

Review

Orthodontic treatment and oral flora

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Abstract: The general aim of orthodontic treatment is to provide ideal occlusion, facial aesthetics and stability in individuals, as well as to provide healthy periodontal structures. A good orthodontic treatment can be possible with healthy gingiva. Plaque accumulation may occur in the tooth areas around the equipment used in orthodontic appliances. The microbiological composition of dental plaque is related to dental and oral health. During the orthodontic treatment process, microbiological changes may occur in the flora. Therefore, before starting orthodontic treatment, the oral hygiene of the patient should be checked. It should be considered that the lack of oral hygiene may cause complications. In this review, information on the relationship between orthodontic treatment and oral flora is summarized.

Keywords: orthodontic treatment; oral flora

1. Introduction

During the orthodontic treatment of various malocclusions with appliances, the inflammatory reaction of the gingival tissue is frequently seen. The emergence of new attachment sites around bands and brackets is considered to be the main factor for increased dental plaque deposition and inflammatory response (Alexander, 1991; Ristic *et al.*, 2008). Based on this fact, researchers initially focused heavily on the effect of fixed orthodontic appliances on oral hygiene and gingival condition (Newbrun, 1992; Leverett *et al.*, 1993). Over time, the development of microbiology has led to an increase in studies to investigate specific microbiological changes of dental plaque in patients treated with fixed appliances (Huser *et al.*, 1990; Sukontapatipark *et al.*, 2001; Ristic *et al.*, 2008; Turkkahraman *et al.*, 2005). *Streptococcus mutans* or *Lactobacillus* spp. such as cariogenic microflora and tooth decalcification have been the main areas of interest for researchers (Forsberg *et al.*, 1991; Ristic *et al.*, 2008; Rosenbloom and Tianoff, 1991). Later, a very complex subgingival flora consisting of periodontopathic anaerobes was examined (Forsberg *et al.*, 1991). Both fixed and removable orthodontic appliances can cause plaque accumulation by preventing proper oral hygiene. Many studies (Paolantonio *et al.*, 1999; Ristic *et al.*, 2008; Vizitiu and Lonescu 2010) report changes in dental flora after starting orthodontic treatment. There are many researchers (Ristic *et al.*, 2008; Vizitiu and Lonescu, 2010) stating that the presence of orthodontic appliances may cause an increase in oral bacteria concentration. It causes plaque accumulation around fixed orthodontic appliances, bands and brackets. Because the microbiological composition of dental plaque is closely related to periodontal tissue health, fixed orthodontic appliances are likely to have effects on subgingival microflora and periodontal status. Inflammatory reaction of the gingival tissue can usually be seen in patients using fixed orthodontic appliances (Boyd and Baumrind, 1992; Davies *et al.*, 1991). Insufficient oral hygiene in these patients is thought to be the main cause of plaque

accumulation, increased number of bacterial colonies, and sequential inflammatory response. The main microorganisms that can cause periodontal damage are *P. intermedia*, *A. actinomycetemcomitans*, *P. gingivalis* (Haffajee and Socransky, 1994; Moore and Moore, 1994). Often, periodontitis is caused by the periodontopathogenic anaerobe *A. actinomycetemcomitans* (Ristic *et al.*, 2008; Sukontapatipark *et al.*, 2001). It was reported that *A. actinomycetemcomitans* increased significantly in dental plaque samples after the application of fixed appliances, persisted during the treatment, and decreased after the removal of the fixed appliance (Paolantonio *et al.*, 1999). After the application of the fixed appliance, the number of bacterial colonies in dental plaque and saliva may increase as the fixed appliance creates new retaining sites. Due to the risk of damage to the periodontal tissue of appliance applications, it may be necessary to inform patients for good oral hygiene and to maintain constant re-motivation and continuous controls throughout orthodontic treatment.

