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Vaginal and Oral Microbes, Host Genotype and Preterm Birth

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Abstract

Preterm birth (PTB) is a leading cause of infant mortality and morbidity in the U.S. and across the globe. Infection and associated inflammation are important initiators for PTB pathways; an estimated 40% of PTBs are attributed to amniochorionic-decidual or systemic inflammation. Historically, intrauterine infections have been implicated in PTB; recent evidence suggests that infections remote from the fetal site may also be causative. There is strong epidemiological evidence that bacterial vaginosis and periodontitis -- two syndromes characterized by perturbations in the normal vaginal and oral bacterial microflora respectively-- are linked to infection-associated PTB. Oral and vaginal environments are similar in their bacterial microbiology; identical bacterial species have been independently isolated in periodontitis and bacterial vaginosis. Periodontitis and bacterial vaginosis also share many behavioral and sociodemographic risk factors suggesting a possible common pathophysiology. Genetic polymorphisms in host inflammatory responses to infection are shared between bacterial vaginosis, periodontitis and PTB, suggesting common mechanisms through which host genotype modify the effect of abnormal bacterial colonization on preterm birth. We review the state of knowledge regarding the risk of PTB attributable to perturbations in bacterial flora in oral and vaginal sites and the role of host genetics in modifying the risk of infection-related PTB. We posit that bacterial species that are common in perturbed vaginal and oral sites are associated with PTB through their interaction with the host immune system.

Keywords

Prematurity; infection; genotype

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Introduction

Preterm birth (PTB) is a leading cause of infant mortality and morbidity in the U.S. and across the globe. Infection and associated inflammation are important initiators for PTB pathways; an estimated 40% of PTB are attributed to amniochorionic-decidual or systemic inflammation (1). PTB can be spontaneous or indicated; spontaneous PTB include births that occur at < 37 weeks gestation following preterm labor with or without premature rupture of membranes (PROM). Genital tract infections such as pyelonephritis and sexually transmitted infections such as trichomoniasis have long been associated with increased risk of PTB (2–7). More recently, a growing body of evidence indicates that even low levels of chronic infection and associated perturbations in the bacterial flora in the mouth or vaginal cavity are sufficient to stimulate a maternal inflammatory response, ultimately leading to PTB (8–11). It is not known when these sub acute infections are acquired and how they lead to PTB; infections early in gestation or even before pregnancy are likely important. The inflammatory response is oftentimes subclinical; the lack of specific histology and apparent clinical symptoms make diagnosis difficult. The association of sub-acute infection and sub-clinical inflammation has been used to explain the strong and consistent two-fold association of PTB with bacterial vaginosis (BV)(12) and periodontitis(13), two clinical syndromes associated with microbial shifts away from the normal bacterial flora in the vaginal and oral sites. Treatment trials of both BV and periodontitis during pregnancy have given mixed results, showing both positive and negative effects on preterm delivery (14–19).

The generally accepted hypothesis for the pathophysiology of infection-associated PTB is that bacteria or bacterial products enter the uterine cavity by ascending from the proximal lower genital tract or systemically from remote sites such as the oral cavity. The pregnant body responds to infection by mounting an immune response to clear pathogen(s) and repair the associated injury; elevated local levels of cytokines and chemokines are important mediators of this process that results in PTB. High cytokine levels are used to indicate subclinical infection even when clinical symptoms of inflammation such as fever are absent (20). Clinical and subclinical bacterial infection trigger a cascade of events that can lead to PTB either when the bacteria directly ascend into the maternal uterine cavity and invade the fetal unit invoking a massive fetal inflammatory response (as measured by elevated cytokines, metalloproteinases and C reactive protein in fetal plasma (21–23)) and/or by triggering a proinflammatory maternal host response in the uterine tissues (1, 23–31). These processes up regulate prostaglandin synthesis and culminate in the onset of myometrial contractility (Figure 1). Invasion of the amniotic cavity through an ascending infection from the vagina is most proximal to the fetal unit; however, the consistent association of PTB with periodontal disease even in the absence of recovery of oral microbiota from the amniotic cavity suggests that periodontal disease may invoke a host response that triggers pathways to PTB (32). Alternatively, PTB may be triggered through initial colonization by bacteria shared between oral and vaginal sites (Figure 1). If the latter is true than personal hygiene and sexual behavioral factors that may aid sharing of bacterial flora between oral and vaginal sites will be strongly associated with risk of PTB. Regardless of the mechanism via which infection triggers PTB, the degree of inflammatory response to acute or sub acute infection is likely modified by innate host immunity; the interaction between host immune

