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ORIGINAL RESEARCH

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Joko Kusnoto<sup>1</sup>, Siti Sara Safrah<sup>2</sup>, Litayana Ria Anggrani Sitorus<sup>3</sup>, Winnie Valentini<sup>4</sup>, Armelia Sari Widyarman<sup>5</sup>

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The Journal of Contemporary Dental Practice (2025); 10.5005/jp-journals-10024-3857

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Corresponding Author: Armelia Sari Widyarman, Department of Oral Biology, Faculty of Dentistry, Universitas Trisakti, Jakarta, Indonesia, Phone: +62 811929379, e-mail: armeliasari@trisakti.ac.id  
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<sup>2-3</sup>Academic Program, Faculty of Dentistry, Universitas Trisakti, Jakarta Indonesia  
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*Fusobacterium nucleatum* is a dominant bacterial species that plays an important role in the formation of dental biofilms and periodontal tissue disease. In the formation of biofilms, *F. nucleatum* being a "bridging" or "linking" organism between initial bacterial colonization and final bacterial colonization, which are unable to bind to each other directly. *F. nucleatum* can also co-aggregate with various microbial species in the oral cavity.<sup>8-10</sup> *F. nucleatum* encodes several adhesion genes involved in interspecies interactions, including fusobacterium adhesion A (*fadA*), fusobacterium outer membrane protein A (*fomA*), *radD* (an arginine-inhibitable adhesin), and adherence inducing determinant gene 1 (*aid1*).<sup>8,11-14</sup> Fusobacterium adhesin A (FadA) is known to be

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**Source of support:** Nil

**Conflict of interest:** None

involved in *F. nucleatum* invasion and adhesion to host cells and is highly conserved among oral *Fusobacterium* species.<sup>8,15,16</sup> FadA has been identified has a major virulence factor in *F. nucleatum* in interspecies interactions with *Streptococcus* mediated by *radD*, as it increases the binding specificity of *F. nucleatum* to other microbial species.<sup>14</sup> The arginine-inhibitable adhesion *radD* is required by *F. nucleatum* for co-adherence with various species of Gram-positive bacteria, such as streptococci (early colonizers), and fungal species, such as *Candida*.<sup>11,12,17</sup>

*Enterococcus faecalis* (*E. faecalis*) is associated with chronic periodontitis and chronic apical periodontitis in failed root canal treatment.<sup>18</sup> *E. faecalis* is a Gram-positive aerobic bacterium. The severity of *E. faecalis* infection depends on the immune response and virulence factors, which can exacerbate infection and play a role in increasing biofilm formation.<sup>19</sup> There are several genes associated with *E. faecalis* biofilm formation, including gelatinase (*gelE*) and autolysin (*atlA*).<sup>20</sup> *gelE* in *E. faecalis* plaque or saliva isolates showed resistance to antibiotics and high biofilm formation ability.<sup>21</sup> *atlA* is the main peptidoglycan hydrolase or autolysin of *E. faecalis*.<sup>22</sup> *AtlA* plays a role in the biofilm maturation stage during which extracellular DNA (eDNA) is released and contributes to biofilm attachment and stability.<sup>23,24</sup>

An increase in the number of colonies of microorganisms also increased, one of which was *Candida albicans*, which causes infections of oral mucosa.<sup>25,26</sup> *C. albicans* has a protein in the form of an adhesive that mediates other microorganisms to adhere to abiotic and host surfaces to form biofilms.<sup>27</sup> Several *C. albicans* gene transcription factors, including biofilm and cell wall regulator 1 (*BCR1*) and angiotensin converting enzyme 2 (*ACE2*), play a role in the formation of biofilms. *BCR1* acts as a major regulator of *C. albicans* biofilm formation.<sup>28</sup> The *ACE2* transcription factor plays a role in fungal adherence, biofilm formation, and hyphal morphogenesis. In addition, *ACE2* plays a role in regulating the expression of genes involved in cell wall separation and metabolism.<sup>29</sup> As shown in previous research, *ACE2* is required for filamentation, and it can increase the number of pseudohyphae cells at the time of biofilm formation.<sup>30</sup>

Biofilm formation plays a role in increasing antibiotic resistance in bacterial cells. Therefore, an effective therapy is needed to prevent biofilm formation. The use of probiotics has been suggested as a promising approach to prevent and treat microbial diseases and biofilm activity in the oral cavity.<sup>31,32</sup> Several studies have proven that the use of probiotics has oral cavity health benefits, such as preventing caries and periodontal disease.<sup>32,33</sup> One commercial probiotic proven to be beneficial for oral health is *Lactobacillus reuteri*. The antimicrobial activity of *L. reuteri* inhibits colonization by pathogenic microbes and interacts the inhibition directly with host cells.<sup>34</sup> *L. reuteri* also inhibits the growth of *C. albicans* and *E. faecalis* biofilms.<sup>35,36</sup> However, no studies have investigated the effect of the probiotic *L. reuteri* on the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atlA* genes in dental plaque biofilms found in patient's oral environment with fixed orthodontic appliances. By analyzing the virulence genes found in several pathogenic bacteria, we can hypothesize that the downregulation of these genes will lead to less biofilm production and healthier oral health conditions during the duration of fixed orthodontic appliances usage. Thus, to bridge the knowledge gap, the aim of this study was to determine the effect of consuming lozenges containing the probiotic *L. reuteri* on the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atlA* genes in biofilms from subjects using fixed orthodontic appliances.

## MATERIALS AND METHODS

### Sample Collection

Subjects undergoing fixed orthodontic therapy were enrolled in this open-label prospective, clinical trial. Ethical approval for the study was granted by the Institutional Review Board of the Faculty of Dentistry, Universitas Indonesia (approval number: 100,701,020). The inclusion criteria specified participants aged 18 years or older who had been undergoing orthodontic treatment with fixed

appliances for a minimum duration of 1 year and had not consumed probiotics or antibiotics in the preceding 3 months. The fixed orthodontic appliances used by the subjects are conventional metal braces fixed appliance. Exclusion criteria encompassed individuals with systemic conditions such as hypertension or diabetes, those on systemic medications including antihypertensives, analgesics, hormonal therapies, sedatives, or anti-seizure medications, as well as individuals presenting with severe periodontal disease or known allergies to probiotics.

The study utilized *L. reuteri* Prodentis lozenges, obtained from BioGaia (Stockholm, Sweden). Each lozenge (800 mg) contained a minimum of  $2 \times 10^8$  live *Limosilactobacillus reuteri* Prodentis (previously classified as *L. reuteri*). This food supplement, specifically formulated for oral health, included a proprietary combination of the *L. reuteri* DSM 17938 and *L. reuteri* ATCC PTA 5289 strains, which are recognized for their potential to support and maintain oral health.

To standardize oral hygiene practices, all participants were provided with a standardized toothbrush and toothpaste for use throughout the study period. Participants received oral hygiene instructions and were instructed to brush their teeth twice daily. Each participant was administered one probiotic lozenge containing *Limosilactobacillus reuteri* daily for 14 days, to be taken once per day after morning toothbrushing and prior to breakfast. Plaque samples were collected from participants on the day of enrolment, prior to the initiation of probiotic lozenge consumption, and again on the 14th day following the completion of the probiotic regimen.

Before sample collection, mandatory rapid antigen test for SARS-CoV-2 detection had to be taken by the subjects in response to the COVID-19 pandemic (as of 30 September 2020 when collecting the samples) and the test result had to be negative for the subject partaking in the study. In brief, the participants were instructed not to eat or drink anything 2 hours prior to collection of sample. Samples were collected using sterile cotton buds and swabbed from buccal/mesial/distal/lingual/occlusal surfaces of the index teeth of the subjects. The plaque samples were stored in sterile falcon tubes with 5 mL of phosphate-buffered saline (PBS).

Furthermore, clinical data, including the Oral Hygiene Index-Simplified score and the Papilla Bleeding Index, were recorded at each visit. Overall, 20 subjects had enrolled and fulfilled all requirements and inclusion criteria, as 20 subjects were proved to be sufficient to provide valid data as a pilot study.<sup>37,38</sup> Plaque samples from the subjects were continued unto the following downstream analysis.

### RNA Extraction, cDNA Synthesis, and Quantification

RNA from the sample was extracted using TRIzol reagent methodology as instructed by the manufacturer (Thermo Fisher, Waltham, MA). The extracted RNA was synthesized into cDNA using ReverTra Ace<sup>TM</sup> qPCR RT Master Mix with gDNA Remover (Toyobo, Japan). The mixture for cDNA synthesis is described in Table 1. The cDNA was then quantified using an Invitrogen<sup>TM</sup> Qubit 3.0 Fluorometer (Thermo Fisher Scientific, Waltham, MA). The cDNA was stored at  $-20^{\circ}\text{C}$  for storage of directly used for downstream analysis.

