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REVIEW ARTICLE

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The role of oral dysbiosis in pregnancy complications: a systematic review and meta-analysis of preterm birth

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ABSTRACT

Objective: To systematically review the association between oral dysbiosis and pregnancy-related complications and to quantitatively assess differences in oral microbial alpha diversity between preterm birth (PTB) and term birth (TB).

Material and methods: A systematic search was conducted in July 2025 following PRISMA 2020 guidelines and registered in PROSPERO. Studies published between 2015 and 2025 assessing oral microbiota composition, alpha/beta diversity, or taxa abundance in relation to preeclampsia, gestational diabetes mellitus, preterm birth, low birth weight, mental health disorders, or pregnancy loss were included. Due to heterogeneity in study design, microbiome metrics, and outcome definitions, meta-analysis was restricted to studies comparing Shannon alpha diversity between PTB and TB. Study quality was assessed using the Newcastle–Ottawa Scale and the Joanna Briggs Institute checklist.

Results: Twenty-one studies met the inclusion criteria, including cohort, case–control, and cross-sectional designs; four were included in the meta-analysis. Pregnancy complications were commonly associated with altered oral microbial profiles, characterized by reduced alpha diversity, changes in beta diversity, and increased abundance of genera such as Prevotella, Veillonella, and Porphyromonas. The meta-analysis suggested a directional trend toward altered alpha diversity in adverse pregnancy outcomes.

Conclusions: Overall, the findings support a potential association between oral dysbiosis and pregnancy-related complications; however, this evidence is limited by the small scale and heterogeneity of the available studies. These results highlight the oral microbiome as a biologically plausible contributor to adverse maternal and neonatal outcomes and a promising focus for future mechanistic and translational research.

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Oral dysbiosis; pregnancy complications; oral microbiota; preeclampsia; gestational diabetes; preterm birth

Introduction

Oral health constitutes a relevant component of general health, and its maintenance acquires significant importance during pregnancy, a period of vulnerability due to the physiological changes experienced by women. The lack of oral healthcare in pregnant women can have negative consequences for both the mother and the newborn [1]. Oral health should not be considered an isolated aspect during pregnancy; rather, it is closely related to maternal systemic health and, consequently, can influence the well-being of the infant [2]. The multiple physiological changes occurring in a woman's body during gestation can alter oral homoeostasis, suggesting a bidirectional relationship between oral and systemic health [3].

In this context, the oral microbiota is defined as a complex and dynamic microbial ecosystem, whose composition varies among individuals based on external factors such as diet, hygiene habits, or tobacco consumption. Maintaining a balanced oral microbiome is crucial for preserving systemic health, whereas its alteration, known as dysbiosis, can promote the development of diseases and complications [4]. Oral

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dysbiosis is characterised as an imbalance or alteration in the composition and functionality of the oral cavity's microbial community, leading to a loss of homoeostasis and the onset of both local and systemic diseases. Under healthy conditions, the oral microbiota comprises a diverse and stable community of bacteria, fungi, archaea, and viruses that coexist in equilibrium, thereby enhancing protection against pathogens, regulating immune responses, and maintaining oral tissues. Conversely, oral dysbiosis contributes to a loss of diversity, an increase in pathogenic microorganisms, and an alteration of metabolic functions, which triggers inflammatory phenomena and diseases [5].

To assess oral dysbiosis, microbiological parameters such as alpha diversity—which quantify the richness and evenness of species within an individual sample—and beta diversity—which evaluates differences in microbial composition between individuals—are commonly used. A decrease in alpha diversity is associated with a higher risk of disease, while an increase in beta diversity reflects greater heterogeneity among individuals, which in turn is linked to inflammatory processes or immune dysfunctions. Techniques such as 16S rRNA sequencing and metagenomic analysis allow for the examination of the abundance of specific taxa and the changes occurring in microbial metabolic functions. The concept of dysbiosis can be approached from both a host-centred perspective and a microbial perspective, considering the overgrowth of pathobionts and the loss of beneficial microorganisms. Most of the studies included in this systematic review define dysbiosis based on changes in alpha and beta diversity, as well as the relative abundance of certain bacterial species [6].

Among the different ecological measures, the Shannon diversity index is one of the most widely used to evaluate alpha diversity, since it accounts for both richness and evenness of species. Because of its frequent application across studies on oral microbiota in pregnancy, this index was chosen as the main outcome for the quantitative synthesis [7].

The implications of the oral microbiota are not limited to oral diseases; it has also been associated with pathologies and complications in distant organs, particularly during pregnancy [5]. Among the most significant complications is gestational diabetes mellitus (GDM), which represents the most common metabolic disorder during pregnancy. GDM is characterised by the onset of glucose intolerance and is associated with risks for both the mother and the foetus. Diagnosis can be performed using either a one-step or two-step approach: in the one-step method, all pregnant women undergo a 75-gram oral glucose tolerance test (OGTT) over 2 hours, with GDM diagnosed if one or more values exceed the established criteria; in the two-step approach, an initial screening test is performed, and if positive, a 100-gram OGTT over 3 hours is conducted, with GDM diagnosed if two or more values are abnormal. Maternal hyperglycaemia leads to foetal hyperinsulinemia, resulting in increased foetal growth, a higher risk of childhood obesity and metabolic problems, and an increased risk of type 2 diabetes in the mother [8].

Another major complication is preeclampsia, a hypertensive disorder affecting 2–3% of pregnant women, which manifests as elevated blood pressure after the 20th week of gestation, accompanied by damage to target organs such as the brain, liver, and platelets. Diagnosis is based on diastolic blood pressure values ≥90 mmHg or systolic values ≥140 mmHg, together with significant proteinuria. Preeclampsia is classified according to its severity and time of onset. Prevention includes the administration of aspirin, vitamins, and folic acid during the first trimester, and treatment involves the use of drugs such as hydralazine, labetalol, and nifedipine [9].

Preterm birth (PTB) is defined as delivery before 37 weeks of gestation and remains the leading cause of neonatal mortality, being associated with significant long-term physical, neurological, and socioeconomic sequelae. The highest incidence of prematurity is observed in South Asia and Sub-Saharan Africa, highlighting the need to improve data quality and to implement evidence-based prevention and care strategies, particularly in countries with the highest rates of preterm birth. Early identification of women at risk and specialised care are essential to reduce the morbidity and mortality associated with preterm birth [10].

Mental health problems during pregnancy, especially depression and anxiety, are also common and can affect any woman, regardless of her previous history. Factors such as a history of psychiatric illness, discontinuation of psychotropic medications, previous miscarriages, relationship problems, stress, and adverse social conditions increase the risk. Maternal depression during pregnancy is associated with low birth weight and other negative effects on the baby's development. Social support, mental health education, and access to interventions such as therapy, exercise, and meditation are fundamental for prevention and treatment [11].

Pregnancy is not a state of immunosuppression, but rather a unique and modulated immunological condition. Pregnancy involves distinct immunological phases: an initial pro-inflammatory phase, a subsequent anti-inflammatory phase, and a final pro-inflammatory phase. This dynamic regulation allows for both protection against infections and the immunological tolerance necessary for successful gestation [12]. Overall, the evidence suggests that oral dysbiosis may play a significant role in the onset and development of these obstetric complications through inflammatory, immunological, and metabolic mechanisms.

The aim of this systematic review and meta-analysis is to analyse the role of oral dysbiosis in the occurrence of complications during pregnancy, with particular emphasis on alpha diversity measured through the Shannon index, as well as to explore underlying mechanisms and the potential clinical implications for prevention and management.

