Study of Porphyromonas gingivalis in periodontal diseases: A systematic review and meta-analysis

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Abstract

Background: The mouth cavity hosts various types of anaerobic bacteria including Porphyromonas gingivalis, which causes periodontal inflammatory diseases. P. gingivalis is a gram-negative oral anaerobe and is considered as a main etiological factor in periodontal diseases. Several studies have reported a relationship between P. gingivalis in individuals with periodontal diseases and a critical role of this bacterium in the pathogenesis of periodontal diseases. The present study aimed at estimating this probability using a meta-analysis.

Methods: We searched several databases including PubMed, Scopus, Google Scholar, and Web of Science to identify case-control studies addressing the relationship between P. gingivalis with periodontal diseases. A total of 49 reports published from different countries from 1993 to 2014 were included in this study. I² (heterogeneity index) statistics were calculated to examine heterogeneity. Data were analyzed using STATA Version 11.

Results: After a detailed analysis of the selected articles, 49 case-control studies with 5924 individuals fulfilled the inclusion criteria for the meta-analysis. The healthy controls included 2600 healthy individuals with a Mean±SD age of 36.56±7.45 years. The periodontal diseases group included 3356 patients with a mean age of 43.62±8.35 years. There was a statistically significant difference between P. gingivalis in periodontal patients and healthy controls; 9.24 (95% CI: 5.78 to 14.77; P = 0.000). In the other word, there was a significant relationship between the presence of P. gingivalis and periodontal diseases.

Conclusion: Analyzing the results of the present study, we found a strong association between the presence of P. gingivalis and periodontal diseases. This result suggests that another research is needed to further assess this subject.

Keywords: Porphyromonas gingivalis, Periodontal Diseases, Chronic Periodontitis, Aggressive Periodontitis, Gingivitis

Introduction

Periodontal diseases are complicated oral diseases, which are specified by bacterial-induced inflammatory destruction of tooth-supporting tissues (1). Periodontal diseases can be described as one of the predominant polymicrobial infections of humans, which can advance and lead to gum retrogression, soft tissue harm, weakness of the bone, eventual osteoporosis and tooth loss (severe periodontitis). Periodontal disease have many risk factors including smoking and diabetes, moreover, several bacteria have been connected to the intensity and progress of periodontitis (2, 3).

The oral cavity is a source of different microorganisms that cause a class of infections and inflammation inside the cavity (4). So far, more than 700 bacterial taxa have been identified in samples taken from oral cavities (2). Evidence for periodontal etiology relies on the performance of several criteria described by Socransky (5).

Of the bacteria believed to be pathogenic in periodontal disease, P. gingivalis has been extensively studied due to its unique ability to evade the immune response (6). P. gingivalis is a gram-negative oral anaerobe and considered as a main etiological factor in periodontal diseases by produc-
Porphyromonas gingivalis in periodontal diseases

ing a number of virulence factors and extracellular prote-
ases such as lipopolysaccharide, fimbia, gingipain etc., re-
sulting in destruction of periodontal tissues (7–11). The
various surface components of P. gingivalis enable the bac-
terium to interact with the external medium and simplify its
growth, nutrient gain, colonization, and formation of a bio-
film that protects it against the host’s defense (12, 13). In
addition to being painful, persistent dental disease is linked
to diabetes, heart disease, high blood pressure, and MS in
later years of life; therefore, extensive studies have been
conducted to control the bacteria causing dental diseases
(14).

The pathogenicity of P. gingivalis has been investigated
in a variety of experimental animal models such as rat,
mouse, rabbit, drosophila, and cell models, showing com-
plicated mechanisms of P. gingivalis-host interplay in the
expansion of periodontal diseases (15–19).

Although many studies aimed to specify the macrobiotic
dependents of specific disease types and the extent of peri-
donatal destruction, there is yet no quantitative data on the
levels of P. gingivalis in periodontal diseases. To authenti-
cate the studies, performing a meta-analysis seemed neces-
sary. Thus, this study aimed at evaluating the prevalence of
P. gingivalis in patients with periodontal diseases.