### qPCR Analysis

Amplification and detection by qPCR (Applied Biosystems, Waltham, MA) were performed. The components of the qPCR Master Mix are listed in Table 2. Using a specific kit, namely HOT FIREpol EvaGreen<sup>®</sup> qPCR Mix (Solis Biotek, Tartu, Estonia) which was activated by

# Probiotic Consumption Reduced Virulence Gene Expression from Fixed Orthodontic Plaque

**Table 1:** Reagent components for DNase I reaction solution

| Component           | Volume          |
|---------------------|-----------------|
| 4 × DN Master Mix   | 2 mL            |
| RNA template        | 0.5 pg – 0.5 mg |
| Nuclease-free water | X mL            |
| Total volume        | 8 mL            |

**Table 2:** Components of Master Mix RT-qPCR

| Component                               | Volume |
|-----------------------------------------|--------|
| 5 × HOT FIREPol EvaGreen® qPCR Mix Plus | 4 mL   |
| Primer Forward                          | 1 mL   |
| Primer Reverse                          | 1 mL   |
| DNA template                            | 2 mL   |
| NFW                                     | 12 mL  |
| Total                                   | 20 mL  |

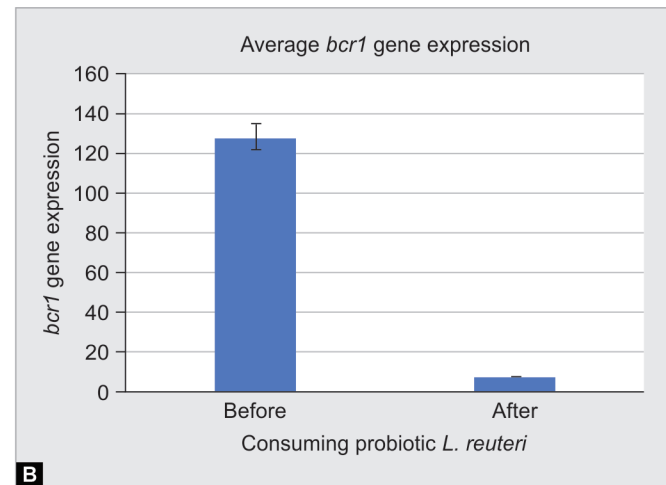
**Table 3:** Primer sequence for RT-qPCR

| Genes                                                        | Primer sequence                                                                               | Temperature and cycle settings                                                                                                                                                                                                         |
|--------------------------------------------------------------|-----------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>BCR1</i> <sup>39</sup>                                    | forward:<br>5'-CTTCAGCAGCTTCATTAACACCTA-3'<br>reverse:<br>5'-TCTTGGATCAGGTGTACTTTTCAA-3'      | Initial denaturation of 95°C for 5 minutes; 40 cycles of denaturation at 95°C for 1 minute and annealing at 58°C for 1 minute.                                                                                                         |
| <i>ACE2</i> <sup>40</sup>                                    | forward<br>5'-AGAATTGACCGTTGTCCGTGAAG-3'<br>reverse:<br>5'-AATGGGTGAATAAATCCCTCCCTAA-3'       | Initial denaturation 95°C for 2 minutes; 40 cycles of denaturation at 95°C for 30 seconds and annealing at 60°C for 1 minute.                                                                                                          |
| Housekeeping gene<br><i>C. albicans: ACT1</i> <sup>41</sup>  | forward:<br>5'-TTTCATCTTCTGTATCAGAGGAAGTATT-3'<br>reverse:<br>5'-ATGGGATGAATCATCAACAAGAG-3'   | Initial denaturation 95°C for 10 minutes; 40 cycles of denaturing 95°C for 15 seconds and annealing 60°C for 1 minute.                                                                                                                 |
| <i>fadA</i> <sup>15</sup>                                    | forward:<br>5'-CAC AAG CTG ACG CTG CTA GA- 3'<br>reverse:<br>5'-TTA CCA GCT CTT AAA GCT TG-3' | Initial incubation for 4 minutes at 94°C followed by 30 cycles of denaturation at 94°C for 30 seconds, annealing at 55.8°C for 30 seconds, and elongation at 72°C for 40 seconds and the final elongation for 6 minutes. <sup>14</sup> |
| <i>aid1</i> <sup>14</sup>                                    | forward:<br>5'-TACAGGAG GTGCCGTAGCAG-3'<br>reverse:<br>5'-TTTTTGTTAATTCT CCAGCTCCA-3'         | Initial incubation for 10 minutes at 95°C followed by 40 cycles of denaturation at 95°C for 15 seconds, annealing and elongation at 60°C for 1 minute. <sup>13</sup>                                                                   |
| Housekeeping gene<br><i>F. nucleatum: rpoB</i> <sup>42</sup> | forward:<br>5'-GGYTWYGAAGTNCGHGACGTDC-3'<br>reverse:<br>5'-TGACGYTGCATGTTBGMR CCCATMA-3'      | Initial incubation for 10 minutes at 95°C followed by 40 cycles of denaturation at 95°C for 15 seconds, annealing and elongation at 60°C for 1 minute.                                                                                 |
| <i>gelE</i> <sup>43</sup>                                    | forward:<br>5'-CGGAACATACTGCCGTTTGA-3'<br>reverse:<br>5'-TGGATTAGATGCACCCGAAAT -3'            | Initial denaturation at 95°C for 3 minutes, 40 cycles of denaturation at 95°C for 5 seconds, and annealing at 60°C for 30 seconds.                                                                                                     |
| <i>atlA</i> <sup>44</sup>                                    | forward:<br>5'-AATAATCAATCAGGAACGAATACG-3'<br>reverse:<br>5'-GCCACACTAACACCGAAT-3'            | Initial denaturation at 95°C for 2 minutes, 40 cycles of denaturation at 95°C for 15 seconds, and annealing at 60°C for 60 seconds.                                                                                                    |
| Housekeeping gene<br><i>E. faecalis: rpoA</i> <sup>44</sup>  | forward:<br>5'-GTGAAACCTGGTCGTGGCTA-3'<br>reverse:<br>5'-CGACGAACGGGTGTGTAGAT-3'              | Initial denaturation at 95°C for 2 minutes, 40 cycles of denaturation at 95°C for 15 seconds, and annealing at 60°C for 60 seconds.                                                                                                    |

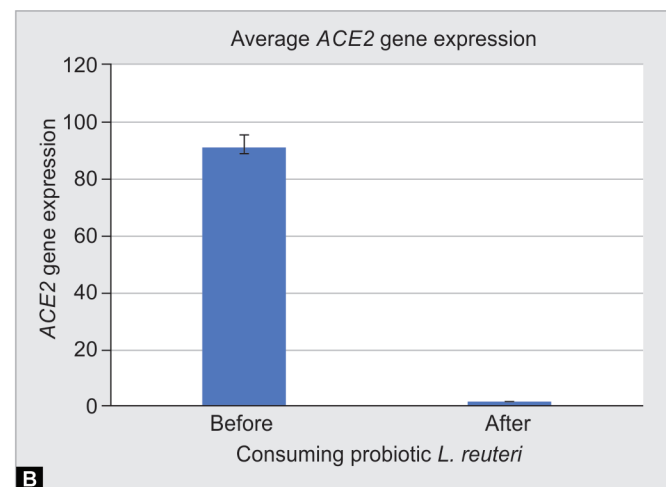
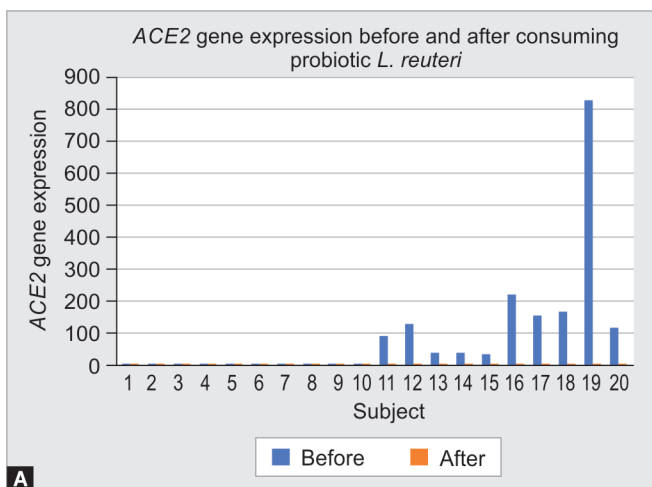
incubation at 95°C for 10 minutes. This was followed by 40 cycles of denaturation at 95°C for 10 seconds, annealing temperature at 60–65°C (Table 3), and elongation at 72°C for 20 seconds. For templates longer than 150 bp, the annealing and elongation times were extended to 30 seconds. Actin gene encoding as the housekeeping gene was used for normalization purposes. qPCR was performed on cDNA. qPCR was performed using the primers listed in Table 3.

## Data Analysis and Outcome Analysis

The data were analyzed using the Shapiro–Wilk normality test ( $p > 0.05$ ). For data with a normal distribution, a paired  $t$ -test was applied ( $p < 0.05$ ). The software used for the analysis is Statistical Package for the Social Sciences (SPSS) version 27 (IBM, Armonk, NY). The outcome analysis are the quantitative data presented from the RT-qPCR instrument. This data can then be correlated with previous study that also conducted such research to ensure the validity of this data.