Materials and methods

Protocol and registration

This systematic review was conducted in accordance with the PRISMA 2020 guidelines, an acronym for 'Preferred Reporting Items for Systematic Reviews and Meta-Analyses' [13]. Furthermore, the review was registered in the PROSPERO database (International Prospective Register of Systematic Reviews) under registration number CRD420251110788.

Eligibility criteria

Various inclusion and exclusion criteria were applied in the preparation of this systematic review. Articles published between 2015 and 2025 were included, as well as those reporting information on the influence of oral dysbiosis during pregnancy, without restrictions regarding age or geographical context, to obtain a comprehensive overview of the relationship between these entities.

With respect to pregnancy, several clinical aspects specific to this stage were considered, including changes in oral microbial composition, the association of oral dysbiosis with the onset of preeclampsia, gestational diabetes, immune regulation, mental health, preterm birth, low birth weight, and even pregnancy loss.

Regarding the oral microbiota, for the term 'oral dysbiosis', studies were considered if they evaluated and analysed both changes in microbial diversity (alpha and beta diversity) and the relative abundance of specific taxa. Observational studies (cross-sectional, case-control, and cohort studies) and clinical trials were included, while reviews and pilot studies were excluded.

Conversely, studies that exclusively analysed dysbiosis of the intestinal or vaginal microbiota were excluded, as were articles in which the evaluated patients were not pregnant. Additionally, articles that did not meet the inclusion criteria or did not specify the diagnostic method employed were also excluded.

The primary outcomes were differences in the composition of the oral microbiota between pregnant women with or without preeclampsia, gestational diabetes, or preterm birth. When available, effect measures such as odds ratios, confidence intervals, and *p*-values were considered.

The PICO model was followed to establish the inclusion criteria: population/problem (*P*): pregnant women; intervention (I): presence of oral dysbiosis; comparison/control (C): pregnant women in healthy conditions; outcome (O): influence of oral dysbiosis on the onset or progression of preeclampsia, gestational diabetes, preterm birth, mental health, and immune regulation. Therefore, the resulting PICO question was: Does the presence of oral dysbiosis influence the occurrence of complications during pregnancy?

Information sources and search strategy

To conduct the article search, PubMed (MEDLINE), SciELO, The Cochrane Library, and Scopus were selected as the databases. This procedure was carried out on July 14, 2025, and articles providing information on the influence of oral dysbiosis on the occurrence of complications during pregnancy were included.

The Medical Subject Headings (MeSH) thesaurus was used to obtain the appropriate search terms. The terms related to 'oral dysbiosis' included: 'dysbiosis,' 'microbial imbalance,' 'oral microbiota,' 'oral microbiome,' and 'oral bacteria.' In contrast, the terms referring to 'pregnancy' were: 'pregnancy,' 'gestation,' 'pregnant woman,' 'maternal,' 'prenatal,' and 'perinatal,' while the terms associated with 'complications during pregnancy' were: 'preterm birth,' 'premature birth,' 'low birth weight,' 'pregnancy outcome,' 'preeclampsia,' 'pregnancy loss,' 'miscarriage,' and 'adverse pregnancy outcomes.'

The Boolean operators 'AND' and 'OR' were used to combine the terms. The search strategy employed was as follows: ('dysbiosis' [MeSH Terms] OR 'microbial imbalance' [MeSH Terms] OR 'oral microbiota' [MeSH Terms] OR 'oral microbiome' OR 'oral bacteria') AND ('pregnancy' [MeSH Terms] OR 'gestation' OR 'pregnant woman' OR 'maternal' [MeSH Terms] OR 'prenatal' OR 'perinatal') AND ('preterm birth' [MeSH Terms] OR 'premature birth' [MeSH Terms] OR 'low birth weight' OR 'pregnancy outcomes' [MeSH Terms] OR 'preeclampsia' [MeSH Terms] OR 'pregnancy loss' OR 'miscarriage' OR 'adverse pregnancy outcomes').

The following limits were applied: publication date (between 2015 and 2025), language (English or Spanish), and study type (original articles evaluating the influence of oral dysbiosis on the occurrence of complications during pregnancy).

In total, 1,105 references were identified from four databases: 431 from PubMed, 627 from Scopus, 44 from The Cochrane Library and 3 from Scielo.

Study selection

After completing the search, the identified studies were imported into the EndNote™ (Clarivate Analytics) reference manager, where duplicates were removed. Subsequently, an initial screening phase was conducted by reviewing the titles and abstracts, excluding studies that did not meet the proposed inclusion criteria. Finally, the selected articles were assessed in full text to determine their eligibility. This process was performed independently by two reviewers (P.G.-R. and F.J.R.-L.).

Data extraction

To conduct a comprehensive analysis of the selected studies, the following categories were considered for each: author and year of publication, type of study included, number and age of participants, characteristics of the oral microbiota analysed, and the conclusions drawn. Data were independently extracted by two reviewers (P.G.-R. and F.J.R.-L.) using a standardised form.

Quality analysis

This systematic review comprises seven cohort studies, eight case-control studies, and four cross-sectional studies. The Newcastle-Ottawa Scale (NOS) [14] and the Joanna Briggs Institute (JBI) [15] guidelines were used to conduct the quality assessment. The former is applied to evaluate the quality of case-control and cohort studies, the latter assesses cross-sectional studies, and a third tool is used for experimental studies.

The Newcastle-Ottawa Scale [14] was used to assess the risk of bias in case-control and cohort studies. This tool evaluates three domains -selection, comparability and exposure (or outcome in cohort studies)- with studies receiving up to nine stars in total. Based on the number of stars awarded, studies were classified as having a low (7 to 9 stars), moderate (4 to 6 stars), or high (0 to 3 stars) risk of bias.

On the other hand, the JBI Critical Appraisal Tool [15] was used to assess the quality of the cross-sectional studies included in this systematic review. This instrument assesses eight criteria related to study design, conduct, and analysis, with each criterion rated as 'yes', 'no', 'unclear', or 'not applicable'. According to the number of criteria met, studies were categorised as having a low (6 to 8 criteria), moderate (4 to 5 criteria), or high (0 to 3 criteria) risk of bias.

To be included in this systematic review, studies were required to meet at least half of the established criteria. The articles were evaluated as follows: two reviewers (PGR and FJRL) independently analysed and rated each study. The results were then compared to identify any discrepancies, which were resolved by consensus.

Quality of evidence assessment

In addition to the Newcastle–Ottawa Scale (NOS) for cohort and case-control studies and the Joanna Briggs Institute (JBI) checklist for cross-sectional studies, the overall quality of the body of evidence for each outcome was evaluated using the Grading of Recommendations Assessment, Development and Evaluation (GRADE) approach. This method considers five domains: risk of bias, inconsistency, indirectness, imprecision, and publication bias. Evidence quality was classified as high, moderate, low, or very low. Where applicable, the quality rating was downgraded due to methodological limitations identified in the included studies, heterogeneity in results, or small sample sizes.