status (genotype) and bacterial exposure (environment) is critical for illuminating the etiology of infection associated PTB. In this review we will focus on the current state of knowledge regarding the risk of PTB attributable to perturbations in bacterial flora shared between oral and vaginal sites and the role of host genetics in modifying the risk of infection-related PTB.

Bacteria in the amniotic fluid and PTB

80% of women who deliver preterm have infections of the amnion or chorion compared to 30% of women who deliver at term (33); detection of microorganisms in the amniotic fluid is a marker for upper genital tract infection and associated with a higher risk of PTB (34). Maternal upper genital tract infections can occur early on and remain asymptomatic for most of gestation; bacteria recovered from amniotic fluid in the absence of clinical symptoms have been associated with subsequent clinical chorioamnionitis and premature rupture of membranes (PROM) (35). Alternatively, bacterial organisms that colonize the lower genital tract and the vagina ascend to the uterus and cause infection; colonization by low virulence non-commensal bacteria in the vaginal sites are thought to be markers of upper genital tract infection (36–40). Additionally, colonization by these microorganisms cause increased vaginal concentrations of pro inflammatory cytokines (41). Microorganisms recovered from the uterine cavity (including from amniotic fluid) following PTB include *Ureaplasma urealyticum* (42), *Chlamydia trachomatis* (43), *Trichomonas vaginalis* (44), *Streptococcus agalactiae* (43), *Escherichia coli* (2, 45, 46) and various anaerobes (Table 1). Some of them including species of *Fusobacterium* and *Streptococcus* are also found in the oral cavity although it is not clear whether a) these organisms share identity at the strain level and b) these organisms are representative of normal or diseased oral conditions (47). Detection of bacteria in amniotic fluid correlates to histological inflammation; higher grades of histological lesions are associated with total colony count of bacteria in amniotic fluid ($p < 0.05$) and with “high-virulence” bacteria in amniotic fluid ($p < 0.05$) (48). However, in approximately 30% of PROM cases, the recovery of bacterial organisms does not correlate with inflammatory changes found during histological chorioamnionitis (23, 49, 50). The detection of bacterial colonization in the absence of host inflammation might result from contamination of the chorion by vaginal organisms at the time of delivery, bacterial infection close to delivery time, or colonization by relatively ‘avirulent’ organisms or strains. Conversely, inflammation occurring in the absence of detected bacterial colonization might result from colonization by non-cultivable organisms, a generalized fetal inflammatory response to infection or from a non-infectious process.

Bacterial organisms recovered from amniotic fluid of women who went on to deliver preterm have been recovered from the vagina as early as in the first trimester. Single or mixed vaginal colonization with *U.urealyticum*, *C. trachomatis* or *T. vaginalis* are commonly associated with PTB, although there is variation between studies (51–55). The inconsistent results across studies may reflect racial and ethnic differences in study populations, since the prevalence of bacterial colonization vary by racial/ethnic group (56, 57); in a study of pregnant women, vaginal colonization with *Mycoplasma hominis* was more prevalent in African American (18.9%) and Hispanic (20.9%) women than in Caucasian women (4.2%, $p = 0.01$) (57). The timing of detection of non commensal

