a total VSC reduction and a reduction in the $(CH_3SH)/H_2S$ ratio. Therefore, the authors suggested that both the TC and periodontal pockets played a role in VSC production [19]. Another study showed that the TC was the main source of VSCs [10]. To conclude, patients with periodontal disease produced higher concentrations of (CH_3SH) than H_2S, whereas subjects with healthy periodontal tissues produced higher concentrations of H_2S than (CH_3SH) [10, 19]. In addition, the presence and the quantity of the TC was strongly correlated with the VSC scores [4, 32].

In addition to causing an objectionable odor, VSCs can penetrate into the oral tissues, increase the permeability of oral mucosa [33], and affect collagen synthesis and degradation [34]. Furthermore, VSCs stimulate IL-1 cytokine production, which induces a reaction that promotes prostaglandin E2-mediated bone resorption. Thus, VSC-induced mucosal permeability may play a role in the transition from gingivitis to periodontitis, but this remains unclear [35].

7. Quantification of tongue coating

An evaluation of the quantity of TC plays a vital role in motivating patients to maintain proper tongue hygiene. Therefore, the standardization of TC quantification is an important step in developing a new paradigm for maintaining tongue hygiene. Current methods used to quantify TC include visual parameters, such as the coated area, TC thickness, and TC discoloration [36]. An alternative method for quantifying the TC is the wet-weight measurement of scrapings collected from the tongue dorsum [10]. The other approach to measure the tongue coat is to collect the coat samples using a sterile toothbrush and to count the number of micro-organisms present in the representative sample of a known area of the tongue, i.e., the total microscopic count of microbial cells and/or a quantitative 'total viable count' by use of serial dilution and plating on a non-selective aerobic and anaerobic nutrient medium [37]. Of these, the most accepted method is the visual index method, which is simple, rapid, and reliable [38]. Table 1 summarizes different types of indices and the criteria for evaluating the TC. The first visual index employed was a simple index based on the presence or absence of TC, on a scale from zero to three (0–3) [39]. Miyazaki *et al* (1995) proposed a visual examination of the TC area, a technique which has been employed in many other studies due to its simplicity [30]. Kojima (1985)

Table 1. The various types of tongue coating indices.

Reference	Source	Description
Gross *et al* (1975)	0	No coating
	1	Light coating
	2	Medium coating
	3	Heavy coating
Kojima index (1985)	0	No coating
	1	Thin coating of $< 1/3$ of the tongue
	2	Thin coating of $< 2/3$ of the tongue or thick coating on $< 1/3$ of the tongue
	3	Thin coating of $> 2/3$ of the tongue or thick coating on $< 2/3$ of the tongue
	4	Thick coating of $> 2/3$ of the tongue
Miyazaki *et al* (1995)	0	None
	1	$< 1/3$ tongue dorsum surface covered
	2	$< 2/3$ tongue dorsum surface covered
	3	$> 2/3$ tongue dorsum surface covered
Mantilla Gomez (2001)	Discoloration	
	0	Pink
	1	White
	2	Yellow/Light Brown
	3	Brown
	4	Black
	Thickness	
	0	No coating
	1	Light, thin coating
	2	Heavy, thick coating
Oho *et al* (2001)	Area	Area score $\times$ thickness score $=$ tongue coating (range 0–6).
	0	No tongue coating
	1	$< 1/3$ tongue dorsum surface covered
	2	1/3–2/3 tongue dorsum surface covered
	3	$> 2/3$ tongue dorsum surface covered
	Thickness	
	0	No tongue coating
	1	Thin tongue coating (papillae visible)
	2	Thick tongue coating (papillae invisible)
Winkel *et al* (2003)	(Six areas grid)	Tongue dorsum is divided into six areas (i.e., three posterior and three anterior)
	Coating	
	0	No coating
	1	Light coating
	2	Severe coating
	Discoloration	
	0	No discoloration
	1	Light discoloration
	2	Severe discoloration
		Score is calculated by adding all six scores (range 0–12)
Kim *et al* (2009)	Tongue coating area	Calculated from digital images obtained by the digital tongue imaging system (DTIS)

evaluated TC status based on both the thickness and the coated area [40]. The two above methods have limitations in the criteria of quantification. To overcome these limitations, the tongue was divided into nine sections and the discoloration and thickness of the coating on those sections were scored on a scale of zero to four (0–4) [14]. In another approach, called the Winkel Tongue Coating Index (WTCI, 2003), the tongue was divided into six sections; in each section, the discoloration and the absence or presence of TC were scored on a scale of zero to two (0–2). The scores from the individual sections were summed, for a total maximum value of 12 [41]. Since the scores from the WTCI were based on clear differentiating criteria that were easy to interpret, this was considered a useful method [38]. However, Lundgren *et al* (2007) defined the WTCI score differently. They defined a score of one as the keratinization of tongue papillae, rather than as the presence of TC. A modified WTCI (mWTCI) was developed, with only two scores (0 and 2), where the score of one was eliminated [42]. Despite improvements, visual methods are prone to inter- and intra-examiner biases; thus, a more objective method is needed for consistent TC measurements. In 2009, Kim *et al* established a digital TC evaluation method [38]. The success of that method was limited mainly by its low feasibility in clinical settings and the lack of patient cooperation in mouth opening. However,