Data synthesis

Inter-investigator reliability was evaluated using Cohen's unweighted kappa (κ) [16] to ensure consistency in the screening process. A meta-analysis was conducted when at least two studies provided comparable quantitative data on the Shannon index. The primary effect size was the difference in the Shannon diversity index between women who delivered at term birth (TB) and those with PTB. Continuous outcomes reported as medians with ranges, interquartile ranges (Q1–Q3), or minimum–maximum values were converted to means and standard deviations using established statistical conversion methods. Specifically, the approach proposed by Luo et al. [17] was applied to estimate means, and the method of Wan et al. [18] was used to calculate standard deviations from medians, ranges, and interquartile ranges. Sensitivity analyses were conducted by repeating the models using alternative conversions following Wan et al. and Hozo et al. [19] to verify the robustness of the results. Meta-analyses were performed using Stata software (version 19.5; StataCorp, College Station, TX, USA). A random-effects meta-analytic model was used as the primary analytical approach, employing the restricted maximum likelihood (REML) estimator to quantify between-study variance, and between-study heterogeneity was explored through subgroup analyses according to sampling site, geographic region, and amplified 16S rRNA region. Between-study heterogeneity was assessed using the I^2 statistic, interpreted as low (<40%), moderate (40–60%), substantial (60–75%), or considerable (>75%). Pooled estimates were expressed with 95% confidence intervals (CIs), and statistical significance was set at $p < 0.05$. Forest plots were generated to display individual and pooled effect sizes.

Results

Study selection and flow diagram

Initially, a total of 1,105 references were identified from four different databases: 431 from PubMed, 627 from Scopus, 44 from The Cochrane Library, and 3 from Scielo. After removing 102 duplicate articles using EndNote™, 1,003 studies remained for title and abstract screening. Subsequently, 978 articles were excluded because they did not meet the inclusion criteria, as they analysed the influence of intestinal or vaginal microbiota on pregnancy complications rather than oral microbiota, did not include pregnant patients in their study, or related these complications to other conditions. Thus, 21 studies met all inclusion criteria and were included in the qualitative synthesis, of which four also provided quantitative data for meta-analysis. The study selection process is summarised in Figure 1.

Data extraction

Types of studies

Among the 21 studies included in this systematic review, eight were case–control, eight were cohort, and five were cross-sectional designs. All investigated the association between oral dysbiosis and one or more pregnancy complications (Table 1). Sample sizes varied widely, ranging from 11 to 375 participants, with maternal ages typically between 18 and 40 years. Most studies used 16S rRNA gene sequencing to characterise oral microbial diversity and composition, assessing both alpha diversity (mainly the Shannon index) and beta diversity to determine interindividual differences. The main oral sites sampled were saliva and supragingival or subgingival plaque. The main characteristics and findings of the included studies are presented in Table 2.

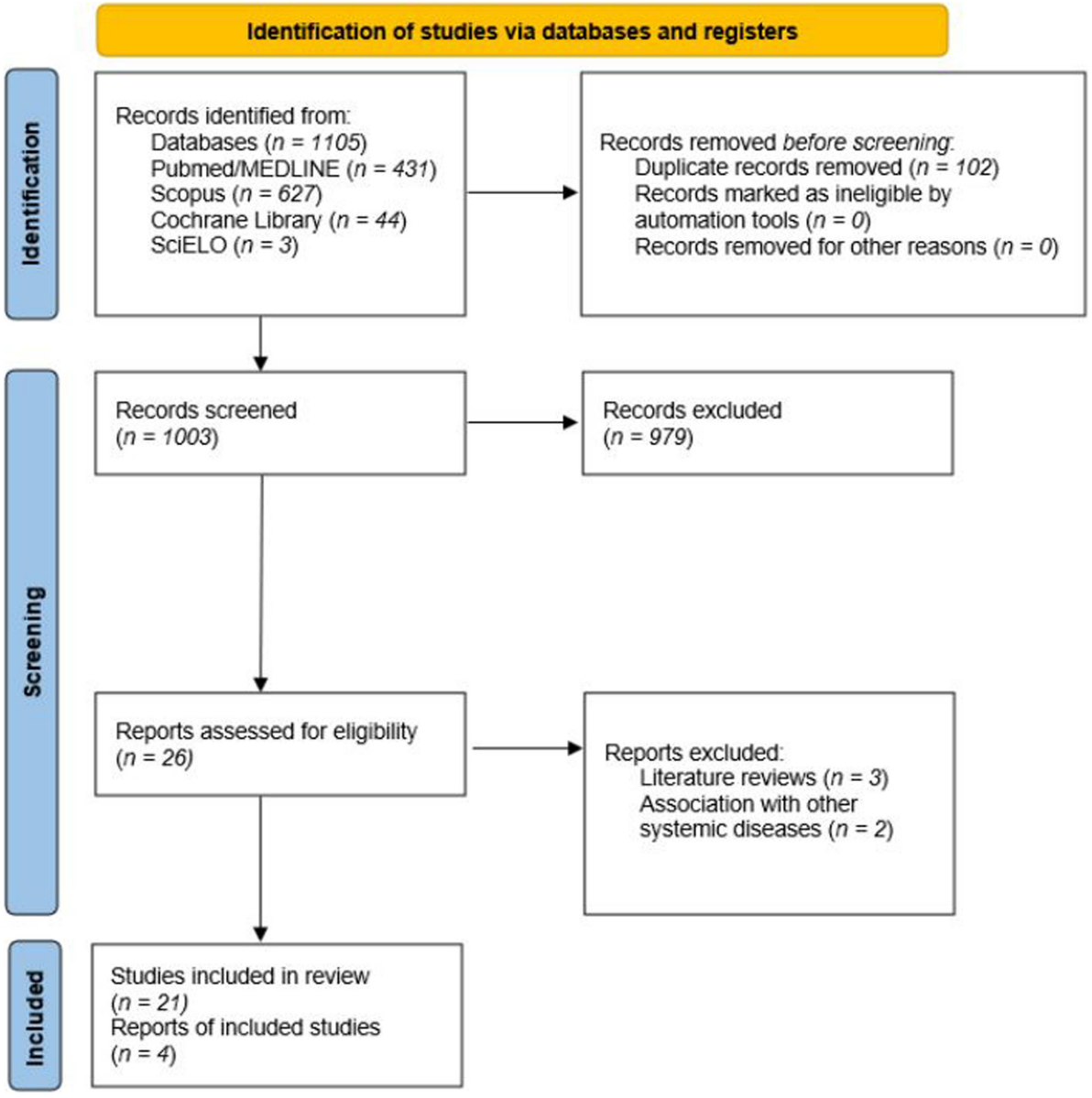

Figure 1. Flow diagram.

Quality Analysis

The methodological quality of the included studies was assessed using the NOS for cohort and case–control designs and the JBI checklist for cross-sectional studies. Of the 21 articles reviewed, 7 were classified as having a moderate risk of bias and 14 as low risk; none showed a high risk of bias. Cohort and case–control studies generally scored be-tween six and eight stars on the NOS, while cross-sectional studies met six to eight of the JBI criteria. The results of these assessments are summarised in Tables 3 and 4 and illustrated in Figure 2.

Meta-analysis results

Four studies provided quantitative data on alpha diversity assessed by the Shannon index, comparing women with PTB and those with (TB). The pooled mean difference was 1.09 (95% CI –0.554 to 2.73; $p = 0.19$), indicating no statistically significant association between Shannon diversity and PTB. The analysis revealed substantial heterogeneity across studies ($I^2 = 97.6\%$, $p < 0.001$). At the individual study

Table 1. Results of the association between oral dysbiosis and pregnancy complications.