bacterial organisms is important in attributing risk of PTB. One study found levels *G.vaginalis*, *M.hominis* and *U.urealyticum* are acquired at a low rate but are highly persistent and significantly associated with PTB while species of *Peptostreptococcus* and *Bacteroides* are frequently acquired only in late pregnancy and found not to be associated with PTB (58). These results imply that abnormal colonization by certain bacteria early in pregnancy or perhaps even before gestation might be important in determining PTB outcome. PTB risk was elevated in women with BV who were also colonized by *U. urealyticum* (OR 3.1, 1.8-5.4) compared to the rate in the presence of *U. urealyticum* only, indicating the potential importance of mixed infections (59).

Antibiotic treatment of patients with PROM without labor decreases risk of chorioamnionitis from 69% to 46%, $p < 0.05$ (60), suggesting that regardless of whether the colonizing bacteria caused rupture of membranes, they contribute to subsequent PTB. There is some indication that it is the relative loads of bacteria rather than their presence or absence *per se* associated with increased risk of PTB; florescence in situ hybridization experiments using a DNA probe specific to the conserved 16S rDNA of bacteria detected higher numbers of bacteria detected in PROM; bacteria were also found to colonize 13–16% of term deliveries, albeit in lesser numbers (61).

Paradoxically, treatment regimens targeting PTB associated bacteria have not changed PTB outcome for the most part (Table 2); this has been variously attributed to differences in type and mechanism of action of antibiotic and formulation of antibiotics prescribed, duration and timing of administration (37, 62–67). These results imply that once abnormal bacteria colonize and trigger inflammatory maternal and/or fetal response, eradication of the bacteria in itself is insufficient to fix the cascade of damaging processes that culminate in PTB.

Bacterial Vaginosis and PTB

Several studies have shown a two to five fold increased risk of PTB in women with bacterial vaginosis (BV) during gestation; this increased risk is independent of previous PTB, smoking and black race (Figure 2) (29, 44, 47, 68–72). BV diagnosed during gestation is also associated with chorioamnionitis and preterm PROM (73). BV is a complex polymicrobial disorder characterized by depletion of *Lactobacilli* dominated flora and overgrowth of a mixed and variable anaerobic and facultative flora, including *Gardnerella vaginalis*, *Prevotella spp*, *Bacteroides spp*, *Mobiluncus spp*, gram-positive cocci, and genital *Mycoplasma*. The number and types of species found in BV are diverse: a metagenomics study found 35 unique species (some not related to any known species) in samples from 27 women with BV (74).

Notably, BV elicits only a low or minimal inflammatory response. The clinical syndrome is characterized by low levels of *Lactobacillus*, discharge, and vaginal odor, but the characteristic microbiology is often detected in the absence of the clinical syndrome. When the diagnosis of abnormal bacterial flora is extended beyond the clinical diagnosis of BV and includes atypical gram-positive rods and *lactobacilli*-dominated smears showing heavy leukorrhea of unknown cause, the risk of PTB increases from 25% to 60%. “Normal” flora by this modified criterion is associated with a four-fold decrease in PTB (95% CI 0.1-0.6, P

< .001) and an abnormal Gram stain with an overall adjusted odds ratio for PTB of 5.2 (95% CI 1.8-14.5, $P < .001$) (75).

The prevalence of BV during pregnancy ranges from 4.9% to 49%, (70, 72, 76–78) and varies by clinical setting, sociodemographic factors, diagnostic criteria and gestational age. In the Vaginal Infections and Prematurity (VIP) study of 13,914 pregnant women (23–26 weeks gestation) enrolled at seven US academic medical centers from 1984 to 1989, 16% (1645/10,397) of women had BV with center-specific prevalence ranging from 9% to 28%. (70) Prevalence of BV was higher among African American (23%) than Caucasian (9%) participants.(79) As BV is very common, and is strongly associated with PTB, treating BV seems a sound strategy to prevent PTB. However, results from clinical treatment trials are conflicting (72, 80–84), and in some cases suggest harm, so treatment of BV during pregnancy currently is not recommended to prevent PTB. Given the importance and substantial attributable risk of preterm birth for BV, there has been intense speculation about the reasons for the failure (16).