comparison of the tongue coating index and tongue biofilm density (tongue scrape from a known measured area (CFU cm^{-2})) has shown no correlation between them [43].

8. The tongue microbiome

The human oral microbiome comprises microbial communities from the mucosal surfaces of the tongue, cheeks, palate, and tonsils, and the microbial biofilms on tooth surfaces [44]. The oral cavity of a newborn baby is free of micro-organisms, but the oral cavity starts acquiring micro-organisms directly after birth [45]. The study of oral microbes was initiated with the standardization of culturing techniques on solid media. Later, the introduction of non-culture-based nucleic acid methods of analysis, such as DNA hybridization, polymerase chain reaction, and Sanger 16S rRNA sequencing, combined with state-of-the-art technologies, such as high-throughput pyro-sequencing-based analyses and metagenomics, led to the development of the Human Oral Microbiome Database, CORE. This 16S rDNA database represents all known bacteria found in the oral cavity [44].

8.1. Tongue surface characteristics and microbial growth

The tongue's surface area is approximately 25 cm^2 [46]. It has several distinct surface characteristics, including fissures, crypts, and papillae. This large surface area and papillary structure can accumulate large amounts of biofilm [21], particularly in the mid-dorsal tongue region [14]. Papillary roughness, crypts and saliva can foster bacterial growth [47]. The frequency of tongue fissures increases with age [48], and a deeply fissured tongue holds nearly twice the quantity of bacteria as a non-fissured tongue. Moreover, a deeply fissured tongue was found to carry high numbers of viable bacteria (measured in colony-forming units, CFUs) compared to a smooth tongue surface [49]. In contrast to this study, other studies found no difference in microbial load between fissured and smooth tongues [14, 32].

The dorsal tongue mucosa is capable of harboring more bacteria than other areas of oral mucosa. For instance, a single desquamated epithelial cell from the tongue dorsum can hold more than 100 bacteria; in contrast, a single detached epithelial cell from other oral mucosal surfaces can hold only 25 bacteria [19]. Thus, the tongue dorsum posterior to the circumvallate papillae carries the highest load of bacteria of all tongue regions [50]. Furthermore, a coated tongue was found to carry a higher load of malodor-associated bacteria than an uncoated tongue [49]. In contrast, another study found that the total bacterial loads were similar in coated and uncoated tongues. Furthermore, VSCs were correlated with TC factors, but the TC was not correlated with the microbial load. Based on those findings, Quirynen *et al* (1998) hypothesized that the TC per se, and not the bacterial load, might be involved in IOH [32]. On the other hand, the findings of Hartley *et al* (1996) showed that the tongue biofilm density plays an important role in the cause of IOH [51].

8.2. The tongue and periodontal bacteria in intra-oral halitosis

The tongue mucosa was shown to be a reservoir for periodontopathic bacteria in both periodontal healthy and periodontal disease states [52]. *In vitro* studies have established that malodorous VSCs were produced by periodontal bacterial species [53]. The periodontal species were isolated from the tongues of patients with periodontitis and identified with targeted molecular approaches. These species were associated with VSCs of IOH, and thus they were found to contribute to IOH [54]. The benzoyl-DL-arginine-2 napthylamide (BANA) test was introduced to detect three periodontopathic species, namely *Treponema denticola, Porphymonas gingivalis,* and *Bacteroides forsythia (Tannerella forsythia*), on the tongue. These bacteria possess an enzyme that hydrolyses the synthetic BANA substrate, which causes it to change color. BANA-positive species were found on the tongues of patients with periodontal diseases and also in the TCs of patients with IOH who were periodontally healthy [55]. In contrast, Kazor *et al* (2003) reported the absence of BANA-positive species in patients with IOH who were periodontally healthy [56], which implied that the bacterial composition associated with IOH differed in periodontal health and periodontal disease states.