Author and year	Type of study	Number of participants and comparison	Age	Characteristics of the oral microbiota	Conclusions
Gilbert et al. [20]	Cross-sectional study	28 non-pregnant women and 179 pregnant women. Comparisons were made between both groups and within the pregnant group.	26–35 years.	During pregnancy, an increase in *Pseudomonas* and a decrease in *Corynebacterium* and *Lachnoanaerobaculum* were detected.	Associates oral microbiome dysbiosis with a higher frequency of oral diseases.
Meriç et al. [21]	Cohort study	96 pregnant women. Comparisons were made within the same group (between pregnancy and postpartum periods).	19–40 years.	*T. denticola* was significantly higher during pregnancy, while *P. gingivalis*, *P. intermedia*, and *F. nucleatum* were significantly higher postpartum.	Evaluates changes in the composition of the oral microbiota in the saliva of women before and 6 months after delivery.
Benslimane et al. [22]	Cohort study	45 pregnant women. Comparisons were made within the same group (between the 2nd and 3rd trimesters).	24–34 years	Significant decrease in alpha diversity and significant change in beta diversity from the 2nd to the 3rd trimester.	Investigates changes in the salivary microbiome from the second to the third trimester of pregnancy. Relates significant biochemical changes to significant changes in the richness and composition of salivary microbiota.
La et al. [23]	Cohort study	101 pregnant women. Comparisons were made within the same group (from preconception to the 3rd trimester).	23–38 years	Significantly lower alpha diversity in the third trimester. More pathogens in saliva during pregnancy.	Characterises the oral microbiome in women from preconception to the end of pregnancy.
Lin et al. [24]	Cohort study	11 pregnant women and 7 non-pregnant women. Comparisons were made between groups and within the pregnant group.	24–29 years	Significantly higher Shannon diversity in the 3rd trimester compared to the non-pregnant group. Increase in *Neisseria*, *Porphyromonas*, and *Treponema* during pregnancy.	Explores changes in the supragingival microbiome in pregnant women compared to non-pregnant women. Studies the segregation of bacterial communities in the gestational state.
Ma et al. [25]	Cross-sectional study	23 healthy pregnant women. Comparisons were made within this group.	28–34 years	Oral microbiota showed greater, unique, and distinct richness compared to placental and intestinal microbiota. Dominant phylum during pregnancy: Firmicutes; predominant genus: *Streptococcus*.	Explores the characteristics of oral, placental, and intestinal microbiota. Significant differences were found among the three groups.
Xu et al. [26]	Case-control study	30 pregnant women with gestational diabetes mellitus and 31 healthy pregnant women. Comparisons were made between groups.	29–37 years	Significantly lower oral alpha diversity in the gestational diabetes group compared to healthy pregnant women.	Compares the characteristics of the oral microbiome in the third trimester between the control and diabetic groups. Shows lower alpha diversity in cases with gestational diabetes.
Li et al. [27]	Case-control study	111 pregnant women (44 with gestational diabetes mellitus and 67 without). Comparisons were made between groups.	Not specified	No significant differences in alpha diversity between groups, but a higher abundance of *Streptococcus* and *Veillonella* in the non-diabetic group.	Identifies biomarkers in the oral microbiota of patients with gestational diabetes mellitus to differentiate them from healthy pregnant women. Significant differences were found in the genera *Lautropia*, *Neisseria*, *Streptococcus*, and *Veillonella* between groups.
Yao et al. [28]	Case-control study	331 pregnant women (65 with gestational diabetes mellitus and 266 non-diabetic). Comparisons were made between groups.	18–24 years	The gestational diabetes group showed a higher rate of bacilli, black-pigmented bacteria, and *Capnocytophaga*; the non-diabetic group had a higher rate of oral *Streptococcus* and lactobacilli.	Studies the association between gestational diabetes and oral microbial imbalance. Detection of tuberculosis bacilli, black-pigmented bacteria, and *Capnocytophaga* was significantly higher in the gestational diabetes group.
Geldenhuys et al. [29]	Cohort study	21 pregnant women (11 normotensive and 10 with preeclampsia). Comparisons were made between groups.	18–35 years	No significant differences in oral alpha or beta diversity compared to the normotensive group.	Determines the diversity of intestinal, vaginal, and oral microbiomes in South African pregnant women, comparing those with and without preeclampsia. No significant differences in the oral microbiome between groups.

(*Continued*)

Table 1. (*Continued*)

Author and year	Type of study	Number of participants and comparison	Age	Characteristics of the oral microbiota	Conclusions
Azevedo et al. [30]	Cohort study	20 pregnant women (10 normotensive and 10 with preeclampsia). Comparisons were made between groups.	26–37 years	The hypertensive group showed higher oral alpha diversity six months postpartum, while the healthy group showed increased levels of *Streptococcus, Prevotella*, and *Veillonella*.	Establishes a possible interaction between hypertension, oral dysbiosis, and the salivary proteome. The composition of the oral microbiome differed significantly between groups, as did Shannon diversity in hypertensive women six months postpartum.
Altemani et al. [31]	Case-control study	36 pregnant women (12 with preeclampsia and 24 normotensive). Comparisons were made between groups.	27–35 years	There was a trend toward lower alpha diversity in the preeclampsia group compared to controls. *Veillonella* was negatively correlated with maternal blood pressure.	Compares the composition of the oral microbiome just before the development of preeclampsia symptoms. Women who developed preeclampsia showed reduced abundance of nitrate-reducing bacteria, and beta diversity differed significantly between groups.
Alex et al. [32]	Cross-sectional study	220 pregnant women (65 with high stress and 155 with mild to moderate stress). Comparisons were made between groups.	18–34 years	The high-stress group showed greater alpha diversity and higher abundance of *Firmicutes* and *Bacteroidetes*.	Relates changes in the oral microbiota to maternal mental health. Differentially abundant microbes were found in pregnant women with high versus low stress.
Yang et al. [33]	Cross-sectional study	26 term pregnant women. Comparisons were made between groups.	28–36 years	Healthy term pregnant women showed elevated levels of *Streptococcus, Veillonella, Haemophilus*, and *Prevotella*, among others.	Correlates the oral microbiome of term pregnant women with local placental immunity and the maternal systemic immune system.
Simic et al. [34]	Case-control study	152 pregnant women (61 preterm birth and 91 term birth). Comparisons were made between groups.	27–35 years	High oral diversity in all pregnant women, with no significant differences in alpha or beta diversity between groups; greater abundance of Firmicutes and Bacteroidetes in the preterm birth group.	Investigated whether oral microbiome composition is associated with preterm birth. Firmicutes and Bacteroidetes were relatively more abundant in women with preterm birth, and Proteobacteria was less prevalent. *Veillonella, Prevotella*, and *Capnocytophaga* in the maternal oral microbiome were associated with preterm birth.
Yang et al. [35]	Cohort study	50 pregnant women (5 preterm birth, 16 early term, 24 full term, and 3 spontaneous). Comparisons were made between groups.	19–29 years	Alpha and beta diversities remained stable throughout pregnancy, but significant differences were observed in late pregnancy. Early pregnancy showed higher abundance of Lautropia mirabilis, and late pregnancy of Prevotella melaninogenica.	Relates changes in the oral microbiome to preterm birth. Differences in alpha diversity were identified at the end of pregnancy between women with preterm and full-term birth. No associations were found between microbiome characteristics and spontaneous abortion or spontaneous preterm birth.
Liu et al. [36]	Case-control study	45 pregnant women (23 with low birth weight and 22 with normal weight). Comparisons were made between groups.	24–36 years	In preterm births with low birth weight infants, the salivary microbiota was less stable, more uneven, and heterogeneous throughout pregnancy.	Establishes changes in the oral microbiome as a predictor of low birth weight. Clostridia, nutritionally variant Streptococcus (NVS), *Leptotrichia buccalis*, and *Gemella sanguinis* were associated with preterm births with low birth weight infants.
Hong et al. [37]	Case-control study	59 pregnant women (30 preterm birth and 29 full term). Comparisons were made between groups.	24–32 years	No significant differences in alpha and beta diversity measures between the full-term and preterm birth groups.	Compares the compositions of the oral microbiome between preterm and full-term birth groups. No significant differences in alpha or beta diversity measures were found between these groups.

