



15 years ESJ
Special edition

Oral Microbiome and Its Role in Oral Lichen Planus Development: A Literature Review

Nazanin Nouraddini

Giorgi Dugashvili, DMD, PhD, Professor

Grigol Robakidze University, School of Medicine, Tbilisi, Georgia

[Doi:10.19044/esj.2025.v21n39p30](https://doi.org/10.19044/esj.2025.v21n39p30)

Submitted: 19 November 2024

Accepted: 20 February 2025

Published: 15 March 2025

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OPEN ACCESS

Cite As:

Nouraddini N. & Dugashvili G. (2025). *Oral Microbiome and Its Role in Oral Lichen Planus Development: A Literature Review*. European Scientific Journal, ESJ, 21 (39), 30.

<https://doi.org/10.19044/esj.2025.v21n39p30>

Abstract

This article aims to explore the oral microbiome, the implications of its dysbiosis and its role in the development of oral lichen planus (OLP) and systemic diseases. This underscores the necessity for additional research to elucidate the connections between oral microorganisms and the pathology of OLP. Furthermore, a deeper understanding of these intricate interactions may pave the way for novel therapeutic strategies and improved disease management. An electronic search was conducted using PubMed and Scopus, complemented by a manual review of the reference lists of the identified articles for full-text evaluation. Initially, titles and abstracts were assessed, followed by a comprehensive review of pertinent articles for potential inclusion. The human body hosts a diverse array of microorganisms that can influence both health and illness. Recent progress in genomic technologies, including next-generation sequencing, has significantly improved our comprehension of these microbial communities and their impact on human health. Importantly, cancer, currently the second leading cause of death worldwide, has been associated with specific oral pathogens. Certain bacterial species, such as *Helicobacter pylori* and various oral periopathogens, have been linked to the development of cancers, especially in the gastrointestinal system. Elevated levels of bacterial populations, including *C. sputigena*, *E. corrodens*, *L. crispatus*, *M. curtisii*, *N. mucosa*, *P. bivia*, *P. intermedia*, *S.*

agalactiae and *S. haemolyticus*, have been identified in the lesions associated with oral lichen planus. Furthermore, it is noteworthy that individuals with oral lichen planus demonstrated increased infection rates of *A. actinomycetemcomitans*, *P. gingivalis*, *P. intermedia*, *T. forsythia* and *T. denticola* when compared to those without oral lichen planus. Oral lichen planus, a chronic inflammatory disorder affecting the oral mucosa, is marked by T cell-mediated immune responses and is frequently correlated with microbial dysbiosis. OLP is classified as a precancerous condition, underscoring the importance of monitoring and investigating its microbial influences.

Keywords: Oral Lichen Planus, Oral Microbiome, Dysbiosis, Bacterial Communities, Human Health

Introduction

This article aims to investigate the intricate relationships between the oral microbiome and systemic diseases, with a particular emphasis on oral lichen planus (OLP) and its possible associations with cancer. It highlights the significance of specific microorganisms, including *Helicobacter pylori* and various oral pathogens, in the development of OLP and other related conditions. The objective of the article is to enhance the understanding of how microbial dynamics, their balance, or disruptions in microbial flora can impact human health and contribute to disease. The human body is home to a wide variety of microbiota, which play crucial roles as communicators and carriers of genetic information (Malla et al., 2019). In recent years, considerable progress has been made in elucidating the microbiome's impact on health and disease, particularly due to advancements in genomic technologies such as next-generation sequencing (NGS), which have improved our understanding of microbial roles in various health conditions (Malla et al., 2019). One such condition is lichen planus, including oral lichen planus, a chronic inflammatory disorder that affects the tissues of the oral mucosa (Baek & Choi, 2017; Farzaneh AghaHosseini et al., 2024). OLP is characterized by multiple clinical subtypes and predominantly affects women, often resulting in symptoms such as pain and discomfort (Di Stasio, 2014; Olson et al., 2016; González-Moles et al., 2020) The connection between OLP and microbial ecosystems, including potential associations with pathogens like *Helicobacter pylori* and *Candida albicans*, continues to be a focus of active research, highlighting the complex interactions between our microbiota and overall health (Kazanowska-Dygdała et al., 2016; He et al., 2020).

Data collection process

The authors conducted a search strategy on electronic databases via PubMed and Scopus. An analysis of titles and abstracts was conducted to evaluate the articles obtained from the literature search. For the inclusion criteria to be met, the studies ought to have contained the following information: 1) the role of different types of oral microbiota; 2) the importance of altered oral microbiota; 3) the role of *H. pylori* in the progression of the OLP.