8.3. The tongue microbiome in intra-oral halitosis

The tongue microbiome is involved in the breakdown of proteins (proteolytic activity) and in the production of volatile sulfur gases that contribute to IOH [51]. Mainly, the Gram-negative tongue bacteria degrade sulfur-containing substrates, such as cysteine and methionine, which are found in the oral cavity. These substrates are degraded to hydrogen sulfide (H_2S) and methyl mercaptan (CH_3SH), which are VSCs [28]. In addition, sulfur substrates can be putrefied to form malodorous VSCs by other components of the TC [10, 19] and by components of the postnasal drip, a yellow mucus discharged from the nasal sinus which drips onto the posterior tongue dorsum [57].

Various microbiological studies have focused on TC samples from periodontal healthy patients with and without IOH. Hartley *et al* established a relationship between the tongue microbiome and IOH; they observed that, compared to the non-IOH group, the IOH group had a significantly larger total bacterial load and more key bacterial groups, specifically Gram-negative anaerobes, such as *Porphyromonas, Prevotella*, and *Fusiforms* [51, 58]. Additionally, cultures of tongue samples from patients with IOH revealed other species associated with IOH [59]. Donaldson *et al* (2005) reported that samples from patients with IOH

displayed greater species diversity than control samples [60]. However, conventional culturing methods employed in previous studies were associated with two major limitations: the difficulties with *in vitro* growth techniques and the paucity of microbial identification. Indeed, 40%–60% of oral bacteria strains are uncultivable [61]. Kazor *et al* (2003) and Riggio *et al* (2008) studied tongue microbiota with culture-independent molecular methods, such as molecular cloning and sequence analyses with 16S rRNA gene sequencing. The Kazor group showed that the tongue possessed unique microbiota; they identified 12–29 phylotypes associated with the tongue dorsum of patients with IOH and 12–21 phylotypes associated with the tongue dorsum of healthy subjects [56]. The Riggio group revealed that the tongue microflora was complex, but similar between patient and control groups; they observed that several species predominated in both groups [62].

To conclude, the above studies showed greater species diversity in patients with IOH than in controls, but those studies were limited to clone numbers. Later, Haraszthy *et al* (2007) isolated different bacterial species in patients with IOH and reported that the Gram-positive *Solobacterium moorei*, a key species associated with IOH, was found only in subjects with IOH [16, 63]. In further studies, *S. moorei* was found to correlate strongly with IOH parameters, such as H_2S, CH_3SH, $(CH_3)_2S$, and total VSC; but *S. moorei* was reportedly found both in the patient and control groups, with a slight predominance in the patient group [64]. When tested *in vitro*, *S. moorei* was found to be a moderate producer of H_2S compared to *Fusobacterium nucleatum* [65]. When *S. moorei* was incubated with saliva, serum or mucin, the production of VSCs was less; and when supplemented with an exogenous source of proteins (such as pancreatic trypsin), significant production of VSCs was found. In addition, Beta galactosidase of *S. moorei* played a role in the production of VSCs from mucin [66].

H_2S-producing bacteria were characterized with samples from the tongues of subjects with malodor and subjects with no/low odor. The study showed a significant increase in the total bacteria and H_2S-producing bacteria, such as the *Veillonella*, *Prevotella*, and *Actinomyces* species, in the malodor group compared to those in the no/low odor group. The results suggested that the groups had qualitatively similar bacterial compositions in their TCs and that an increase in bacterial density might be responsible for IOH [18]. Also, more recently, a 16S amplicon sequencing study on the tongue microbiome of IOH and control group revealed similar qualitative microbial compositions in the IOH and healthy groups [67]. Further, a pyrosequencing study on the bacterial 16S rRNA genes of tongue microbiomes was conducted to identify species related to different levels of H_2S in IOH. They showed that *leptotrichia* spp and *Prevotella* spps were strongly associated with high H_2S levels, and that *Haemophilus* spp and *Gemella* spp were negatively associated with H_2S concentrations [68].

The complexity of the oral microbiome clearly implies that the oral cavity maintains micro-organisms by providing a rich supply of nutrients from the diet, saliva, and gingival crevicular fluid [69]. Salivary secretions provide only 1 mg% of free glucose and 15 mg% of carbohydrates in the form of glycoproteins. These amounts represent 0.5 mg of carbohydrate per 3 ml of saliva [28]. Therefore, it is thought that the existence of micro-organisms depends on their metabolic ability to degrade nutrients that are present in small quantities [70]. Moreover, putrefactive activity for VSC production requires a low oxygen and low carbohydrates environment, with alterations in physiological pH [28]. The interplay among these factors requires more extensive investigation.

9. Tongue coating and taste

The TC covers the taste-sensing papillae on the dorsal tongue surface. The TC biofilm may block substances from reaching these cells, which could result in reduced taste sensitivity. A recent study investigated the effect of removing the TC on taste perceptions at the threshold level. The results clearly indicated that removing the TC brought about an improvement in salt taste perception [71]. Moreover, a study on the mechanical removal of the tongue coating showed a significant increase in salt taste intensity after tongue cleaning (unpublished data). Thus, tongue cleaning can influence taste, and therefore, tongue cleaning should be included in our routine oral hygiene procedures.