Table 1. (*Continued*)

Author and year	Type of study	Number of participants and comparison	Age	Characteristics of the oral microbiota	Conclusions
Park et al. [38]	Cross-sectional study	60 pregnant woman (30 preterm birth and 30 full term). Comparisons were made between groups.	31–37 years	No significant differences were observed in oral microbiota alpha or beta diversity between groups; however, distinctions became apparent when participants were reclassified according to the level of gingival inflammation. Mothers who experienced preterm birth with high gingival inflammation exhibited significantly lower microbial diversity compared with full-term birth mothers with similar levels of inflammation.	The composition of the maternal subgingival microbiome differed between preterm and term births. This difference was more pronounced in the high-inflammation group, where mothers who experienced preterm birth exhibited significantly reduced diversity scores and distinct microbial profiles compared with full-term birth mothers with comparable levels of inflammation.
Saadaoui et al. [39]	Cohort study	54 pregnant woman (18 preterm birth and 36 full term). Comparisons were made between groups.	18–49 years	The oral microbiome was dominated by the phyla *Firmicutes, Bacteroides, Proteobacteria* and *Fusobacteria*. The preterm birth group exhibited distinct microbial profiles, with significantly higher diversity in the second trimester, characterised by increases in species such as *Treponema maltophilum* (a PTB risk biomarker) and *Prevotella buccae*.	Whereas in term pregnancies the placental microbiome resembles the oral microbiome, in cases of preterm birth the placental microbiome shows greater similarity to the vaginal microbiome. Furthermore, distinct oral profiles were identified in PTB, including an increased abundance of *Treponema maltophilum* in the second trimester, suggesting its potential as a early risk biomarker.
Liu et al. [40]	Case-control study	182 women of reproductive age (70 with a history of pregnancy loss and 112 without adverse pregnancy outcomes). Comparisons were made between groups.	21–38 years	The control group showed greater richness and diversity in the oral microbiome compared to the pregnancy loss group. There was greater enrichment of *Firmicutes* and a decrease in *Proteobacteria*, *Bacteroidetes*, and *Actinobacteria* in the pregnancy loss group.	Determines whether alterations in the composition and function of the oral microbiome are associated with pregnancy loss. The oral microbiome of women with pregnancy loss showed significantly lower richness and diversity compared to the control group.

Table 2. The quality assessment of the studies using the adapted version of NOS for case-control studies.

Case-control studies (NOS)	Selection	Comparability	Exposure	Total score
Xu et al. [26]	★★★	★	★★	6
Li et al. [27]	★★★	★	★★	6
Yao et al. [28]	★★★	★★	★★	7
Altemani et al. [31]	★★★	★★	★★	7
Simic et al. [34]	★★★	★★	★★★	8
Liu et al. [36]	★★★	★★	★★★	8
Hong et al. [37]	★★★	★	★★★	7
Liu et al. [40]	★★	★	★★	5

level, Yang et al. [35]. reported a markedly higher Shannon diversity in the PTB group compared with TB, while the other studies showed minimal differences, with confidence intervals overlapping zero. This variability may reflect methodological differences such as sample type (saliva vs subgingival plaque), timing of sampling during pregnancy, and sequencing approaches. The forest plot summarising the pooled analysis is shown in Figure 3.

Sensitivity and subgroup analyses

Sensitivity analyses using alternative statistical conversions produced consistent results. Applying the methods of Wan et al. [18] and Hozo et al. [19] yielded pooled mean differences of 1.07 (95% CI –0.48 to

Table 3. The quality assessment of the studies using the adapted version of NOS for cohorts 'studies.

Cohorts' studies (NOS)	Selection	Comparability	Outcome	Total score
Meriç et al. [21]	★★★	★★	★★★	8
Benslimane et al. [22]	★★★	★★	★★	7
La et al. [23]	★★★	★★	★★★	8
Lin et al. [24]	★★	★	★★★	6
Geldenhuys et al. [29]	★★★	★★	★	6
Azevedo et al. [30]	★★	★★	★★★	7
Yang et al. [35]	★★★	★	★★	6
Saadaoui et al. [39]	★★★	★★	★★★	8

Table 4. JBI checklist evaluation.

Article title	Clear inclusion criteria	Subjects and setting described	Exposure measured validly	Standard criteria for condition	Confounding factors identified	Strategies to deal with confounding	Outcomes measured validly	Appropriate statistical analysis	Overall appraisal	%
Gilbert et al. [20]	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes	Yes	Include	**75**
Ma et al. [25]	Yes	Yes	Unclear	Unclear	Yes	Yes	Unclear	Yes	Included	**62.5**
Alex et al. [32]	Yes	Yes	Unclear	Unclear	Yes	Yes	Unclear	Yes	Included	**62.5**
Yang et al. [33]	Yes	Yes	Yes	Unclear	Unclear	Yes	No	Yes	Included	**62.5**
Park et al. [38]	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes	Yes	Included	**75**

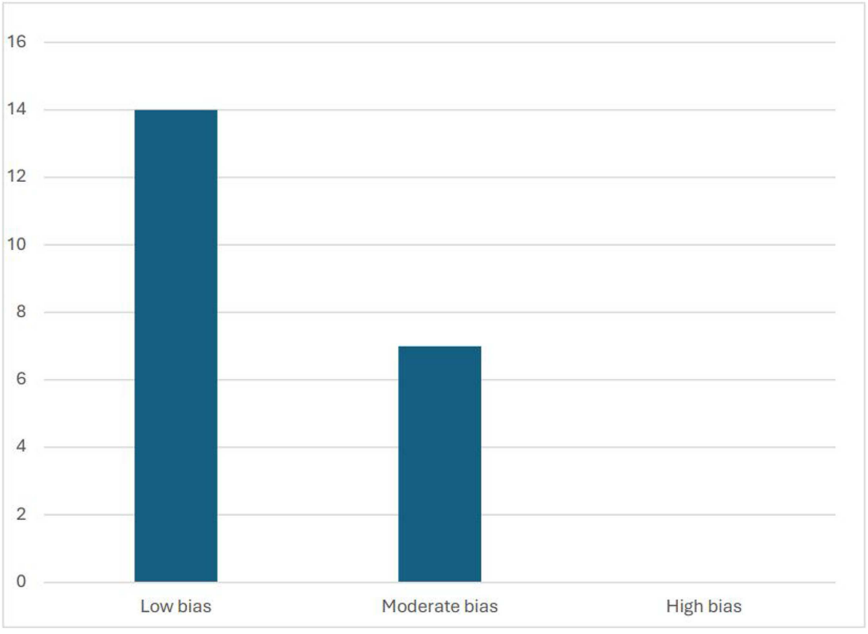

Figure 2. Distribution of studies according to bias.