**Figs 1A and B:** (A) A graph showing *bcr1* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *bcr1* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges



**Figs 2A and B:** (A) A graph showing *ACE2* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *ACE2* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges

## RESULTS

Based on the results of the qPCR test, the expression of *BCR1* (Fig. 1), *ACE2* (Fig. 2), *fdaA* (Fig. 3), *aid1* (Fig. 4), *gelE* (Fig. 5), and *atIA* (Fig. 6), on average, were decreased when comparing the day-0 prior to probiotic consumption and day-14 after the subjects consumed the probiotic *L. reuteri*.

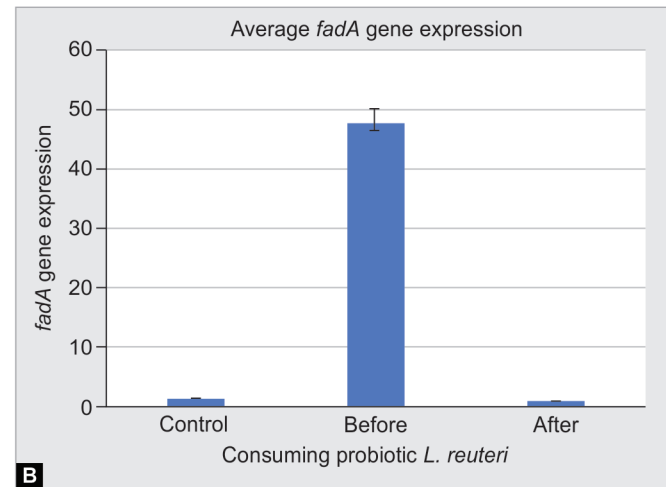
As shown by the results of the Shapiro–Wilk normality test, all the data were normally distributed ( $p > 0.05$ ). The data were analyzed using a paired *t*-test, with a significance level of  $p < 0.05$ . The results of the paired *t*-test revealed a significant difference in the comparison of the *BCR1* and *ACE2* gene expression data. There was a significant difference ( $p < 0.05$ ) in the expression of *BCR1*, *ACE2*, *fdaA*, *aid1*, *gelE*, and *atIA* genes after consuming the probiotic *L. reuteri*.

## DISCUSSION

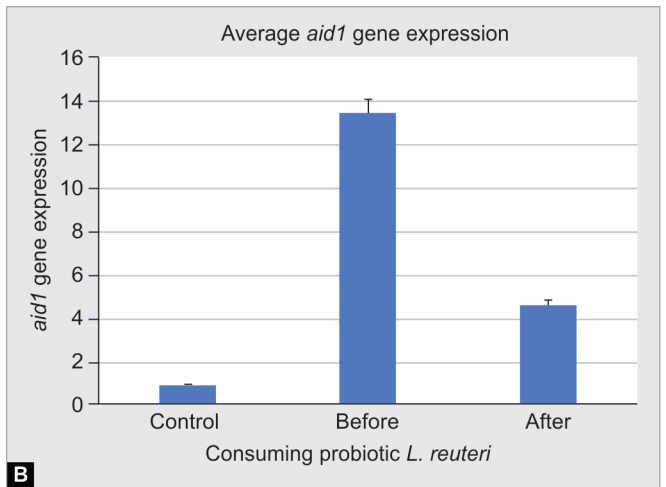
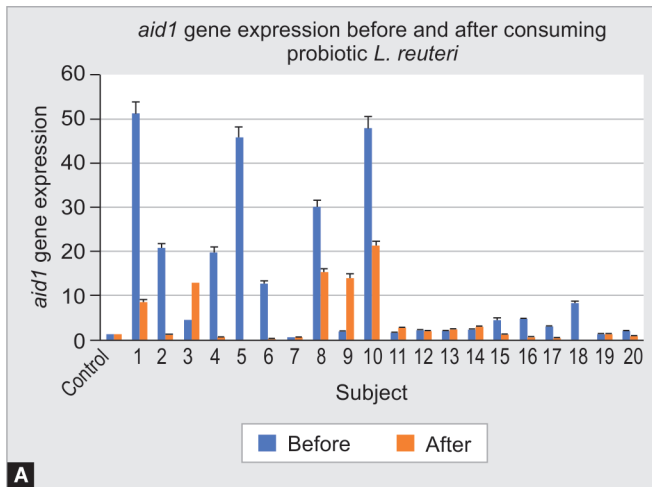
The use of fixed orthodontic appliances often causes poor oral hygiene, thus facilitating microorganism accumulation and various

pathological conditions in the oral cavity, such as fungal infections.<sup>45</sup> A previous study revealed an increase in *Candida* in saliva after using fixed orthodontic appliances. The authors attributed this to the design of fixed orthodontic appliances, which creates a space for the retention of food waste.<sup>46</sup> Thus, patients must be instructed about good oral hygiene practices after orthodontic treatment.<sup>38</sup> Fixed orthodontic appliances also induce changes in buffer capacity, salivary flow rates, and acidity (pH), leading to plaque accumulation and an increase in caries and periodontal disease.<sup>47–49</sup> Based on this information, we attempted this study to prove the benefits of consuming probiotics lozenges as a supplement for patients using fixed orthodontic appliances.

Biofilm formation is an important virulence factor of *F. nucleatum* due to its higher resistance to host defense or antibacterial agents compared to planktonic cells.<sup>50</sup> Several studies detected increased numbers of *Porphyromonas gingivalis*, *F. nucleatum*, *P. intermedia*, and *Tannerella forsythia* after the use of fixed orthodontic appliances.<sup>15,51,52</sup> They also reported that *F. nucleatum* increased



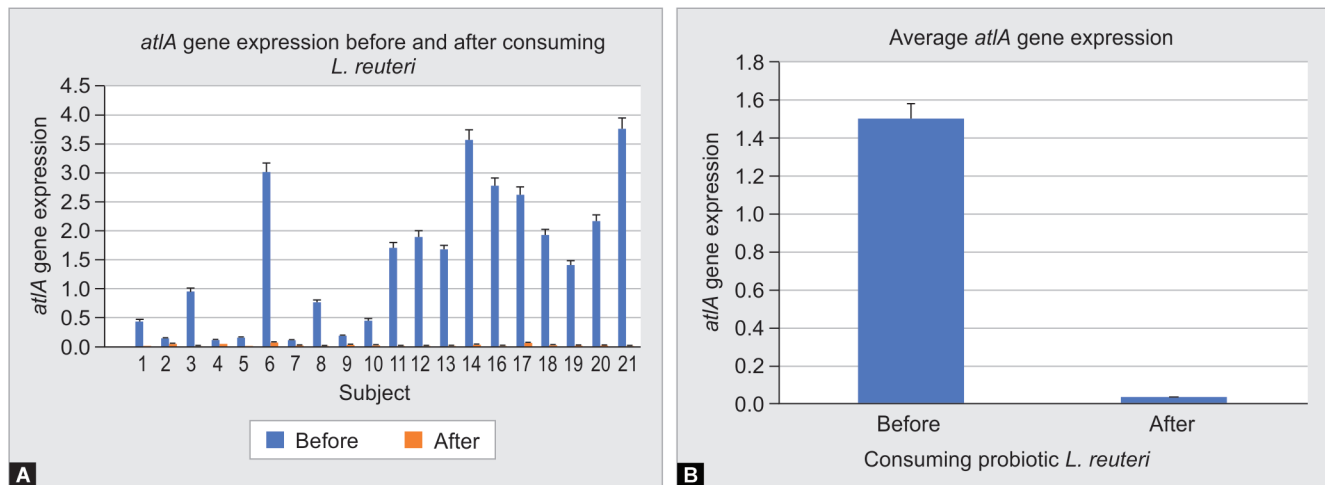
**Figs 3A and B:** (A) A graph showing *fadA* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *fadA* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges



**Figs 4A and B:** (A) A graph showing *aid1* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *aid1* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges



**Figs 5A and B:** (A) A graph showing *gelE* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *gelE* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges



**Figs 6A and B:** (A) A graph showing *atIA* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *atIA* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges

the risk of periodontitis in orthodontic patients due to a conducive environment for anaerobic bacteria.<sup>15,51,52</sup> Biofilm formation is also a contributing factor to *E. faecalis* colonization and infection. Biofilms develop through various processes by which bacteria adhere to surfaces, decompose complex matrices, and develop into bacterial colonies, which adhere to surfaces.<sup>53</sup>

In this study, we used the qPCR method and  $2^{-\Delta\Delta CT}$  formula to calculate target gene expression. As shown by the results, the probiotic *L. reuteri* affected the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes and the formation of *C. albicans*, *F. nucleatum*, and *E. faecalis* biofilms. Based on the Shapiro–Wilk normality test, all the data were normally distributed, with  $p > 0.05$ . The paired *t*-test results revealed significant differences in the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes (all  $p < 0.05$ ).