BV is reported more frequently among women who are poor (70), less educated (70), young (36, 70), or unmarried (70). Until recently, the only behavioral factors reported were early age at first intercourse(70) and smoking (85). Psychosocial stress was found to be strongly and independently associated with BV prevalence in a cross sectional multi-racial sample of pregnant women. (76) An increased risk of BV was associated with stress measured using the Perceived Stress Scale in a one-year prospective study of multi-racial nonpregnant women aged 15 to 44. Behavioral factors such as douching may also influence PTB outcomes. In the 1988 National Survey of Family Growth, women who reported currently douching two to three times per week were more likely to have a history of delivering a low birth weight infant, but that women who douched less often experienced no increase in risk. (86) However other case control studies show contradicting results (87). In a recent study of preterm birth among a cohort of low-income African-American women, women who reported douching less than three times per month in the six months before pregnancy were significantly less likely to deliver preterm than women who reported never douching (prevalence ratio (PR), 95% CI: 0.63, 0.42-0.95) after adjusting for potential confounding. Compared to women reporting never douching, women reporting douching during the pregnancy were at a higher risk of delivering preterm, although not statistically significant (PR, 95% CI: 1.64, 0.97-2.76) (88). It is not known whether women with vaginal infections are more likely to douche because of associated symptoms or whether douching leads to an increase in vaginal infections; consequently the association of douching with PTB is not yet explained.

Most pregnant women with BV do not deliver prematurely and a high percentage of PTB women whose placenta/ membranes show inflammation do not have BV. This has led investigators to hypothesize that BV is a marker for upper genital tract infection. Elastase, mucinase, sialidase, prolidase and other proteolytic enzymes produced by anaerobic bacteria involved in the pathogenesis of BV likely alter the immune signals and promote the degradation of host mucosal epithelial barrier, permitting bacteria access to the uterus as well as impairing fetal membrane strength and elasticity; elevated levels of these enzymes are implicated in increased risk of PTB (89–91). The deleterious effects of these bacterial

byproducts have been shown to induce preterm birth in rat models (92, 93). BV is associated with higher levels of sialidase activity (84% of 50 women with BV compared to none in 19 normal women) and > 70 % of sialidase activity can be accounted for by the presence of *Prevotella*, *Bacteroides* and *Gardnerella* species (94). High rates of phospholipase A2 (a precursor of prostaglandin synthesis) are produced by *Bacteroides spp.*, anaerobic *Streptococci*, *Fusobacterium spp.*, and *G. vaginalis* and high concentrations of these anaerobes as seen in BV may induce prostaglandin synthesis and resultant PTB (reviewed in 73). A study on Danish pregnant women showed that high sialidase and/or prolidase activity combined with elevated vaginal pH 5 or greater, are strong risk factors for early preterm birth (< 32 weeks of gestation), low birthweight (LBW), and very LBW (< 1500 g) (95). Although BV organisms are known to produce high levels of these enzymes, clinically diagnosed BV was not found to be associated with risk of PTB in this population; understanding the functional determinants of BV organisms may allow for a better quantitative measure of the risk of BV associated PTB. In the same population, high levels of specific immunoglobulin A (IgA) against the toxin produced by *G. vaginalis* (anti- Gvh IgA) were protective for adverse pregnancy outcomes (90). In contrast, *Lactobacilli* are found not to increase synthesis of prostaglandins in fetal membranes and may have a protective effect against PTB. This has led investigators to postulate that preventing perturbations in *Lactobacilli* dominated vaginal flora is critical to achieving a decreased risk of PTB. Clinical trials using *L. acidophilus* and *L. reuterii* strains along with antibiotics for treating BV, revealed that use of the *Lactobacilli* strains lengthened the time to BV recurrence for women who were initially cured using antibiotics, however the effect of probiotics on PTB outcomes has not been reported (96). Recent studies using 16S rDNA phylogenetic analysis indicates that vaginal bacterial flora of healthy African American may differ from Caucasian women. *Lactobacilli* were less likely to be the dominant organisms in healthy African American women (68% vs. 91% in healthy Caucasian women) and African American women were more likely to be colonized primarily by anaerobes (32% in African American women vs. 8% in Caucasians) (97). This implies that a non-*Lactobacilli* dominated vaginal flora in itself is not indicative of poor vaginal health; establishing the bacterial signatures of normal (and altered flora) is an essential first step towards determining the subset of bacteria that contribute to infection associated PTB.