2.62; $p = 0.18$; $I^2 = 97.24\%$) and 0.98 (95% CI −0.43 to 2.38; $p = 0.17$; $I^2 = 96.7\%$), respectively. These findings confirm that the overall direction and magnitude of the effect remained stable regardless of the conversion approach, although no statistically significant associations were observed and heterogeneity persisted at a considerable level (Figure 4). Between-study heterogeneity was further explored through subgroup analyses according to sampling site, geographic region, and amplified 16S rRNA region

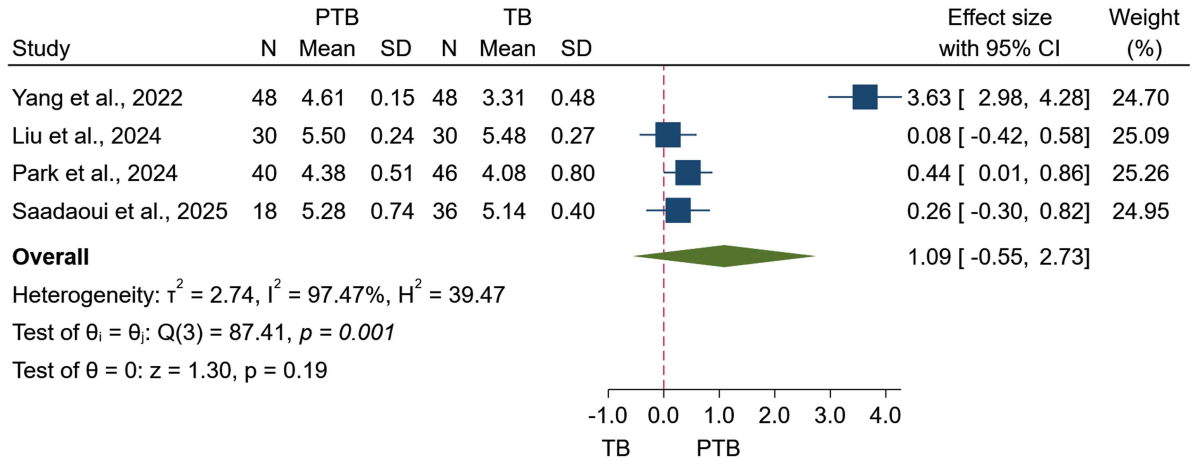

Figure 3. Forest plot of pooled mean differences in Shannon diversity index between preterm birth (PTB) and term birth (TB) groups.

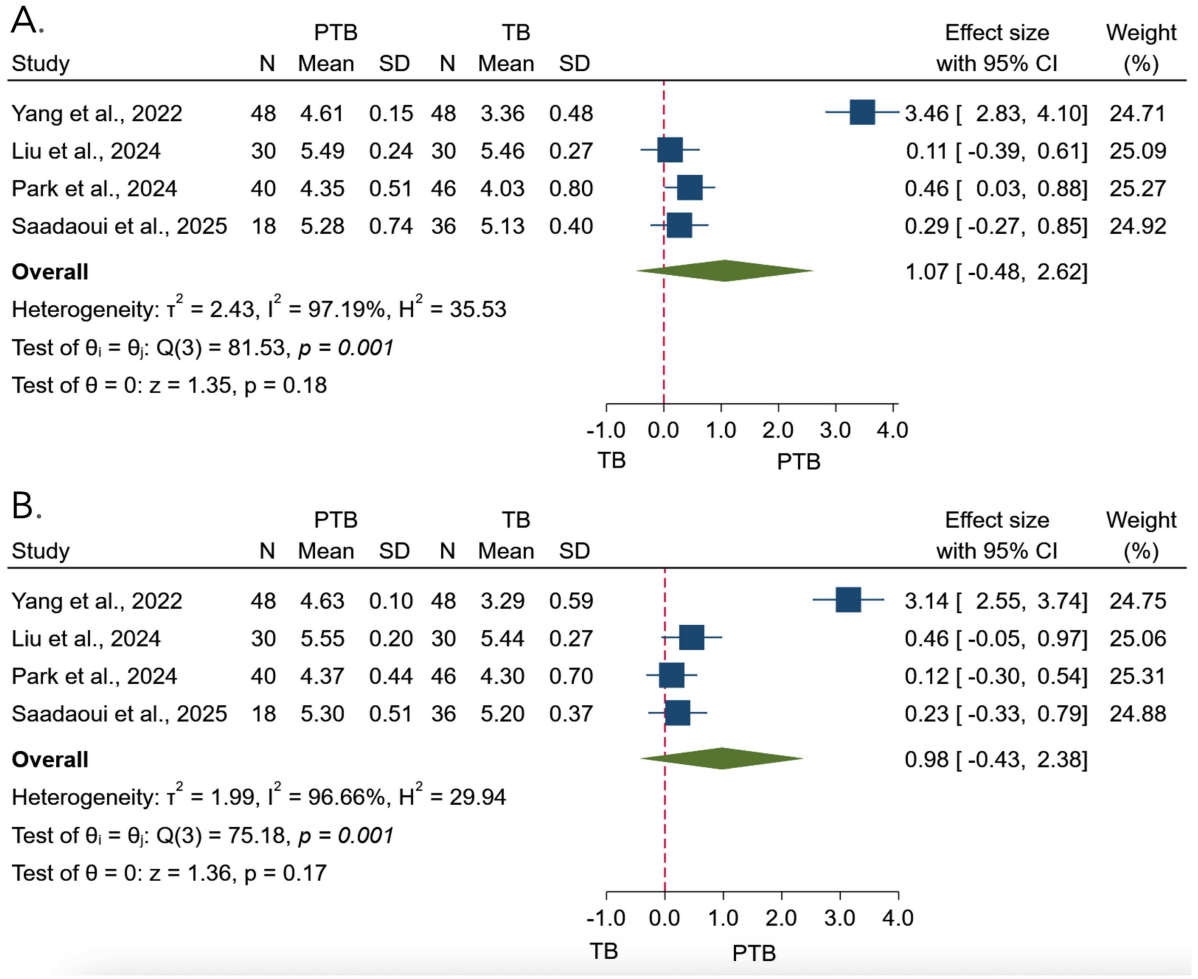

Figure 4. Sensitivity analyses of the meta-analysis on Shannon diversity index comparing preterm birth (PTB) versus term birth (TB). (A) Forest plot using the Hozo method for conversion of summary statistics. (B) Forest plot using the Wan method.