Based on the results of this study, the probiotic *L. reuteri* significantly downregulated the transcription of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes. In gene expression, the process of translating genetic information in the form of sequence of bases of DNA or RNA into proteins.<sup>54</sup> Through gene expression measurement, it is possible to assess qualitatively and quantitatively the effect of a treatment, such as the administration of a drug compound.<sup>55</sup> Gene expression in microorganisms is involved in regulating cell-cell communication, carbohydrate metabolism, adherence, and adaptation to the surrounding environment. A decrease in the expression of specific genes can reduce microorganism colonization and microorganism numbers.<sup>56</sup>

*BCR1*, a major gene transcription factor, produces an adhesin protein, which facilitates *C. albicans* attachment to mucosal surfaces, which is a critical stage of infection.<sup>39</sup> Deletion of *BCR1* eliminates *C. albicans* gene function, resulting in a decrease in biofilm formation.<sup>57</sup> This was supported by the results of the present study, which revealed a statistically significant decrease in *BCR1* gene expression after consuming the probiotic.

The expression of *ACE2* also decreased based on the results of the statistical tests. With deletion of *ACE2*, *C. albicans* is unable to form hyphal cells, and thus biofilm formation is inhibited.<sup>30</sup> An earlier in vitro study showed that probiotics have antifungal effects against *C. albicans* in the oral cavity. Regular use of probiotics helped to inhibit *Candida* biofilms and reduced *Candida* colonization in the oral cavity, thereby reducing the possibility of candidiasis infection.<sup>58</sup>

*FadA* protein is the main *F. nucleatum* virulence factor and mediates microbial attachment and colonization.<sup>8</sup> Based on the results of this study, the probiotic *L. reuteri* appears to influence the pathogenicity of *F. nucleatum* adhesion molecules and colonization and affect biofilm formation through decreased expression of the *fadA* gene.<sup>35</sup> Various *F. nucleatum* adhesins mediate adhesion and aggregation and function as coaggregation intermediaries in the formation and maturation of dental biofilms.<sup>59</sup> The interaction of *Fusobacterium* with other species is largely mediated by the adhesin genes *radD* and *aid1*.<sup>60</sup> The *aid1* gene plays a role in interspecies interactions, colonization, and aggregation of *F. nucleatum*. In a previous study, inactivation of the *aid1* gene decreased the ability of *F. nucleatum* to aggregate, especially with *Streptococcus* spp. or *E. faecalis*.<sup>14</sup> As shown in earlier studies, probiotics can affect the expression of genes involved in cell adhesion, quorum sensing (QS), virulence factors, and biofilm formation.<sup>61,62</sup>

The *E. faecalis gelE* gene has the ability to hydrolyse gelatine, collagen, fibrin, and other peptides.<sup>63</sup> Gene *gelE* is a virulence factor in infection formation through bacterial attachment and biofilm formation.<sup>22</sup> In *E. faecalis*, biofilm formation is regulated by QS, where *Fsr* regulates the expression of the *gelE* gene.<sup>64</sup> *Fsr* regulates the formation of *E. faecalis* biofilms through its product *gelE* and serine proteases.<sup>43</sup> QS is a molecular mechanism by which bacterial cells communicate with each other via signaling molecules in biofilms. If the protease encoded by a signaling factor is decreased, communication between bacteria and biofilm formation will be disrupted.<sup>62</sup> *GelE* can also activate *atIA*, which is responsible for eDNA release at the biofilm maturation stage.<sup>65</sup>

*AtIA* is involved in the hydrolysis of peptidoglycan, which plays an important role in separating cells division after replication.<sup>22</sup> *AtIA* plays a role in the biofilm maturation stage of *E. faecalis*, during which eDNA is released and contributes to biofilm attachment and stability, biofilm defects in primary attachment, and decreased biofilm production.<sup>20,23</sup> This study focused on the probiotic *L. reuteri*, which has ability to secrete antimicrobial substances and compete with oral pathogens for adhesion to mucosa. In addition, *L. reuteri* can adapt and change the pH of the surrounding environment, thereby inhibiting the growth of oral pathogens.<sup>66</sup> The antimicrobial substances secreted by *L. reuteri* are reuterin and

reutericycline.<sup>67</sup> Reuterin and reutericycline are broad-spectrum antimicrobial agents that are effective against Gram-positive and -negative bacteria, fungi, and protozoa by inhibiting microbial DNA synthesis.<sup>35,47</sup>

Many dental and oral health care products used daily now include probiotics. The use of probiotics is increasing due to their advantages over chemical agents, namely reducing the risk of antibiotic resistance.<sup>68</sup> Probiotics work by modulating the immune system, producing antimicrobial substances, and inhibiting certain pathogenic organisms by interfering with adhesion, colonization, and biofilm formation. They inhibit the growth of pathogens via the production of various substances, such as lactic acid and acetic acid, which penetrate the bacterial cell membrane and lower the cytoplasmic pH of pathogenic bacteria. Hydrogen peroxide and bacteriocin can destroy the cell membrane of pathogenic bacteria and inhibit the synthesis of pathogenic DNA.<sup>32,33,35,69</sup> Based on the results of this study, 2 weeks of daily consumption of the probiotic *L. reuteri* affected the process of biofilm formation by downregulating the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atlA* genes, which function as adherent regulators and regulators of hyphae formation in biofilm formation. Many previous studies demonstrated that the addition of probiotics to dental and oral health care products. Probiotic can reduce pathogenic microorganisms in plaque samples from patients using fixed orthodontic appliances.<sup>47,68,70–72</sup> Therefore, it can be stated that the probiotic *L. reuteri* has good ability as an additional treatment for dental and oral health in patients using fixed orthodontic appliances.

The limitation of this study is the small sample size and the fact that the sampling had to be done during COVID-19 pandemic. Although the sample size is small, the result of this study can still provide concise and significant result. In the future, there should be larger sample size for conducting this research so the results can more accurately represent the actual population. Daily consumption of probiotic lozenges duration can also be increased for more precise and accurate results. On the other hand, consumption of probiotic lozenges research can also be conducted for other aspect of oral health diseases to promote the functionality and health-inducing aspect of probiotic lozenges, such as antiinflammation.

## CONCLUSION

Within the limitation of this study, it can be concluded that the probiotic *L. reuteri* influences the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atlA* genes in biofilm formation. By reducing the expression of those genes, the probiotic *L. reuteri* can reduce biofilm formation, such as dental plaque, in patients using fixed orthodontic appliances.

## Clinical Significance

Consumption of probiotic lozenges were confirmed to reduce bacterial and fungal biofilm, as proven by the reduction of virulence gene expression, hence, helping increasing oral health of consumer. The results of this study help clinicians provide probiotic lozenges for patients to promote and maintain their oral health.

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## ORIGINAL RESEARCH

# *Lactobacillus Reuteri* Probiotic Consumption Reduced Various Virulence Gene Expression in Dental Plaque of Fixed Orthodontic Subjects

Joko Kusnoto<sup>1</sup>, Siti Sara Safirah<sup>2</sup>, Litayana Ria Anggriani Sitorus<sup>3</sup>, Winnie Valentini<sup>4</sup>, Armelia Sari Widyarman<sup>5</sup>

Received on: 11 April 2025; Accepted on: 15 May 2025; Published on: 18 June 2025

## ABSTRACT

**Aims:** The aim of this study was to determine the effect of consuming lozenges containing *Lactobacillus reuteri* probiotic Prodentis lozenges on the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes in dental biofilms of subjects using fixed orthodontic appliances.

**Materials and methods:** Plaque samples ( $n = 20$ ) obtained from a previous study were used in this research. Each subject consumed *L. reuteri* probiotic lozenges ( $2 \times 10^8$  CFU/mL) each day for 2 weeks. RNA was extracted from the samples and synthesized into cDNA. The expression of the gene transcription factors *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes in biofilms of subjects who used fixed orthodontic appliances was detected using real-time quantitative polymerase chain reaction (RT-qPCR).

**Results:** The expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes were decreased after consuming the *L. reuteri* probiotic lozenges for 2 weeks ( $p < 0.05$ ).

**Conclusion:** Consuming *L. reuteri* probiotic lozenges would affect the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* in plaque from patients using fixed orthodontic appliances. By reducing the expression of the virulence genes, bacterial number would be reduced and biofilm production can also be reduced.

**Clinical significance:** Consumption of probiotic lozenges were confirmed to reduce bacterial and fungal biofilm, as proven by the reduction of virulence gene expression. Routine consumption of probiotic lozenges can help reduce potential bacterial infection and increase the oral health of patients using fixed orthodontic appliances.