10. Future directions of research

10.1. Formation of the tongue coating

Although the formation of the TC seems to be a natural process, why, how, and when the coating forms is unknown. Subjects with IOH have greater TC quantities than subjects without IOH. Therefore, factors that influence TC formation should be better explored. These endeavors require long-term longitudinal studies, and also require standardized methods for accurately quantifying the TC. Though the visual tongue coating scoring methods are easy and convenient, this method has been considered as a weak approach since the scoring techniques have not been validated against any of the conventional methods used in microbiology. A more specific direction would better determine how the coating index relates to other methods of quantitative analysis of biofilm coat, to determine the proportionality of the scale used in scoring system.

10.2. Improved understanding of bacteriological compositions in tongue coating

The TC has several components, and the bacterial content has been widely studied. However, a knowledge gap remains regarding the composition of the tongue microbiome in relation to health and IOH conditions which demands an in-depth analysis of microbiological compositions in IOH and healthy states. Although information on the composition of the tongue microbiome might provide some clues regarding the key organisms involved, this information is insufficient to unravel the relationship between the microbiome and IOH. In this context, once the species involved in IOH are accurately identified, the roles of specific organisms, and how they change from health to IOH, can be determined only after disclosing their functional activities *in situ*. Furthermore, the microbiome should be studied with advanced technologies, including combinations of transcriptomic analyses (gene expression profiles of microbial communities), metaproteomic analyses (identification and quantifications of proteins expressed by microbial communities), and metabolomic analyses (identification of the final products of bacterial metabolism in the community). These approaches have initiated a new era in the study of the oral microbiome and its functions under varying environmental conditions [72]. Implementing these technologies in IOH studies will facilitate the diagnosis and treatment of IOH.

10.3. Tongue coating, intra-oral halitosis, and food consumption

Sulfur substrates are essential for VSC production. These substrates are naturally produced in the oral cavity, from saliva, gingival fluid, and crevicular fluid. These substrates are also readily available in the foods we consume. For instance, milk and dairy products are rich sources of casein. Casein is rich in cysteine, which is a precursor of H_2S formation in the oral cavity and essential for VSC production. These factors might contribute to IOH [73]. Evaluation of the food products consumed by patients with IOH, and a detailed study of how these food products contribute to VSC production, might provide clues to the cause of IOH.

10.4. Importance of volatile sulfur compounds in the development of periodontitis

According to Wåler (1997), the pH of the tongue and the concentration of sulfur-containing substrates influence the amount of VSCs produced. For instance, in individuals who are periodontally healthy, with no history of halitosis, the amount of VSCs increases with an increase in the cysteine (sulfur substrate) concentration. That study also showed that age, sex, and periodontal disease did not influence VSC production [73]. The enzymatic reactions involved in VSC production in the oral cavity are known only superficially. Hence, detailed studies are needed to elucidate the enzymatic or metabolic pathways involved. Moreover, the role of VSCs in the transition of gingivitis to periodontitis should be studied.

10.5. Impact of tongue coating on general health

In Chinese traditional medicine, the TC plays an important role in the diagnosis of diseases. In Western medicine, the tongue is ignored, and scientific studies relating the tongue to health issues are currently limited. Future epidemiological studies on tongue conditions might provide a picture of the tongue in systemic illnesses, which might facilitate disease diagnosis. According to recent studies, tongue cleaning influences taste, particularly salt taste. Salt is used more often in our daily food than other taste substances. Salt intake in humans normally ranges from 5g to 9 g salt/day, which is nearly twice the amount recommended by the World Health Organization (WHO) [74]. The WHO guidelines on sodium intake advise 2 g sodium/day, which is equivalent to 5 g salt/day [74]. Therefore, tongue cleaning and salt research require extensive study, and the results might support the reducing of excess salt intake.

11. Conclusion

Halitosis causes psychological problems for the patient, which is a serious health concern. Health care professionals must acquire sufficient knowledge about the different aspects of halitosis if they are to diagnose and treat patients adequately. Moreover, knowledge about the TC is of utmost importance in distinguishing IOH from other types of halitosis. Additionally, the diagnostic importance of the tongue might not be negligible in relation to diseases. In this respect, it is of paramount importance to examine both hard and soft tissues in the oral cavity. General physicians and dental professionals require motivation and additional training skills in the proper procedures for examining the oral cavity, particularly the tongue.

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Author contributions

KS designed the review and drafted the manuscript. PJW and EW reviewed the manuscript. All authors read and approved the manuscript.

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