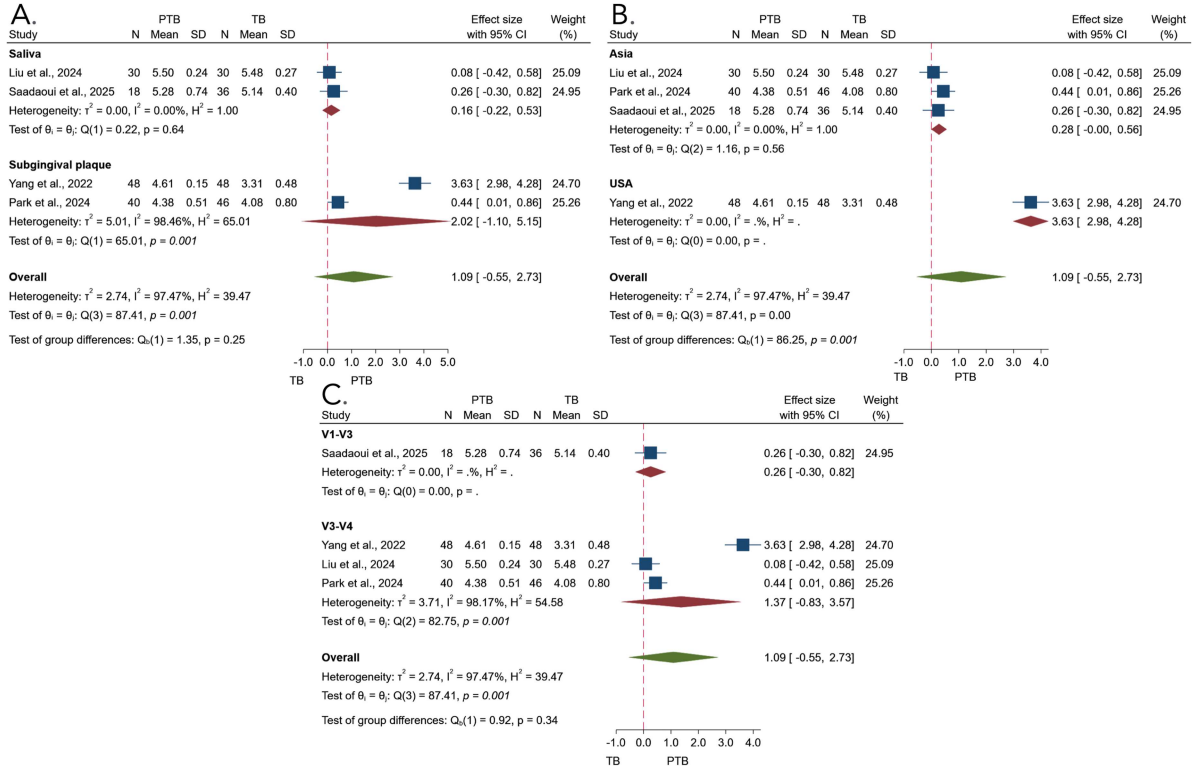

Figure 5. Exploratory subgroup analyses of the meta-analysis on the Shannon diversity index comparing preterm birth (PTB) versus term birth (TB) by (A) sample site, (B) geographic region, and (C) amplified 16S rRNA hypervariable region.

(Figure 5). When stratified by sample type, saliva studies showed small and consistent effect estimates with no evidence of heterogeneity ($I^2 = 0\%$), whereas analyses based on subgingival plaque retained very high heterogeneity, largely driven by a single study with an extreme effect size. Subgroup analyses by geographic region revealed a significant between-group difference (Qb = 86.25, $p < 0.001$), with Asian studies showing homogeneous and small effect estimates ($I^2 = 0\%$) in contrast to the U.S. study, which reported a markedly larger effect. In contrast, stratification by amplified 16S rRNA region did not explain heterogeneity, as analyses focusing on the V3-V4 region continued to show substantial between-study variability. Overall, these findings indicate that heterogeneity was primarily attributable to a single influential study rather than to sampling site or sequencing region, and do not support a consistent association between Shannon diversity and PTB.

Discussion

This systematic review examined the role of oral dysbiosis in pregnancy complications. Several studies demonstrated that pregnancy induces notable shifts in the composition and diversity of the oral microbiota. Gilbert et al. [20] reported significant differences in beta diversity and taxonomic composition between pregnant and nonpregnant women, with higher abundance of *Pseudomonas* and reduced levels of *Corynebacterium* and *Lachnoanaerobaculum* among pregnant women. Meriç et al. [21] observed increased salivary levels of *P. gingivalis, P. intermedia*, and *F. nucleatum* after delivery, alongside decreased *T. denticola* and progressive enrichment of *Proteobacteria* and *Actinobacteria* during gestation. Similarly, Benslimane et al. [22] found a decline in alpha diversity and Shannon index between the second and third trimesters, with *Streptococcus* remaining predominant and increased abundance of *Granulicatella* and *Veillonella*. Studies comparing oral microbiota across different stages of pregnancy have shown progressive changes from preconception to the third trimester, with enrichment of genera such as *Prevotella, Selenomonas, and Veillonella* as gestation advances [23–25]. Variations in both alpha and beta diversity have been observed, with *Proteobacteria, Firmicutes, Fusobacteria, and* Actinobacteria

identified as the predominant phyla. Evidence also suggests that oral dysbiosis during pregnancy is associated with an imbalance in Th1/Th2 immune responses, which may contribute to adverse outcomes such as preterm birth and preeclampsia. Collectively, these findings indicate that pregnancy modulates the oral microbiome toward a dysbiotic profile potentially linked to obstetric complications.

One of the most relevant complications of pregnancy is gestational diabetes mellitus (GDM). Several studies have examined the potential association between the composition of the oral microbiota and the development of this metabolic disease. Xu Y. et al. [26] reported that, although *Leptotrichia, Neisseria, Porphyromonas, Prevotella, Streptococcus,* and *Veillonella* dominated the salivary microbiota of pregnant women, those with GDM exhibited higher proportions of *Proteobacteria* and lower levels of *Firmicutes* and *Leptotrichia.* Moreover, *Streptococcus, Leptotrichia, and Veillonella* abundances were significantly correlated with maternal glucose levels, indicating a potential link between oral dysbiosis and glycemic regulation. Similarly, Li X. et al. [27] identified significant differences in the oral microbiome between healthy pregnant women and those with GDM in the third trimester, supporting the feasibility of using specific oral microbes as biomarkers of GDM. In this study of 111 pregnant women (44 with GDM), salivary *Leptotrichiaceae, Lautropia*, and *Neisseria* were enriched in the GDM group, along with a depletion of *Selenomonas* and *Leptotrichia.* In supragingival plaque, *Lautropia* and *Neisseria* also increased significantly, whereas *Streptococcus* and *Veillonella* were decreased in GDM. *Lautropia* and *Neisseria* thus emerged as characteristic taxa in both plaque and saliva; together with their relationship to glucose metabolism, this finding suggests their potential as indicators of the presence and progression of GDM. On this basis, the development of predictive models for GDM using support vector machine (SVM) and random forest (RF) algorithms leveraging oral microbiota features has been proposed. Along the same lines, Yao H. et al. [28] demonstrated reduced levels of *Streptococcus* and *Lactobacillus* and increased abundance of opportunistic bacteria (*E. coli, S. aureus, P. aeruginosa*) in GDM, linking hyperglycaemia-induced vascular and oxygenation changes to the proliferation of anaerobic species. Collectively, these studies support the hypothesis that oral dysbiosis contributes to GDM pathophysiology and may enable early, noninvasive risk assessment based on microbiome-derived biomarkers.

Several studies have examined the relationship between oral dysbiosis and preeclampsia. Evidence indicates that women with this condition tend to exhibit higher α-diversity compared with normotensive controls, although differences are not always statistically significant [29]. The oral microbiota of affected women is typically characterised by a relative depletion of health-associated genera such as *Streptococcus, Granulicatella, Veillonella, Neisseria, and Capnocytophaga*, and an enrichment of potentially proinflammatory taxa including *Prevotella* and *Haemophilus* [30]. Moreover, alterations in microbial composition persist postpartum, suggesting a long-term imbalance of the oral ecosystem. Overall, these findings support a possible link between pregnancy-associated hypertension and shifts in the oral microbiome toward a proinflammatory profile that may contribute to the pathophysiology of preeclampsia. By contrast, Altemani F. et al. [31] analysed 36 pregnant women (12 with preeclampsia) and found that the oral microbiota of those with preeclampsia tended to exhibit lower α-diversity (not significant). The preeclampsia group showed greater abundances of *Methanosaeta, Desulfomicrobium, Enterococcus, Mycobacterium, Thiobacillus*, and *Ochrobactrum*, whereas normotensive women had higher levels of *Roseomonas, Johnsonella, Caulobacter, Prevotella*, and *Veillonella.* In addition, maternal systolic and diastolic blood pressure at 36 weeks' gestation correlated negatively with *Veillonella* and positively with *Mycoplasma* and *Methanobrevibacter.* Overall, the findings consistently indicate compositional changes in the oral microbiome associated with preeclampsia, although the direction of changes in α-diversity varies across studies. As in the literature on GDM, discrepancies likely reflect limited sample sizes, heterogeneity in sampling time points, and population and methodological differences. Nevertheless, the convergence around taxa with proinflammatory potential and the associations with blood pressure parameters support the hypothesis that oral dysbiosis may contribute to the pathophysiology of preeclampsia.