**Keywords:** Biofilm, Gene expression, *Lactobacillus reuteri*, Orthodontic, Probiotic.

*The Journal of Contemporary Dental Practice* (2025): 10.5005/jp-journals-10024-3857

## INTRODUCTION

Orthodontic treatment is common today in the community. Among adults and children, orthodontic treatment may be undertaken for dental care or esthetic reasons.<sup>1</sup> Orthodontic treatment using fixed appliances aims to ensure proper occlusion and esthetic function, with appropriate tooth movement. Fixed orthodontic treatment can lead to changes in the oral environment and oral flora composition and an increase in the amount of plaque due to difficulty in maintaining oral hygiene.<sup>2-5</sup> In addition, excess composite around the base of the bracket that used in orthodontic treatment is an important factor that can cause plaque accumulation due to the presence of rough surfaces and cracks on the enamel composite surfaces.<sup>3-5</sup> Biofilm accumulation on teeth and soft tissues in the oral cavity can lead to caries, gingivitis, and periodontitis.<sup>6,7</sup>

*Fusobacterium nucleatum* is a dominant bacterial species that plays an important role in the formation of dental biofilms and periodontal tissue disease. In the formation of biofilms, *F. nucleatum* being a "bridging" or "linking" organism between initial bacterial colonization and final bacterial colonization, which are unable to bind to each other directly. *F. nucleatum* can also co-aggregate with various microbial species in the oral cavity.<sup>8-10</sup> *F. nucleatum* encodes several adhesion genes involved in interspecies interactions, including fusobacterium adhesion A (*fadA*), fusobacterial outer membrane protein A (*fomA*), *radD* (an arginine-inhibitable adhesin), and adherence inducing determinant gene 1 (*aid1*).<sup>8,11-14</sup> Fusobacterium adhesin A (FadA) is known to be

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**How to cite this article:** Kusnoto J, Safirah SS, Sitorus LRA, et al. *Lactobacillus Reuteri* Probiotic Consumption Reduced Various Virulence Gene Expression in Dental Plaque of Fixed Orthodontic Subjects. *J Contemp Dent Pract* 2025;26(4):339-347.

**Source of support:** Nil

**Conflict of interest:** None

involved in *F. nucleatum* invasion and adhesion to host cells and is highly conserved among oral *Fusobacterium* species.<sup>8,15,16</sup> FadA has been identified has a major virulence factor in *F. nucleatum* in interspecies interactions with *Streptococcus* mediated by *radD*, as it increases the binding specificity of *F. nucleatum* to other microbial species.<sup>14</sup> The arginine-inhibitable adhesion *radD* is required by *F. nucleatum* for co-adherence with various species of Gram-positive bacteria, such as streptococci (early colonizers), and fungal species, such as *Candida*.<sup>11,12,17</sup>

*Enterococcus faecalis* (*E. faecalis*) is associated with chronic periodontitis and chronic apical periodontitis in failed root canal treatment.<sup>18</sup> *E. faecalis* is a Gram-positive aerobic bacterium. The severity of *E. faecalis* infection depends on the immune response and virulence factors, which can exacerbate infection and play a role in increasing biofilm formation.<sup>19</sup> There are several genes associated with *E. faecalis* biofilm formation, including gelatinase (*gelE*) and autolysin (*atlA*).<sup>20</sup> *GelE* in *E. faecalis* plaque or saliva isolates showed resistance to antibiotics and high biofilm formation ability.<sup>21</sup> *atlA* is the main peptidoglycan hydrolase or autolysin of *E. faecalis*.<sup>22</sup> *AtlA* plays a role in the biofilm maturation stage during which extracellular DNA (eDNA) is released and contributes to biofilm attachment and stability.<sup>23,24</sup>

An increase in the number of colonies of microorganisms also increased, one of which was *Candida albicans*, which causes infections of oral mucosa.<sup>25,26</sup> *C. albicans* has a protein in the form of an adhesive that mediates other microorganisms to adhere to abiotic and host surfaces to form biofilms.<sup>27</sup> Several *C. albicans* gene transcription factors, including biofilm and cell wall regulator 1 (*BCR1*) and angiotensin converting enzyme 2 (*ACE2*), play a role in the formation of biofilms. *BCR1* acts as a major regulator of *C. albicans* biofilm formation.<sup>28</sup> The *ACE2* transcription factor plays a role in fungal adherence, biofilm formation, and hyphal morphogenesis. In addition, *ACE2* plays a role in regulating the expression of genes involved in cell wall separation and metabolism.<sup>29</sup> As shown in previous research, *ACE2* is required for filamentation, and it can increase the number of pseudohyphae cells at the time of biofilm formation.<sup>30</sup>

Biofilm formation plays a role in increasing antibiotic resistance in bacterial cells. Therefore, an effective therapy is needed to prevent biofilm formation. The use of probiotics has been suggested as a promising approach to prevent and treat microbial diseases and biofilm activity in the oral cavity.<sup>31,32</sup> Several studies have proven that the use of probiotics has oral cavity health benefits, such as preventing caries and periodontal disease.<sup>32,33</sup> One commercial probiotic proven to be beneficial for oral health is *Lactobacillus reuteri*. The antimicrobial activity of *L. reuteri* inhibits colonization by pathogenic microbes and interacts the inhibition directly with host cells.<sup>34</sup> *L. reuteri* also inhibits the growth of *C. albicans* and *E. faecalis* biofilms.<sup>35,36</sup> However, no studies have investigated the effect of the probiotic *L. reuteri* on the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atlA* genes in dental plaque biofilms found in patient's oral environment with fixed orthodontic appliances. By analyzing the virulence genes found in several pathogenic bacteria, we can hypothesize that the downregulation of these genes will lead to less biofilm production and healthier oral health conditions during the duration of fixed orthodontic appliances usage. Thus, to bridge the knowledge gap, the aim of this study was to determine the effect of consuming lozenges containing the probiotic *L. reuteri* on the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atlA* genes in biofilms from subjects using fixed orthodontic appliances.

## MATERIALS AND METHODS

### Sample Collection

Subjects undergoing fixed orthodontic therapy were enrolled in this open-label prospective, clinical trial. Ethical approval for the study was granted by the Institutional Review Board of the Faculty of Dentistry, Universitas Indonesia (approval number: 100,701,020). The inclusion criteria specified participants aged 18 years or older who had been undergoing orthodontic treatment with fixed

appliances for a minimum duration of 1 year and had not consumed probiotics or antibiotics in the preceding 3 months. The fixed orthodontic appliances used by the subjects are conventional metal braces fixed appliance. Exclusion criteria encompassed individuals with systemic conditions such as hypertension or diabetes, those on systemic medications including antihypertensives, analgesics, hormonal therapies, sedatives, or anti-seizure medications, as well as individuals presenting with severe periodontal disease or known allergies to probiotics.

The study utilized *L. reuteri* Prodentis lozenges, obtained from BioGaia (Stockholm, Sweden). Each lozenge (800 mg) contained a minimum of  $2 \times 10^8$  live *Limosilactobacillus reuteri* Prodentis (previously classified as *L. reuteri*). This food supplement, specifically formulated for oral health, included a proprietary combination of the *L. reuteri* DSM 17938 and *L. reuteri* ATCC PTA 5289 strains, which are recognized for their potential to support and maintain oral health.

To standardize oral hygiene practices, all participants were provided with a standardized toothbrush and toothpaste for use throughout the study period. Participants received oral hygiene instructions and were instructed to brush their teeth twice daily. Each participant was administered one probiotic lozenge containing *Limosilactobacillus reuteri* daily for 14 days, to be taken once per day after morning toothbrushing and prior to breakfast. Plaque samples were collected from participants on the day of enrolment, prior to the initiation of probiotic lozenge consumption, and again on the 14th day following the completion of the probiotic regimen.

Before sample collection, mandatory rapid antigen test for SARS-CoV-2 detection had to be taken by the subjects in response to the COVID-19 pandemic (as of 30 September 2020 when collecting the samples) and the test result had to be negative for the subject partaking in the study. In brief, the participants were instructed not to eat or drink anything 2 hours prior to collection of sample. Samples were collected using sterile cotton buds and swabbed from buccal/mesial/distal/lingual/occlusal surfaces of the index teeth of the subjects. The plaque samples were stored in sterile falcon tubes with 5 mL of phosphate-buffered saline (PBS).

Furthermore, clinical data, including the Oral Hygiene Index-Simplified score and the Papilla Bleeding Index, were recorded at each visit. Overall, 20 subjects had enrolled and fulfilled all requirements and inclusion criteria, as 20 subjects were proved to be sufficient to provide valid data as a pilot study.<sup>37,38</sup> Plaque samples from the subjects were continued unto the following downstream analysis.

### RNA Extraction, cDNA Synthesis, and Quantification

RNA from the sample was extracted using TRIzol reagent methodology as instructed by the manufacturer (Thermo Fisher, Waltham, MA). The extracted RNA was synthesized into cDNA using ReverTra Ace<sup>TM</sup> qPCR RT Master Mix with gDNA Remover (Toyobo, Japan). The mixture for cDNA synthesis is described in Table 1. The cDNA was then quantified using an Invitrogen<sup>TM</sup> Qubit 3.0 Fluorometer (Thermo Fisher Scientific, Waltham, MA). The cDNA was stored at  $-20^{\circ}\text{C}$  for storage of directly used for downstream analysis.