Methods

Search Strategies

A database was built for the prevalence of P. gingivalis
periodontal diseases from 1993 to 2014 using PubMed,
Web of Science, Google scholar Medline, Embase, the
Cochrane Library, and Scopus databases. The search was
restricted to original articles published in English that pre-
vented the prevalence of P. gingivalis among patients with
periodontal diseases. The following keywords were used
from medical subject headings, titles, or abstracts were
with the help of Boolean operators (and, or): P. gingival-
chronic periodontitis, aggressive periodontitis, and
gingivitis. We also searched bibliographies of the retrieved
articles for additional references. The titles from the search
results were examined closely and determined to be suit-
able for potential inclusion into the study. In addition, the
references from the selected articles were examined as a
further search tool. Relevant trials noted in the reference
lists of each selected article were also evaluated for inclu-
sion. All papers whose keywords were present in their titles
or abstracts were used in the initial list and other unrelated
articles were eliminated.

Inclusion and Exclusion Criteria

All original articles presenting case-control studies on the
prevalence of P. gingivalis in periodontal diseases were
considered. The selection of articles for review was com-
pleted based on 3 stages: titles, abstracts, and full texts.
When necessary, authors were contacted for additional in-
formation. Studies were excluded if they presented insuffi-
cient data, if they were not epidemiologic studies, and if
they focused on the prevalence of P. gingivalis in diseases
other than periodontal diseases. Review articles, congress
abstracts, studies reported in languages other than English
or Persian, meta-analyses or systematic reviews, and dupli-
cate publication of the same study were also excluded. The
STROBE (strengthening the reporting of observational
studies in epidemiology) statement was used for quality
control of the studies. We assessed the quality of studies
according to variables related to the study objectives, char-
acteristics of the study population, clearly explained inclu-
sion/exclusion criteria, data collection method, as well as
the validity, explicit findings, and appropriate data analysis
methods of the studies.

Data Extraction

For all studies, the following data were extracted: first
author, year of publication, location, sample size, sample
age, P. gingivalis screening method, and sample specimens,
percentage of P. gingivalis in patients and healthy individ-
uals. Abstracts and full articles were reviewed indepen-
dently by 2 of the authors, and if results were discord-
ant, papers were reviewed jointly until the differences were
resolved.

Data Synthesis and Analysis

Studies were combined based on the sample size, mean
and standard deviation. The difference between the average
variance of the normal distribution was calculated using the
formula of 2 integrated variance. To assess the heterogen-
ity of the studies, Cochran test and the I² (heterogeneity
index) were used. Due to the significant heterogeneity in the
studies, random effects model was used. The findings are
described in forest plots (the point estimations and their
95% CI). To examine publication bias, Begg plot and re-
ductions method were used. P value less than 5% was con-
sidered as a significant heterogeneity test. Sensitivity anal-
yses were prespecified. Statistical analyses were performed
using STATA version 11.

Results

Our initial search strategy yielded 172 potential articles
for inclusion; in a secondary screening, 48 of them were
excluded based on title and abstract evaluation, and 124
were retained for detailed full text evaluation. We excluded
another 75 articles (9 review articles, 18 articles with other
diseases, 13 for lack of enough information, 23 articles with
percentage of P. gingivalis only in patients group, and 12
duplicates). After a detailed analysis of the selected articles,
49 case- control studies with 5924 individuals (3356 pa-
tients and 2600 healthy individuals) fulfilled the inclusion
criteria for the meta-analysis (Fig. 1). The characteristics of
the 49 trials and the quality scores included in the meta-
analysis are summarized in Table 1.

The healthy controls comprised 2600 healthy individuals,
with the age range of 14 to 67 years and a mean age of
36.56±7.45 years. The periodontal diseases group included
3356 patients with periodontal diseases, ranging from 14 to
59 years, and with a mean age of 43.62±8.35 years.