Previous studies have suggested that maternal psychological status and immune regulation during pregnancy may be influenced by the oral microbiota. Evidence indicates that higher levels of stress, anxiety, and depressive symptoms are associated with increased microbial richness, although the overall community structure often remains stable. Specific bacterial shifts have been observed, including an enrichment of Proteobacteria in women with high stress, Bacteroidetes and Firmicutes in those with

elevated anxiety, and Firmicutes and Spirochaetes in women with greater depressive symptoms [32]. Other research has revealed significant correlations between the composition of the oral microbiota and placental immune mediators such as IFN-γ, IL-4, IL-5, IL-6, and GM-CSF [33]. In particular, a negative association between Streptococcus abundance and IL-5 levels, along with links to the CD4 + /CD8 + T-cell ratio, supports the existence of an oral microbiota–immune axis relevant to maternal health during pregnancy.

Preterm birth (PTB), defined as delivery before 37 weeks of gestation, remains a major cause of neonatal morbidity and mortality. Recent studies have explored its potential association with oral dysbiosis, suggesting that alterations in the oral microbiota may precede or contribute to this outcome. Across cohorts, no consistent differences have been observed in overall alpha or beta diversity between women with preterm and term births, yet compositional changes in specific taxa are recurrent. The dominant phyla generally include Firmicutes, Proteobacteria, Bacteroidetes, Fusobacteria, and Actinobacteria [34–39]. At finer taxonomic levels, women who delivered preterm often show enrichment of potentially pathogenic or inflammatory genera such as Prevotella, Campylobacter, Veillonella, and Actinomycetales, whereas Haemophilus, Neisseria, Lautropia, and Streptococcus tend to predominate in term births. In particular, depletion of Lautropia mirabilis and overrepresentation of Prevotella melaninogenica have been proposed as microbial risk markers [35]. Longitudinal analyses also indicate that imbalances in the oral microbiome—detectable as early as the second trimester—may precede preterm delivery, as shown by alterations in the Streptococcus/Saccharibacteria ratio and enrichment of opportunistic taxa such as Leptotrichia buccalis and Gemella sanguinis [36]. Other studies have found that dysbiosis is more evident in women with concomitant gingival inflammation, reinforcing the role of local oral conditions as potential modifiers of pregnancy outcomes [38].

Overall, these findings suggest that a dysbiotic oral environment may contribute to preterm birth by promoting systemic inflammation or microbial translocation to the fetoplacental unit. This hypothesis is further supported by evidence linking oral microbial imbalance to pregnancy loss. Women with a history of miscarriage exhibit reduced richness and evenness of the oral microbiota, with an increase in Firmicutes and depletion of Proteobacteria and Bacteroidetes, as well as overrepresentation of Roseburia, Bacteroides, Neisseria sicca, and Streptococcus mitis/oralis [40]. These compositional patterns may reflect disrupted microbial homoeostasis and immune dysregulation, emphasising the potential of the oral microbiome as an early, noninvasive biomarker for adverse pregnancy outcomes.

In line with these observations, the meta-analysis performed in the present systematic review provides additional insights. In the pooled analysis, mean Shannon diversity was numerically higher in women with PTB than in those with TB; however, this difference was not statistically significant and was accompanied by very high between-study heterogeneity ($I^2 = 97\%$), indicating that the pooled estimate should not be interpreted as evidence of a consistent association. Subgroup analyses revealed that this heterogeneity was largely driven by a single influential study reporting an extreme effect size, rather than by systematic differences across methodological features [41]. Geographic region significantly differentiated subgroup effects; however, this distinction was largely attributable to the U.S. study and does not indicate a consistent regional pattern. Specifically, studies based on saliva samples and those conducted in Asian cohorts showed small, non-significant differences with I^2 values close to 0%, whereas marked heterogeneity emerged when analyses included the U.S. study, which was based on subgingival plaque samples, indicating that the observed variability was primarily driven by this influential study rather than by a consistent pattern across studies [35]. From a biological perspective, these patterns are plausible: saliva samples integrate bacteria from multiple oral niches and may capture a more stable 'background' community [41], whereas subgingival plaque reflects a highly site-specific biofilm that is more strongly influenced by local inflammation and periodontal status, which could amplify between-study variability. Likewise, differences in geographic region may mirror variation in host genetics, diet, oral-hygiene practices, and healthcare access, while differences in sequencing strategies, including the amplified 16S rRNA region, may introduce additional technical variability in taxonomic resolution and abundance estimates [35,42]. This counterintuitive pattern suggests that increased microbial diversity should not always be interpreted as a marker of eubiosis [43]. Instead, it may reflect the expansion of opportunistic taxa that artificially elevate diversity indices while undermining ecological stability [44]. These inconsistencies highlight the importance of standardised approaches and larger cohorts to clarify whether alpha diversity, as measured by the Shannon index, can serve as a reliable biomarker of adverse pregnancy outcomes [45].

This systematic review presents several limitations that should be acknowledged. The included studies were highly heterogeneous regarding design, sample size, and population characteristics, which limits comparability and the strength of meta-analytic conclusions. Differences in sampling sites, sequencing methods, and diagnostic criteria for pregnancy complications may have introduced methodological bias. Moreover, most studies focused on late pregnancy, with few assessing longitudinal microbiome changes. Confounding factors such as diet, antibiotic use, and oral hygiene were often uncontrolled. Finally, the predominance of small-scale studies and potential publication bias restrict the generalisability of the findings and highlight the need for standardised, multicenter research.

Conclusions

This systematic review demonstrates that pregnancy is associated with distinct alterations in the oral microbiota and that oral dysbiosis may be linked to a range of adverse pregnancy outcomes, including gestational diabetes, preeclampsia, preterm birth, low birth weight, and pregnancy loss. Across studies, compositional shifts and enrichment of pathogenic taxa appear more relevant than absolute changes in microbial diversity.

Importantly, although the meta-analysis of alpha diversity (Shannon index) did not reach statistical significance, the observed trend toward altered diversity in complicated pregnancies supports a potential association between oral microbial imbalance and adverse outcomes. Together, these findings reinforce the biological relevance of the oral microbiome in maternal–foetal health and highlight its promise as a target for future mechanistic and translational research in prenatal care.

Author contributions

CRediT: **Paula García-Rios:** Conceptualization, Investigation, Validation; **Francisco Javier Rodríguez-Lozano:** Investigation, Validation, Visualization, Writing – original draft, Writing – review & editing; **Raquel González-Murcia:** Conceptualization, Investigation, Writing – original draft; **Laura Murcia:** Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing; **Desirée Victoria-Montesinos:** Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Writing – original draft; **Ana María García-Muñoz:** Investigation, Methodology, Resources, Software, Supervision, Validation.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The data that support the findings of this study are available from the corresponding author, upon reasonable request.

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