### qPCR Analysis

Amplification and detection by qPCR (Applied Biosystems, Waltham, MA) were performed. The components of the qPCR Master Mix are listed in Table 2. Using a specific kit, namely HOT FIREpol EvaGreen<sup>®</sup> qPCR Mix (Solis Biotek, Tartu, Estonia) which was activated by

21

16

1

2

**Table 1:** Reagent components for DNase I reaction solution

| Component           | Volume          |
|---------------------|-----------------|
| 4 × DN Master Mix   | 2 mL            |
| RNA template        | 0.5 pg – 0.5 mg |
| Nuclease-free water | X mL            |
| Total volume        | 8 mL            |

**Table 2:** Components of Master Mix RT-qPCR

| Component                               | Volume |
|-----------------------------------------|--------|
| 5 × HOT FIREPol EvaGreen® qPCR Mix Plus | 4 mL   |
| Primer Forward                          | 1 mL   |
| Primer Reverse                          | 1 mL   |
| DNA template                            | 2 mL   |
| NFW                                     | 12 mL  |
| Total                                   | 20 mL  |

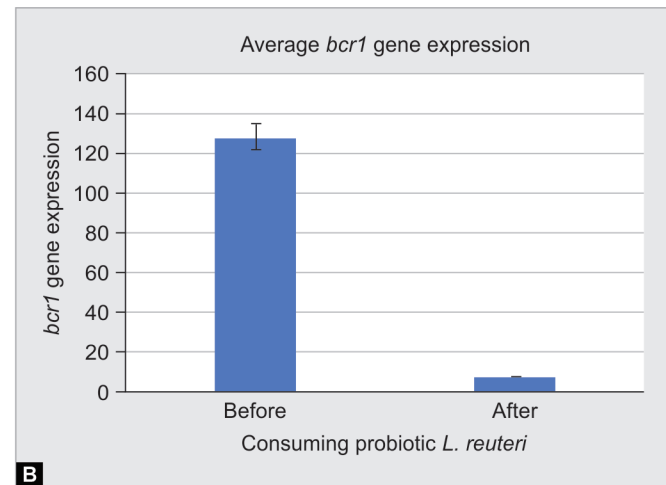
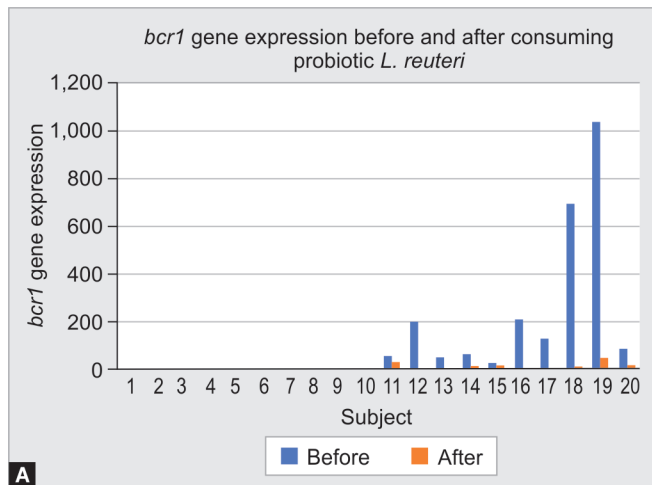
**Table 3:** Primer sequence for RT-qPCR

| Genes                                                        | Primer sequence                                                                               | Temperature and cycle settings                                                                                                                                                                                                         |
|--------------------------------------------------------------|-----------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>BCR1</i> <sup>39</sup>                                    | forward:<br>5'-CTTCAGCAGCTTCATTAACACCTA-3'<br>reverse:<br>5'-TCTTGGATCAGGTGTACTTTTCAA-3'      | Initial denaturation of 95°C for 5 minutes; 40 cycles of denaturation at 95°C for 1 minute and annealing at 58°C for 1 minute.                                                                                                         |
| <i>ACE2</i> <sup>40</sup>                                    | forward<br>5'-AGAATTGACCGTGTCCGTGAAG-3'<br>reverse:<br>5'-AATGGGTGAATAAATCCCTCCCTAA-3'        | Initial denaturation 95°C for 2 minutes; 40 cycles of denaturation at 95°C for 30 seconds and annealing at 60°C for 1 minute.                                                                                                          |
| Housekeeping gene<br><i>C. albicans: ACT1</i> <sup>41</sup>  | forward:<br>5'-TTTCATCTTCTGTATCAGAGGAAGTATT-3'<br>reverse:<br>5'-ATGGGATGAATCATCAACAAGAG-3'   | Initial denaturation 95°C for 10 minutes; 40 cycles of denaturing 95°C for 15 seconds and annealing 60°C for 1 minute.                                                                                                                 |
| <i>fadA</i> <sup>15</sup>                                    | forward:<br>5'-CAC AAG CTG ACG CTG CTA GA- 3'<br>reverse:<br>5'-TTA CCA GCT CTT AAA GCT TG-3' | Initial incubation for 4 minutes at 94°C followed by 30 cycles of denaturation at 94°C for 30 seconds, annealing at 55.8°C for 30 seconds, and elongation at 72°C for 40 seconds and the final elongation for 6 minutes. <sup>14</sup> |
| <i>aid1</i> <sup>14</sup>                                    | forward:<br>5'-TACAGGAG GTGCCGTAGCAG-3'<br>reverse:<br>5'-TTTTGTGAATTCT CCAGCTCCA-3'          | Initial incubation for 10 minutes at 95°C followed by 40 cycles of denaturation at 95°C for 15 seconds, annealing and elongation at 60°C for 1 minute. <sup>13</sup>                                                                   |
| Housekeeping gene<br><i>F. nucleatum: rpoB</i> <sup>42</sup> | forward:<br>5'-GGYTWYGAAGTNCGHGACGTDC-3'<br>reverse:<br>5'-TGACGYTGCATGTTBGMR CCCATMA-3'      | Initial incubation for 10 minutes at 95°C followed by 40 cycles of denaturation at 95°C for 15 seconds, annealing and elongation at 60°C for 1 minute.                                                                                 |
| <i>gelE</i> <sup>43</sup>                                    | forward:<br>5'-CGGAACATACTGCCGTTTGA-3'<br>reverse:<br>5'-TGGATTAGATGCACCCGAAAT-3'             | Initial denaturation at 95°C for 3 minutes, 40 cycles of denaturation at 95°C for 5 seconds, and annealing at 60°C for 30 seconds.                                                                                                     |
| <i>atlA</i> <sup>44</sup>                                    | forward:<br>5'-AATAATCAATCAGGAACGAATACG-3'<br>reverse:<br>5'-GCCACACTAACACCGAAT-3'            | Initial denaturation at 95°C for 2 minutes, 40 cycles of denaturation at 95°C for 15 seconds, and annealing at 60°C for 60 seconds.                                                                                                    |
| Housekeeping gene<br><i>E. faecalis: rpoA</i> <sup>44</sup>  | forward:<br>5'-GTGAAACCTGGTCGTGGCTA-3'<br>reverse:<br>5'-CGACGAACGGGTGTGTAGAT-3'              | Initial denaturation at 95°C for 2 minutes, 40 cycles of denaturation at 95°C for 15 seconds, and annealing at 60°C for 60 seconds.                                                                                                    |

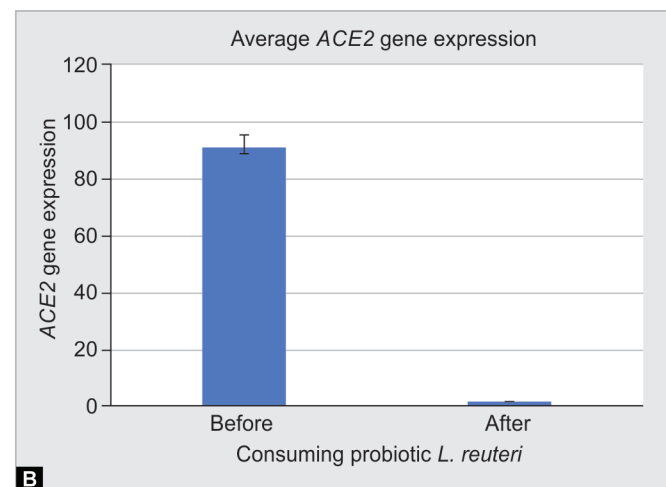
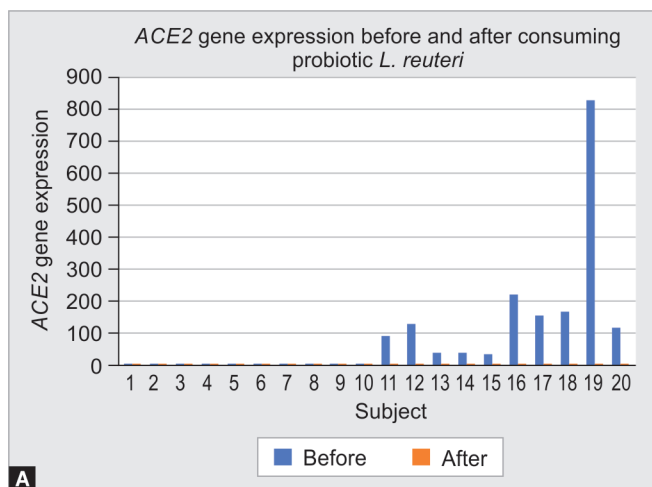
incubation at 95°C for 10 minutes. This was followed by 40 cycles of denaturation at 95°C for 10 seconds, annealing temperature at 60–65°C (Table 3), and elongation at 72°C for 20 seconds. For templates longer than 150 bp, the annealing and elongation times were extended to 30 seconds. Actin gene encoding as the housekeeping gene was used for normalization purposes. qPCR was performed on cDNA. qPCR was performed using the primers listed in Table 3.