In the present study, a statistically significant difference
was found between P. gingivalis in periodontal patients and
healthy controls; 9.24 (95% CI: 5.78 to 14.77; p<0.001)
(Fig. 2). In the other word, on analyzing the results of the
present study, a strong association was found between the

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presence of *P. gingivalis* and periodontal diseases (Fig. 2).

According to publication bias figure, the effect of bias in these studies was not significant. In fact, most studies were located inside the Funnel Plot, and thus the results of most relevant studies, considering the title, were included into the analysis (p > 0.005) (Fig. 3).

**Discussion**

It is widely accepted that the etiology of periodontal diseases is polymicrobial in nature. Worsening or improvement of periodontal situation goes along by a change in the bacterial composition of subgingival plaque (20). It has, therefore, been suggested that microbial testing be used to diagnose and optimize periodontal therapy and assess its outcome. However, this strategy may be confusing as the beginning and the progress of periodontal diseases are impressed by interaction of myriad genetic, environmental, host, and microbial factors (20-23). Furthermore, molecular studies reveal an unexpectedly high diversity of microorganisms and progression of disease remains to be investigated. Nevertheless, current microbiological testing

**Table 1. Study characteristics**

<table>
<thead>
<tr>
<th>First author (Reference)</th>
<th>Country</th>
<th>Case</th>
<th>Control</th>
<th>Mean age</th>
<th>Case Control</th>
<th>Percent Low</th>
<th>Percent High</th>
<th>Type of disease</th>
<th>Sample Specimens</th>
<th>Methods of Cupper Measurement</th>
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<tr>
<td>Kim J et al. (2017)</td>
<td>Japan</td>
<td>17</td>
<td>58</td>
<td>52.4±11</td>
<td>49.1±10.2</td>
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<td>0.32</td>
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<td>salivary plaque</td>
<td>PCR method</td>
</tr>
<tr>
<td>M. Rafiei, et al. (2017)</td>
<td>Iran</td>
<td>39</td>
<td>40</td>
<td>52.11±11</td>
<td>49.1±10.2</td>
<td>1.88</td>
<td>13.29</td>
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<td>salivary plaque</td>
<td>PCR method</td>
</tr>
<tr>
<td>Araújo C (2007)</td>
<td>Brazil</td>
<td>50</td>
<td>50</td>
<td>45.1±8.7</td>
<td>32.3±18.9</td>
<td>0.68</td>
<td>3.56</td>
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<td>salivary plaque</td>
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<tr>
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<td>20</td>
<td>10</td>
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<td>28.7±3.2</td>
<td>2.95</td>
<td>1587.72</td>
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<td>5.06</td>
<td>87.12</td>
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<td>93.89</td>
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<td>subgingival plaque</td>
<td>PCR method</td>
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<td>36.6±15.3</td>
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<td>0.30</td>
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<td>subgingival plaque</td>
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</tr>
<tr>
<td>Zhou T (2012)</td>
<td>Japan</td>
<td>150</td>
<td>60</td>
<td>54.6±1.2</td>
<td>52.9±1.4</td>
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<td>6.33</td>
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<td>subgingival plaque</td>
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</tr>
<tr>
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<td>93.89</td>
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<td>subgingival plaque</td>
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<td>gingival crevicular fluid</td>
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<td>53.6 ± 10</td>
<td>54.8 ± 10</td>
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<tr>
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<td>29</td>
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Porphyromonas gingivalis in periodontal diseases

The aim of this study was to evaluate the association between the presence of *P. gingivalis* and periodontal diseases. *P. gingivalis* has been known to be a risk factor for periodontal diseases although its exact roles in the initiation and progression of the oral diseases remain unclear (15, 24).

In the present study, a significantly strong positive correlation was found between the presence of *P. gingivalis* and periodontal diseases. Published data suggests that the flora associated to chronic periodontal diseases is dominated by

Fig. 1. The flow diagram of studies identified the systematic review and meta-analysis

Fig. 2. Meta-analysis of the association of *P. gingivalis* with periodontal diseases. Square represents effect estimate of individual studies with their 95% confidence intervals with size of squares proportional to the weight assigned to the study in the meta-analysis. In this chart, studies are stored in order of the year of publication and author’s names, based on a random effects model.