2. Oral Microflora

Bacteria are the most dominant group of organisms in the oral cavity. There are about 700 common types of oral microorganisms. Many different microorganisms can be found in the oral cavity. The reason for this is the teeth and gums, which are anatomical structures found nowhere else in the body. Under normal conditions, this wide array of organisms, including bacteria, archaea, fungi, mycoplasma, protozoa, and viral flora, often lives in harmony. However, caries and periodontal diseases occur when there is an ecological imbalance in the oral cavity for internal or external reasons. All oral microorganisms, their genetic information and the oral environment with which they interact are called the oral microbiome, and all living microbes that make up the oral microbiome are called the oral microbiota. The oral microbiome can be divided into three main subdivisions, bacterial, fungal, and viral, respectively. Even healthy individuals differ significantly in the composition of the established oral microbiota. Although much of this diversity cannot be explained, diet, environment and host genetics play an active role in shaping the flora. The oral microbiota exists either suspended in saliva as planktonic phase organisms or adhered to oral surfaces in the biofilm phase. Overall, despite the high diversity of the salivary microbiome within and between individuals, minor geographic differences can be discerned. Individuals from different parts of the world harbor similar salivary microbiota, suggesting that host species is the primary determinant of the oral microbiome. Some microorganisms in the mouth (e.g., *Porphyromonas gingivalis*) are more closely associated with the disease than others, but they can usually be hidden in the normal oral flora without harming oral health (Samaranayake, 2018).

3. Orthodontics and oral flora

Both fixed and removable orthodontic appliances can create problems in oral hygiene and cause plaque accumulation. In many studies (Paolantonio *et al.*, 1999) it has been reported that after starting orthodontic treatment, changes occur in the oral flora, especially pathogenic microorganisms increase. However, there are also studies that state that there is no significant difference in the dental flora after orthodontic treatment and even that some microorganisms in the flora decrease (Ristic *et al.*, 2008). During orthodontic treatment of various malocclusions with appliances, an inflammatory reaction of the gingival tissue can be observed. The formation of new retention areas around the bands and brackets is one of the main reasons for increased dental plaque deposition and inflammatory response (Alexander, 1991). Therefore, the effects of fixed orthodontic appliances on oral hygiene and gingival status have been studied in detail (Sadowsky and BeGole, 1981; Polson *et al.*, 1988). Microbiological changes are usually caused by *Streptococcus mutans*, *Lactobacillus* spp. some other microorganisms (Forsberg *et al.*, 1991; Ristic *et al.*, 2008; Rosenbloom and Tianoff, 1991) and periodontopathic anaerobes can occur in the subgingival flora (Paolantonio *et al.*, 1999). Some specific forms of subgingival bacteria can directly disrupt periodontal tissues, the most dangerous microorganisms that can cause periodontal damage belong to the group of *P. intermedia*, *A. actinomycetemcomitans*, *P. gingivalis* and some other anaerobes (Haffajee and Socransky, 1994; Moore and Moore, 1994). In addition to virulence of microorganisms, bacterial serotype and individual host susceptibility are also the main factors in the development of periodontal damage (Paolantonio *et al.*, 1999).

Ristic *et al.* (2008) reported that treatment with fixed appliances temporarily increases the growth of periodontopathic bacteria and may result in a gingival inflammatory response without a destructive effect on deep periodontal tissues. In this study, it was determined that the total number of bacteria generally increased in the subgingival dental plaque samples examined. These researchers (Ristic *et al.*, 2008) identified *P. intermedia* and *Actinobacillus actinomycetemcomitans* as periodontopathic anaerobes. Inflammatory reaction of the gingival tissue can be seen more frequently in patients using fixed orthodontic appliances (Boyd

and Baumrind, 1992; Davies *et al.*, 1991). Insufficient oral hygiene in these patients is thought to be the main cause of plaque accumulation, increased number of bacterial colonies, and sequential inflammatory response.

Schie *et al.* (2007) concluded that fixed orthodontic appliance application created a transitory decrease in the number of *S. mutans* colonies. These researchers (Schie *et al.*, 2007) found that three months after the application of the fixed appliance, the number of bacterial colonies in dental plaque and saliva increased as the fixed appliance created new retainer sites. These researchers especially emphasized that the placement of the fixed appliance initially causes microbial elimination, and it takes time for the bacterial colonies to regain their initial numbers. As a result of the study, they reported that treatment with fixed appliances could increase the growth of pathogenic bacteria and anaerobes, and they stated that these microbiological changes were limited to the subgingival dental plaque collected from the teeth and had no adverse effects on periodontal tissues. Because these changes in the subgingival microflora increase the risk of damaging periodontal tissue, it is necessary to provide instructions for good oral hygiene in patients receiving fixed therapy and to maintain constant re-motivation and constant control throughout orthodontic treatment.