## Data Analysis and Outcome Analysis

The data were analyzed using the Shapiro–Wilk normality test ( $p > 0.05$ ). For data with a normal distribution, a paired  $t$ -test was applied ( $p < 0.05$ ). The software used for the analysis is Statistical Package for the Social Sciences (SPSS) version 27 (IBM, Armonk, NY). The outcome analysis are the quantitative data presented from the RT-qPCR instrument. This data can then be correlated with previous study that also conducted such research to ensure the validity of this data.



**Figs 1A and B:** (A) A graph showing *bcr1* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *bcr1* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges



**Figs 2A and B:** (A) A graph showing *ACE2* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *ACE2* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges

## RESULTS

Based on the results of the qPCR test, the expression of *BCR1* (Fig. 1), *ACE2* (Fig. 2), *fdaA* (Fig. 3), *aid1* (Fig. 4), *gelE* (Fig. 5), and *atIA* (Fig. 6), on average, were decreased when comparing the day-0 prior to probiotic consumption and day-14 after the subjects consumed the probiotic *L. reuteri*.

As shown by the results of the Shapiro–Wilk normality test, all the data were normally distributed ( $p > 0.05$ ). The data were analyzed using a paired *t*-test, with a significance level of  $p < 0.05$ . The results of the paired *t*-test revealed a significant difference in the comparison of the *BCR1* and *ACE2* gene expression data. There was a significant difference ( $p < 0.05$ ) in the expression of *BCR1*, *ACE2*, *fdaA*, *aid1*, *gelE*, and *atIA* genes after consuming the probiotic *L. reuteri*.

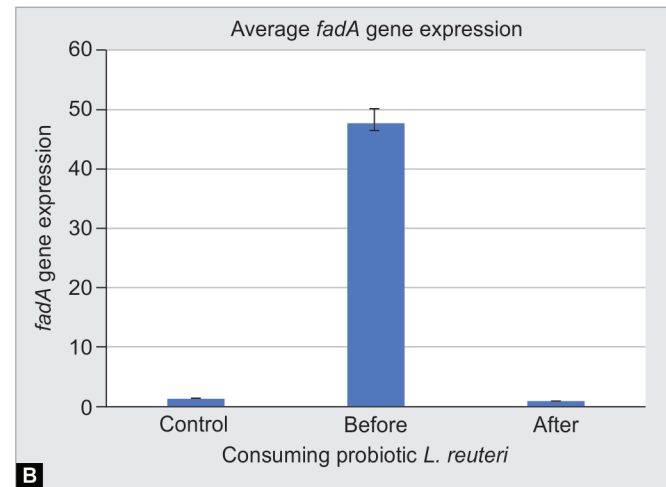
## DISCUSSION

The use of fixed orthodontic appliances often causes poor oral hygiene, thus facilitating microorganism accumulation and various

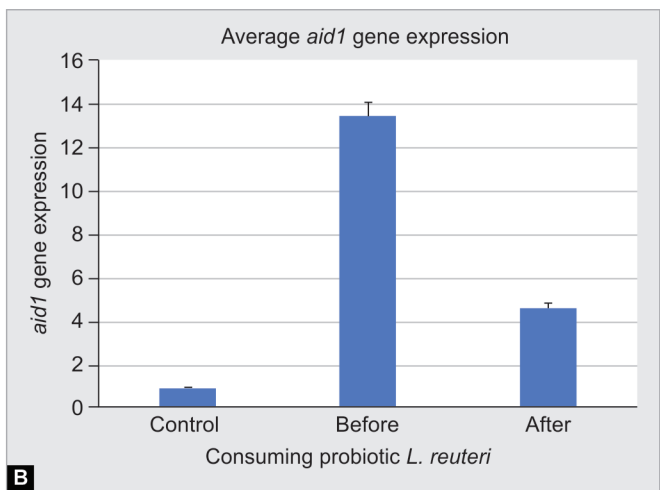
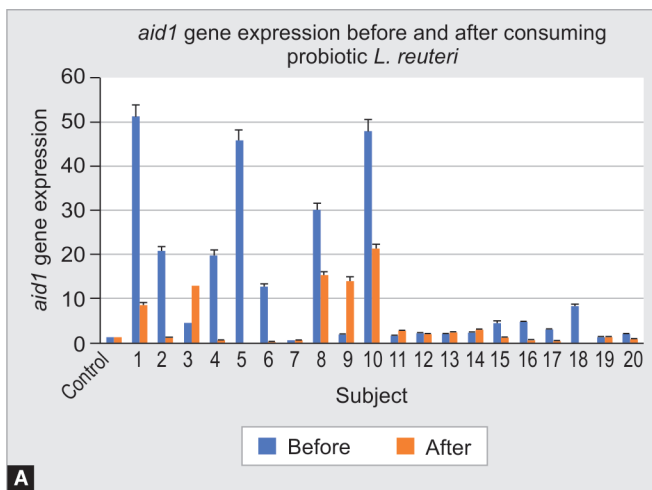
pathological conditions in the oral cavity, such as fungal infections.<sup>45</sup> A previous study revealed an increase in *Candida* in saliva after using fixed orthodontic appliances. The authors attributed this to the design of fixed orthodontic appliances, which creates a space for the retention of food waste.<sup>46</sup> Thus, patients must be instructed about good oral hygiene practices after orthodontic treatment.<sup>38</sup> Fixed orthodontic appliances also induce changes in buffer capacity, salivary flow rates, and acidity (pH), leading to plaque accumulation and an increase in caries and periodontal disease.<sup>47–49</sup> Based on this information, we attempted this study to prove the benefits of consuming probiotics lozenges as a supplement for patients using fixed orthodontic appliances.

Biofilm formation is an important virulence factor of *F. nucleatum* due to its higher resistance to host defense or antibacterial agents compared to planktonic cells.<sup>50</sup> Several studies detected increased numbers of *Porphyromonas gingivalis*, *F. nucleatum*, *P. intermedia*, and *Tannerella forsythia* after the use of fixed orthodontic appliances.<sup>15,51,52</sup> They also reported that *F. nucleatum* increased

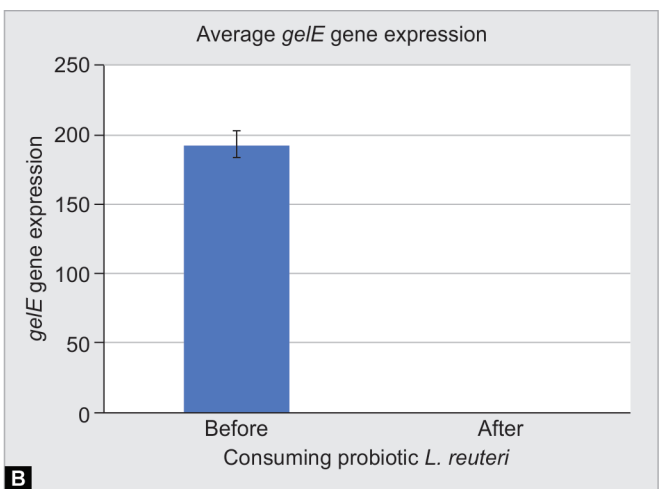
Probiotic Consumption Reduced Virulence Gene Expression from Fixed Orthodontic Plaque



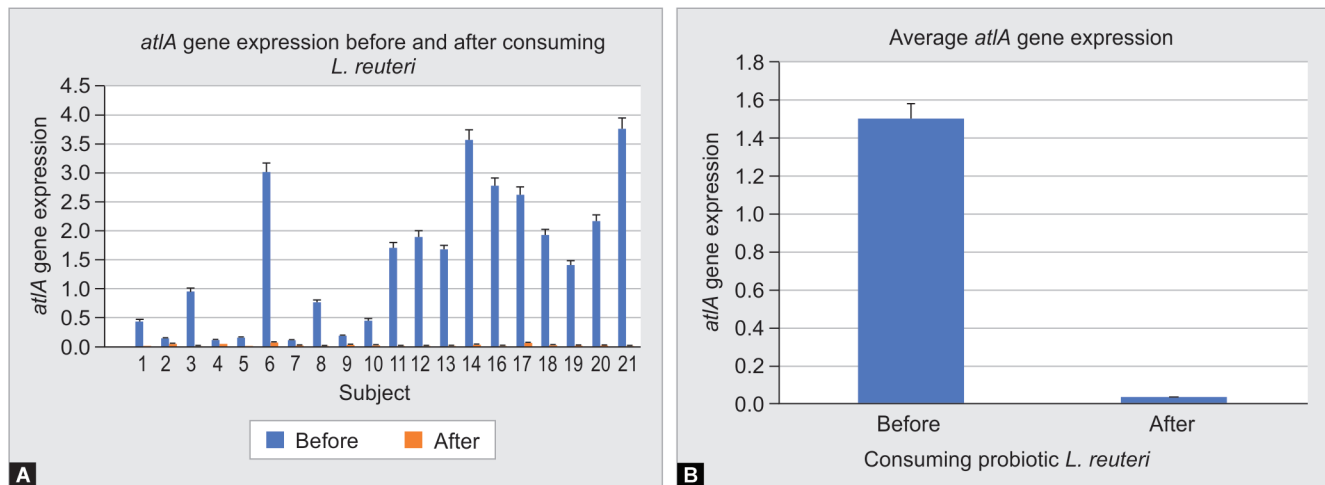
**Figs 3A and B:** (A) A graph showing *fadA* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *fadA* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges



**Figs 4A and B:** (A) A graph showing *aid1* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *aid1* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges



**Figs 5A and B:** (A) A graph showing *gelE* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *gelE* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges



**Figs 6A and B:** (A) A graph showing *atIA* gene expression in plaque samples ( $N = 20$ ) as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges; (B) A graph showing the average of *atIA* gene expression in plaque samples as assessed by the RT-qPCR method and the formation of *C. albicans* biofilms before and after consuming *L. reuteri* probiotic lozenges

the risk of periodontitis in orthodontic patients due to a conducive environment for anaerobic bacteria.<sup>15,51,52</sup> Biofilm formation is also a contributing factor to *E. faecalis* colonization and infection. Biofilms develop through various processes by which bacteria adhere to surfaces, decompose complex matrices, and develop into bacterial colonies, which adhere to surfaces.<sup>53</sup>

In this study, we used the qPCR method and  $2^{-\Delta\Delta CT}$  formula to calculate target gene expression. As shown by the results, the probiotic *L. reuteri* affected the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes and the formation of *C. albicans*, *F. nucleatum*, and *E. faecalis* biofilms. Based on the Shapiro–Wilk normality test, all the data were normally distributed, with  $p > 0.05$ . The paired *t*-test results revealed significant differences in the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes (all  $p < 0.05$ ).

Based on the results of this study, the probiotic *L. reuteri* significantly downregulated the transcription of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atIA* genes. In gene expression, the process of translating genetic information in the form of sequence of bases of DNA or RNA into proteins.<sup>54</sup> Through gene expression measurement, it is possible to assess qualitatively and quantitatively the effect of a treatment, such as the administration of a drug compound.<sup>55</sup> Gene expression in microorganisms is involved in regulating cell-cell communication, carbohydrate metabolism, adherence, and adaptation to the surrounding environment. A decrease in the expression of specific genes can reduce microorganism colonization and microorganism numbers.<sup>56</sup>

*BCR1*, a major gene transcription factor, produces an adhesin protein, which facilitates *C. albicans* attachment to mucosal surfaces, which is a critical stage of infection.<sup>39</sup> Deletion of *BCR1* eliminates *C. albicans* gene function, resulting in a decrease in biofilm formation.<sup>57</sup> This was supported by the results of the present study, which revealed a statistically significant decrease in *BCR1* gene expression after consuming the probiotic.

The expression of *ACE2* also decreased based on the results of the statistical tests. With deletion of *ACE2*, *C. albicans* is unable to form hyphal cells, and thus biofilm formation is inhibited.<sup>30</sup> An earlier in vitro study showed that probiotics have antifungal effects against *C. albicans* in the oral cavity. Regular use of probiotics helped to inhibit *Candida* biofilms and reduced *Candida* colonization in the oral cavity, thereby reducing the possibility of candidiasis infection.<sup>58</sup>

*FadA* protein is the main *F. nucleatum* virulence factor and mediates microbial attachment and colonization.<sup>8</sup> Based on the results of this study, the probiotic *L. reuteri* appears to influence the pathogenicity of *F. nucleatum* adhesion molecules and colonization and affect biofilm formation through decreased expression of the *fadA* gene.<sup>35</sup> Various *F. nucleatum* adhesins mediate adhesion and aggregation and function as coaggregation intermediaries in the formation and maturation of dental biofilms.<sup>59</sup> The interaction of *Fusobacterium* with other species is largely mediated by the adhesin genes *radD* and *aid1*.<sup>60</sup> The *aid1* gene plays a role in interspecies interactions, colonization, and aggregation of *F. nucleatum*. In a previous study, inactivation of the *aid1* gene decreased the ability of *F. nucleatum* to aggregate, especially with *Streptococcus* spp. or *E. faecalis*.<sup>14</sup> As shown in earlier studies, probiotics can affect the expression of genes involved in cell adhesion, quorum sensing (QS), virulence factors, and biofilm formation.<sup>61,62</sup>

The *E. faecalis gelE* gene has the ability to hydrolyse gelatine, collagen, fibrin, and other peptides.<sup>63</sup> Gene *gelE* is a virulence factor in infection formation through bacterial attachment and biofilm formation.<sup>22</sup> In *E. faecalis*, biofilm formation is regulated by QS, where *Fsr* regulates the expression of the *gelE* gene.<sup>64</sup> *Fsr* regulates the formation of *E. faecalis* biofilms through its product *gelE* and serine proteases.<sup>43</sup> QS is a molecular mechanism by which bacterial cells communicate with each other via signaling molecules in biofilms. If the protease encoded by a signaling factor is decreased, communication between bacteria and biofilm formation will be disrupted.<sup>62</sup> *GelE* can also activate *atIA*, which is responsible for eDNA release at the biofilm maturation stage.<sup>65</sup>

*AtIA* is involved in the hydrolysis of peptidoglycan, which plays an important role in separating cells division after replication.<sup>22</sup> *AtIA* plays a role in the biofilm maturation stage of *E. faecalis*, during which eDNA is released and contributes to biofilm attachment and stability, biofilm defects in primary attachment, and decreased biofilm production.<sup>20,23</sup> This study focused on the probiotic *L. reuteri*, which has ability to secrete antimicrobial substances and compete with oral pathogens for adhesion to mucosa. In addition, *L. reuteri* can adapt and change the pH of the surrounding environment, thereby inhibiting the growth of oral pathogens.<sup>66</sup> The antimicrobial substances secreted by *L. reuteri* are reuterin and

reutericycline.<sup>67</sup> Reuterin and reutericycline are broad-spectrum antimicrobial agents that are effective against Gram-positive and -negative bacteria, fungi, and protozoa by inhibiting microbial DNA synthesis.<sup>35,47</sup>

Many dental and oral health care products used daily now include probiotics. The use of probiotics is increasing due to their advantages over chemical agents, namely reducing the risk of antibiotic resistance.<sup>68</sup> Probiotics work by modulating the immune system, producing antimicrobial substances, and inhibiting certain pathogenic organisms by interfering with adhesion, colonization, and biofilm formation. They inhibit the growth of pathogens via the production of various substances, such as lactic acid and acetic acid, which penetrate the bacterial cell membrane and lower the cytoplasmic pH of pathogenic bacteria. Hydrogen peroxide and bacteriocin can destroy the cell membrane of pathogenic bacteria and inhibit the synthesis of pathogenic DNA.<sup>32,33,35,69</sup> Based on the results of this study, 2 weeks of daily consumption of the probiotic *L. reuteri* affected the process of biofilm formation by downregulating the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atlA* genes, which function as adherent regulators and regulators of hyphae formation in biofilm formation. Many previous studies demonstrated that the addition of probiotics to dental and oral health care products. Probiotic can reduce pathogenic microorganisms in plaque samples from patients using fixed orthodontic appliances.<sup>47,68,70-72</sup> Therefore, it can be stated that the probiotic *L. reuteri* has good ability as an additional treatment for dental and oral health in patients using fixed orthodontic appliances.

The limitation of this study is the small sample size and the fact that the sampling had to be done during COVID-19 pandemic. Although the sample size is small, the result of this study can still provide concise and significant result. In the future, there should be larger sample size for conducting this research so the results can more accurately represent the actual population. Daily consumption of probiotic lozenges duration can also be increased for more precise and accurate results. On the other hand, consumption of probiotic lozenges research can also be conducted for other aspect of oral health diseases to promote the functionality and health-inducing aspect of probiotic lozenges, such as antiinflammation.

## CONCLUSION

Within the limitation of this study, it can be concluded that the probiotic *L. reuteri* influences the expression of *BCR1*, *ACE2*, *fadA*, *aid1*, *gelE*, and *atlA* genes in biofilm formation. By reducing the expression of those genes, the probiotic *L. reuteri* can reduce biofilm formation, such as dental plaque, in patients using fixed orthodontic appliances.

## Clinical Significance

Consumption of probiotic lozenges were confirmed to reduce bacterial and fungal biofilm, as proven by the reduction of virulence gene expression, hence, helping increasing oral health of consumer. The results of this study help clinicians provide probiotic lozenges for patients to promote and maintain their oral health.

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