Mostly involves the classic doubtful oral pathogens (20).

172 of the studies were identified through Google scholar, PubMed and Scopus database searching

76 articles were excluded
- Review articles: 9
- Articles with other diseases: 18
- Lack of enough information: 13
- Articles with percentage of *P. gingivalis* only in patients group: 23
- Duplicates: 12

Abstract evaluation
N= 139

Full text evaluation
n=124

Articles included
N= 49

Excluded:
Titles not relevant, n=33

Excluded:
Topic not relevant, n=15

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the presence of Gram-negative anaerobic bacteria, and especially P. gingivalis (25). Slots and Ting described a synergistic association of P. gingivalis in presentations with evolutive lesions (26). Van Winkelhoff et al. concluded that P. gingivalis was the marker of a destructive lesion (27). Authors of previous studies reported similar results. The authors of various studies on P. gingivalis have reported that these pathogens are able to pollute soft tissues and flee the surgical debridement of periodontal lesions (28, 29).

Many epidemiological studies report a positive association between the presence of P. gingivalis and periodontal diseases (7, 25, 30-36), whereas in some studies, no association was found between the presence of P. gingivalis and periodontal diseases (20, 37-41). This has also been shown by Kumar et al. (42). The fact that all types of bacteria studied could be detected, even in healthy controls, might indicate that the presence of periodontal pathogens does not necessarily lead to periodontal diseases (1). However, these species show just a small percentage of whole bacteria, and the open-ended approach of their study may not be geared to indicate an association of this species with the disease (20). In another study, Kumar et al. demonstrated a significant association of P. gingivalis with chronic periodontitis using PCR amplification of 16S rRNA genes (43).

Some studies have reported a strong association between the presence of P. gingivalis and periodontitis, but did not find any association between the presence of P. gingivalis and gingivitis (1, 12, 44, 45). Although a number of putative bacteria are considered to be associated with chronic periodontitis, it has become clear that other factors are involved in the etiology of several types of periodontitis. In the other word, P. gingivalis is one of the risk factors responsible for periodontitis.

P. gingivalis is one of the bacteria that form the classic ‘red complex’ described by Socransky et al. (46). It is the bacteria most frequently found in patients with periodontal disease (12). Wara-aswapati et al. (47) found that the mean age of patients was higher than that of the healthy participants. P. gingivalis has been reported to be related to adult periodontitis (48, 49). In a study by Liu et al (15), they analyzed the correlation of patients’ age and occurrence of P. gingivalis and found that the age of P. gingivalis positive and negative was statistically different, implying that the prevalence of P. gingivalis may increase as the patients’ age increase.

The association of certain putative pathogens with periodontal diseases shown in many studies may be explained in part by deeper pockets in these patients. In the present study, the association between probing severely and the occurrence of periodontal disease has not studied because most previous studies conducted on the association of particular bacteria with periodontitis did not test the influence of probing depth. Some studies found that the search depth had a much greater impact on the species than did the diagnosis. In study of Riep et al. (20), the prevalence of P. gingivalis was highly associated (p< 0.001) with pocket depth. Ali et al. (50) studied the existence of P. gingivalis in very deep pockets (≥ 6 mm) and deep pockets (4–5 mm) of 36 Romanian patients presenting with chronic periodontitis. P. gingivalis was recognized in 75.8% of the patients and 63.6% of the sampled sites.

Listgarten and Loomer (51) also questioned whether microbial identification should be considered as a strategy in managing this disease. They found no strong evidence supporting the benefit of microbial testing, partly due to a lack of standardization among diagnostic methods.

In summary, on analyzing the results of the present study, a strong association was found between the presence of P. gingivalis and periodontal diseases. Furthermore, the results of the present study indicated that P. gingivalis is one of the risk factors responsible for periodontitis. This result suggests that further research is needed to investigate their pathogenicity.

Acknowledgments

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Conflict of Interests

The authors declare that they have no competing interests.

References


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