In instances where the abstracts were ambiguous, a comprehensive analysis of the full texts was conducted to ensure that no potentially relevant articles were overlooked. Articles that failed to satisfy the inclusion criteria were thereafter excluded.

Each eligible article's reference lists were manually reviewed to identify articles that were more relevant to the search.

Discussion

In the last ten years, numerous efforts have been undertaken to identify and comprehend the role of the microbiota in relation to human health and disease. The emergence of advanced genomic technologies, such as next-generation sequencing (NGS), which contrasts with traditional culture-based identification methods, has enhanced our understanding of the human microbiome's impact on health through the application of bioinformatics (Malla et al., 2019).

Oral lichen planus is characterized as a chronic inflammatory condition that affects mucocutaneous tissues, including the skin, nails, eyes, urogenital tract and oral mucosa (Baek & Choi, 2017; Wang et al., 2021).

OLP has been observed to occur significantly more frequently in women than in men (Olson et al., 2016; Ioannides et al., 2020) with a prevalence rate ranging from 0.5% to 2% among individuals aged 30 to 60 (Li et al., 2020; González-Moles et al., 2020b; Marwa Saadaoui et al., 2025) and can lead to a variety of symptoms and discomforts, including altered taste sensations, as well as chronic burning and tingling sensations.

While the advancement of OLP has been linked to T cell-mediated immune responses affecting the oral mucosa (WANG et al., 2021; El-Howati et al., 2022), various microorganisms, such as *Helicobacter pylori*, may also contribute to the onset of OLP (Attia et al., 2010; Kazanowska-Dygdala et al., 2016; Li et al., 2021b).

Di Stasio (2014) posits that Th2-mediated inflammation plays a role in the advancement of oral lichen planus. There are six recognized clinical subtypes of OLP: reticular, atrophic, plaque, erosive, papular, and bullous (González-Moles et al., 2019; Shavit et al., 2020). The reticular subtype, characterized by white lines and plaques, and the erosive subtype, which

presents with ulceration, are the most frequently observed. Erosive and atrophic lesions are typically associated with pain, whereas reticular lesions are generally asymptomatic (Cassol-Spanemberg et al., 2018). The buccal mucosa is the most commonly affected area in all forms of OLP, often exhibiting symmetrical involvement (Boñar-Alvarez et al., 2019).

The roles of *Mycoplasma salivarium* (Mizuki et al., 2017), periodontopathogenic bacteria (Seckin Ertugrul et al., 2013), *Candida albicans* (Zeng et al., 2008; He et al., 2020), human papillomavirus (Ma et al., 2016), Epstein-Barr virus (Fu et al., 2015) and Hepatitis C virus (Lodi et al., 2010; Petti et al., 2011; Alaizari et al., 2016) in the progression of OLP remain disputed or controversial.

The significance of the human microbiome in both physiological and pathological processes

The concept of "microbiome" was introduced by Joshua Lederberg, a Nobel Prize laureate in 2001, who is well-known for his contributions to the Human Genome Project. The term originally refers to an ecosystem comprising symbiotic, commensal, and pathogenic microorganisms that reside in various regions of the human body (Kilian et al., 2016; Haque & Haque, 2017).

The human body encompasses a wide variety of microorganisms, including bacteria, fungi and viruses, which are essential for maintaining health and contributing to disease processes (Qin et al., 2010; Kilian et al., 2016). The microorganisms that inhabit the human body, including those found on the skin, in the gastrointestinal tract, respiratory tract and urogenital tract, are collectively referred to as the human microbiota. The human microbiota is composed of archaea, bacteria, viruses, protists and fungi, with bacteria being the most dominant group (Qin et al., 2010; Yatsunenkov et al., 2012; Shkoporov & Hill, 2019). Each type of microorganism within the human microbiota can function as either a pathogen or a commensal organism. The interactions that occur among the microbiota, as well as between the microbiota and their host, can significantly influence the host's health. For example, *Porphyromonas gingivalis* can induce periodontal bone loss by disrupting the balance between commensal microbiota and the host's immune responses, rather than directly attacking the bone (Hajishengallis et al., 2011). The human microbiota exerts a substantial influence on health and disease by modulating various physiological processes in areas such as the skin, stomach and oral cavity. It is estimated that over 700 different bacterial species (Deo & Deshmukh, 2019; Marwa Saadaoui et al., 2025) and around 100 species of fungi inhabit the oral cavity (Peters et al., 2017; Escapa et al., 2018). Changes in the oral cavity microbiome can disrupt the bidirectional relationship between oral inflammatory diseases, such as periodontitis and systemic

conditions like systemic lupus erythematosus and autoimmune disorders, including rheumatoid arthritis (Graves et al., 2018).