Vizitiu and Ionescu (2010) in their study to evaluate the changes in the oral microbial flora in the first 3 months of orthodontic treatment; reported that the presence of orthodontic appliances causes an increase in oral bacterial concentration. In this study, a small number of anaerobic strains were isolated (one *Aggregatibacter actinomycetemcomitans* and one *Porphyromonas gingivalis* strain from each group) and an increase in the isolation percentages of oral streptococci and anaerobic bacteria involved in dental and periodontal pathological processes was observed after starting treatment with orthodontic appliances:

Researchers (Vizitiu and Ionescu, 2010) reported that the concentration of aerobic and anaerobic bacteria (CFU/sample) increased in the first 3 months of orthodontic treatment. It was emphasized that the isolation percentages of oral streptococci and anaerobic bacteria increased after treatment with orthodontic appliances was started. *Streptococcus mutans*, *Aggregatibacter actinomycetemcomitans*, *Porphyromonas gingivalis* and Lactobacilli were reported among the detected groups of microorganisms. In addition, other studies on aerobic and anaerobic CFU/sample number (Paolantonio *et al.*, 1999; Ristic *et al.*, 2008; Vizitiu and Ionescu, 2010) emphasized that the presence of orthodontic appliances increases oral bacteria concentration.

Lucas *et al.* (2000) in their study to determine the dominant streptococcal species in the mouths of healthy children and to investigate the composition of the oral streptococcal flora over a 4-month period, they found that the dominant species were *Streptococcus salivarius*, *S. oralis* and *S. mitis*, and there was no significant change in the composition of the oral streptococcal flora during the 4-month period.

In a study conducted to determine the qualitative and quantitative microbiological changes after the application of orthodontic appliances (Reichardt *et al.*, 2019). They reported that they identified inflammatory symptoms after the placement of fixed orthodontic appliances, and observed an increase in plaque accumulation, bleeding on probing, and pocket depth within 1 week. In the study, the formation of biofilm-forming bacteria was determined and it was stated that the total number of bacteria increased. After the placement of fixed orthodontic appliances, an increase in *Streptococcus* spp, *Actinomyces*, *Neisseria* and *Rothia* species was detected in premolars and molars.

Researchers (Gorton and Featherstone, 2003; O'Reilly and Featherstone, 1987) found that demineralization occurred 4 weeks after the placement of fixed orthodontic appliances. Øgaard *et al.* (2001) reported that 50-70% of orthodontic patients developed an initial caries lesion during orthodontic treatment. Reichardt *et al.* (2019) in their study, in addition to changes in microflora, clinical indices describing gingivitis increased significantly; Significant gingivitis symptoms were observed in all patients one week after the placement of fixed orthodontic appliances. Deinzer *et al.* (2007) stated that chronic gingivitis appeared 4 weeks after the application of fixed orthodontic appliances.

Orthodontic treatment causes significant changes in the oral bacterial environment associated with gingivitis and an increased risk of cariogenic reactions in the first days of orthodontic treatment. Reichardt *et al.* (2019) showed that the total germ count increased significantly 1 week after the placement of fixed orthodontic appliances. These researchers demonstrated that the growth of some bacteria is faster under the ecological conditions of orthodontic treatment. In particular, cariogenic *Streptococcus* spp was found to grow significantly in microbial plaque isolated from the niches between the metal surfaces and the adjacent tooth surface. This rapid process increases the risk of caries development. It was stated that one week after the fixed orthodontic appliances were inserted, significant gingivitis symptoms were observed in all patients. In order to reduce the side effects of orthodontic treatment, it is very important to give oral hygiene instructions to the patients and to control the oral hygiene of the patients before and during the treatment, especially in the early period (Reichardt *et al.*, 2019).

4. Oral microbiota microorganisms

Major microorganisms that can be found in the oral microbiota (Samaranayake, 2018):

Gram positive cocci

Streptococcus

Mutans group: *Streptococcus mutans* serotypes c, e, f, k; *Streptococcus sobrinus* serotypes d, g; *Streptococcus criceti* serotype a; *Streptococcus rattii* serotype b.

Saliva group: *Streptococcus salivarius*; *Streptococcus vestibularis*.

Anginosus group: *Streptococcus constellatus*; *Streptococcus intermedius*; *Streptococcus anginosus*.

Mitis group: *Streptococcus mitis*, *Streptococcus sanguinis*, *Streptococcus gordonii*, *Streptococcus oralis*, *Streptococcus cristatus*, *Streptococcus parasanguinis*, *Streptococcus oligofermentans*, *Streptococcus sinensis*, *Streptococcus australis*, *Streptococcus infantreptococcus percoccus*.

Anaerobic streptococci: *Peptostreptococcus anaerobius*, *Micromonas micros*, *Finegoldia magna*, *Peptoniphilus asaccharolyticus*

Stomatococcus: *Stomatococcus mucilaginous*

Granulicatella: *Granulicatella adiacens*, *Granulicatella elegans*, *Granulicatella balaenopterae*.