There has been a limited amount of research conducted on the roles of the oral microbiome in oral lichen planus (Treede et al., 2019).

Microbial ecosystems in the oral cavity

The oral cavity, similar to other regions of the human body, serves as a habitat for a diverse array of microorganisms. Within this cavity, various microenvironments are present, including the hard surfaces of teeth and the epithelial layers of mucosal membranes. The oral cavity comprises multiple ecosystems, such as the tongue, gingival sulcus, tonsils, hard palate and soft palate, which create a conducive environment for microbial proliferation (Dewhirst et al., 2010). Additionally, specific areas like the supra-gingiva, sub-gingiva, interdental spaces and tongue exhibit distinct combinations of microbiota (Camelo-Castillo et al., 2015; Carrouel et al., 2016; Espinoza et al., 2018; Asakawa et al., 2018; Inquimbert et al., 2019). These regions are primarily exposed to saliva and gingival crevicular fluid, which help to keep the bacteria hydrated and provide a medium for nutrient delivery to these microorganisms (Faran & Tanwir, 2012). The consistent temperature and pH levels further enhance the ideal conditions for microbial growth. The human oral cavity typically maintains a stable temperature ranging from 35 to 37 degrees Celsius, which is essential for the survival and proliferation of various microorganisms (Deo & Deshmukh, 2019). According to Lim et al. (2017), saliva maintains a stable pH of 6.5 to 7, which is advantageous for the majority of bacterial species. Saliva is regarded as the primary factor in sustaining the neutral pH of the oral cavity; however, research indicates that different regions within the oral cavity can exhibit varying pH levels (Matzeu et al., 2021).

Comparing healthy oral cavity micro flora with dysbiotic micro flora in OLP cases

The human oral microbiome in a healthy state is predominantly composed of members from the *phyla Actinobacteria, Proteobacteria, Firmicutes, Bacteroidetes, and Fusobacteria*, with Spirochaetes being present in lesser quantities (Dewhirst et al., 2010). Analyses of partial 16S ribosomal RNA (rRNA) sequences from various global regions indicate that the genus *Streptococcus* is the most prevalent in human microflora, representing 22.7% of the 101 identified bacterial genera. Most studies utilizing 16S ribosomal RNA analysis have primarily classified oral bacteria at the genus level, limiting species differentiation (Kilian et al., 2016). Elevated bacterial populations of *C. sputigena, E. corrodens, L. crispatus, M. curtisii, N. mucosa, P. bivia, P. intermedia, S. agalactiae* and *S. haemolyticus* have been observed at the sites of oral lichen planus lesions (Seckin Ertugrul et al., 2013). Choi et

al. (2016) noted that cases of oral lichen planus exhibited higher levels of infection with *A. actinomycetemcomitans*, *P. gingivalis*, *P. intermedia*, *T. forsythia* and *T. denticola* compared to non-OLP cases. Furthermore, Souza et al. (2018) found that patients demonstrated reduced expression of proteins associated with the lubrication and viscosity of saliva. This finding may correlate with the frequent occurrence of xerostomia in individuals with oral lichen planus (Larsen et al., 2017).

Possible role of *Helicobacter pylori* in the development of OLP

The human oral cavity serves as a temporary reservoir for *Helicobacter pylori* outside the gastrointestinal tract. Infection with *H. pylori* has been linked to various oral health issues, including periodontitis and recurrent oral ulcers (Dewhirst et al., 2010c; Matamala-Valdés et al., 2018b; Cristina et al., 2024). Certain pathogens, such as *Helicobacter pylori* and *Candida albicans*, have been associated with oral lichen planus, although their specific contributions remain a subject of debate (Kazanowska-Dygdala et al., 2016; He et al., 2020; Li et al., 2021). OLP has also been associated with an increased risk of malignant transformation (Siegel et al., 2018). Oral dysbiosis is recognized as one of the potential causes of OLP. While *H. pylori* infection is connected to several oral diseases, the relationship between *H. pylori* and OLP is somewhat ambiguous. Alterations in the oral microbiome, or dysbiosis, may play a role in the onset and worsening of OLP and other oral conditions (Liu et al., 2019; Treede et al., 2019). Furthermore, dysbiosis within the oral microbiome is thought to be involved in the pathogenesis of Alzheimer's disease as well (Liu et al., 2019).

H. pylori is classified as a primary carcinogen by the World Health Organization and is associated with the onset of gastric ulcers and gastric cancer (Camilo et al., 2017; Choi et al., 2017). Various molecular techniques have successfully detected *H. pylori* in dental plaques and saliva (Ansari et al., 2018; Matamala-Valdés et al., 2018). The connection between *H. pylori* infection and oral lichen planus remains incompletely understood. Notably, *H. pylori* has been identified in the periodontal pockets of individuals suffering from OLP. Additionally, the presence of *H. pylori* in the oral cavity has been linked to leucoplakia and lesions associated with OLP (Jonas et al., 2001). Research by Li et al. (2021) indicates a significant association between *H. pylori* and alterations in the microbial flora in patients with OLP. Inflammatory cytokines produced in response to *H. pylori* infection in the stomach may enter the bloodstream, reach the oral cavity, and affect the local immune environment, potentially intensifying the inflammatory response (Chua et al., 2019). A study by Li et al. (2015) found increased levels of IL-6, IL-8, and IL-17, all of which are known to play a role in the development of erosive OLP (Basha et al., 2021; Husein Husein-ElAhmed & Steinhoff, 2022)

Implications

The investigation into the role of the human microbiome in conditions such as Oral Lichen Planus may yield valuable insights into the mechanisms underlying chronic inflammatory diseases. Understanding the influence of microbial communities on immune responses could facilitate the development of more targeted therapeutic approaches (Di Stasio, 2014; Malla et al., 2019). The connection between oral health and systemic diseases emphasizes the necessity of prioritizing oral hygiene and addressing dysbiosis as key public health concerns. Initiatives aimed at promoting oral health may significantly decrease the prevalence of OLP and related systemic conditions (Graves et al., 2018). These findings highlight the urgent need for additional research into the specific contributions of various microorganisms in OLP and other oral health issues. Future investigations should aim to elucidate the relationships among microbial composition, immune responses, and disease progression, particularly in relation to contentious associations with pathogens such as *Helicobacter pylori* (Kazanowska-Dygdala et al., 2016; Matamala-Valdés et al., 2018).

In the future, there is the potential for an accurate diagnosis that could help prevent misdiagnoses, especially when healthcare professionals acknowledge the important role of *H. pylori* in the onset of oral lichen planus.

The significant function of non-pathogenic oral microbiota, commonly referred to as normal oral flora, and their changes in the development of oral lichen planus cannot be overlooked. A particularly crucial and contemporary consideration is the potential detection of *Helicobacter pylori* within OLP lesions in the oral cavity, which may be addressed or managed prior to the progression to oral carcinoma or the establishment of a chronic condition.

It is essential for healthcare professionals to be informed about the implications of the microbiome for both oral and systemic health, which will enhance their ability to evaluate and manage conditions like OLP. This includes acquiring skills to interpret microbiome data and understanding its potential influence on treatment strategies (Loré et al., 2018; Frederik K L Spijkervet et al., 2019).

Conclusion

The human oral microbiome is integral to both health and disease, particularly in conditions such as oral lichen planus and various forms of cancer. OLP is recognized as a precancerous condition, highlighting the necessity of monitoring and exploring its microbial impacts (Siegel et al., 2018). Recent advancements in genomics and bioinformatics have significantly improved comprehension of microbial interactions and their effects on human physiology. Certain bacterial species, including *Helicobacter pylori*, *Fusobacterium nucleatum*, and *Porphyromonas*

gingivalis, have been associated with cancer progression and inflammatory diseases, notably OLP. The pathogenesis of OLP is characterized by intricate immune responses and microbial dysbiosis, which may be affected by factors such as diet, stress, and genetic predispositions. Although substantial evidence links oral dysbiosis to OLP, the exact mechanisms involved remain elusive, highlighting the need for further research to investigate the connections between the microbiome, inflammation, and the potential for malignant transformation in patients with OLP. A deeper understanding of these interactions could facilitate the development of improved diagnostic and therapeutic approaches for managing OLP and related disorders (Jung and Jang, 2022).

Conflict of Interest: The authors reported no conflict of interest.

Data Availability: All data are included in the content of the paper.

Funding Statement: The authors did not obtain any funding for this research.

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