Staphylococcus and *Micrococcus*

Gram positive rods and filaments

Actinomyces: *Actinomyces israelii*, *Actinomyces gerencseriae*, *Actinomyces odontolyticus*, *Actinomyces naeslundii*, *Actinomyces meyeri*, *Actinomyces georgiae*.

Lactobacillus: *Lactobacillus casei*, *Lactobacillus fermentum*, *Lactobacillus acidophilus*

Eubacterium: *Eubacterium brachy*, *Eubacterium nodatum*, *Eubacterium saphenum*.

Propionibacterium: *Propionibacterium acnes*

Other important Gram-positive organisms

Rothia dentocariosa, *Bifidobacterium dentium*

Gram negative cocci

Neisseria: *Neisseria subflava*, *Neisseria mucosa*, *Neisseria sicca*.

Veillonella: *Veillonella parvula*, *Veillonella dispar*, *Veillonella atypica*.

Haemophilus: *Haemophilus parainfluenzae*, *Haemophilus segnis*, *Haemophilus aphrophilus*, *Haemophilus haemolyticus*, *Haemophilus parahaemolyticus*.

Aggregatibacter: *Aggregatibacter actinomycetemcomitans* (serotypes a–e).

Eikenella: *Eikenella corrodens*.

Capnocytophaga: *Capnocytophaga gingivalis*, *Capnocytophaga sputigena*, *Capnocytophaga ochracea*, *Capnocytophaga granulosa*, *Capnocytophaga haemolytica*.

Prevotella: *Prevotella intermedia*, *Prevotella nigrescens*, *Prevotella loescheii*, *Prevotella corporis*, *Prevotella melaninogenica*; nonpigmented species include *Prevotella buccae*, *Prevotella oralis*, *Prevotella oris*, *Prevotella oulora*, *Prevotella veroralis*, *Prevotella dentalis*

Fusobacterium: *Fusobacterium nucleatum*, *Fusobacterium alocis*, *Fusobacterium sulci*, *Fusobacterium periodonticum*.

Leptotrichia: *Leptotrichia buccalis*.

Treponema: *Treponema denticola*, *Treponema macrodentium*, *Treponema scoliodontium*, *Treponema socranskii*, *Treponema maltophilum*, *Treponema amylovarum*, *Treponema vincentii*.

Usually, the various types of bacteria in the mouth are in balance. If the number of certain bacteria, namely mutans streptococci or lactobacilli increases significantly, the risk of developing disease may be increased by insufficient protective factors. Excessive sugar intake together with low pH values can lead to an increase in the number of *S. mutans* and *S. sobrinus* in the oral cavity. Mutans streptococci have an efficient transport system that transports sugar to their cells (Hamada and Slade, 1980). During metabolic processes in cells, they produce various substances that significantly contribute to their pathogenicity. When high levels of sugar are consumed, mutans streptococci mainly produce lactic acid. This degradation proceeds much faster than other bacteria (Hamada and Slade, 1980; Loesche, 1986). Metabolism takes place in both neutral and acid environments with continued activity at low pH values (Köhler *et al.*, 1995). Mutans streptococci produce intracellular and extracellular polysaccharides.

Extracellular polysaccharides are also produced during enzymatic reactions. Their stickiness facilitates the adhesion of bacteria to tooth surfaces, which allows them to settle even on very smooth surfaces (Loesche, 1986). Mutans streptococci can grow in an acid environment. This can make them dominant against other microorganisms. While low pH levels restrict the growth of many bacteria, numbers of mutans streptococci may increase (Harper and Loesche, 1984). Mutans streptococci are considered the initiators of caries. They trigger the process that leads to initial mineral loss and allows bacteria to penetrate the tooth structure (CRT, 2021).

Lactobacilli are responsible for caries progression (Featherstone, 2000). These; They play a role in colonization and acid production in holding niches. Usually only a few lactobacilli are found in saliva. Mutans streptococci produce an acid environment suitable for lactobacilli, and when they begin to colonize the oral cavity, their numbers increase and thus the pH value decreases (Newbrun, 1992). If lactobacilli are present in an environment where protective factors are lacking, the risk of caries development is high (Leverett *et al.*, 1993).

5. Conclusions

In this review, information on the relationship between orthodontic treatment and oral flora is summarized. As a result, it can be said that gingivitis may develop from time to time in patients receiving orthodontic treatment and there may be changes in the oral flora.

Data availability

Not applicable.

Conflict of interest

None to declare.

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