Oral flora and PTB

A strong association has been observed between poor oral health and PTB although the results are not uniform (13, 98–101). In 1996, Offenbacher first reported a case-control study where women with PTB and low birth weight babies were found to be more likely to have significant periodontal disease compared to control women with normal birth weight babies. In a meta-analysis of 17 observational studies on periodontal disease and preterm birth conducted in 2007, a positive association was found between periodontitis and preterm birth (pooled odds ratio, 95% confidence interval, p-value: 2.27 (1.06-4.85), $p < 0.001$) but the authors recommended that large multi-center trials be completed prior to instituting changes in clinical practice (102). The meta-analysis identified considerable statistical heterogeneity, at least some of which was accounted for by differences in study quality, and study population. The observational studies that were included did not examine specific

microbes or their relative abundance; periodontal disease was measured using a variety of measures including bleeding on probing, pocket depth, clinical attachment loss, plaque index, and gingival index (102). Results from a pilot clinical treatment trial showed a 3.8-fold reduction in the rate of preterm delivery, a decrease in periodontal pathogen load, and a decrease in local and serum inflammatory factors (32). Bacterial organisms which are significantly associated with periodontal disease in the “red cluster” (*Porphyromonas gingivalis*, *Tanerella forsythensis*, and *Tanerella denticola*) and “orange cluster” (*Prevotella intermedia*, *Prevotella nigrescens*, *Campylobacter rectus*) were also associated with PTB, albeit at borderline significance ($p = 0.012-0.069$) (103). Postpartum levels of all selected bacteria were at least two times higher in the preterm group than in the term group, with significant differences in *P. gingivalis*, *T. forsythensis*, *T. denticola*, *P. intermedia*, *P. nigrescens*, and *C. rectus* ($P < 0.05$). Subsequently many studies have confirmed this association of periodontitis with PTB, although a few results from large studies have contradicting results (Figure 3).

A wide range of gram positive and gram negative bacterial species, yeasts, mycoplasmas and protozoa are found in the healthy oral cavity (104). The hard enamel surface of teeth provides surfaces for microbial colonization in a three dimensional architecture resulting in plaque. From initial colonization by aerobic and facultative anaerobes in infancy, mainly *Streptococcus oralis*, *Streptococcus mitis* and *Streptococcus salivarius*, the diversity of oral microbes increases to contain gram positive bacteria from *Actinomyces*, *Lactobacillus*, *Rothia* genus and gram negative organisms including *Neisseria*, *Capnocytophaga* and *Prevotella* genus (105). Diet and social behaviors such as smoking affect the composition of the dental flora; diets rich in sugar provide for acidification of teeth surfaces that encourage colonization by acid tolerant cariogenic species such as *Streptococcus mutans*. Smoking increases the risk of periodontitis and levels of periodontal pathogens such as *P. gingivalis* and *A. actinomycetemcomitans*. Using 16S rRNA analysis, several species of *Fusobacteria*, *Peptostreptococcus*, *Prevotella*, *Capnocytophaga*, *Eikenella* and *Porphyromonas* are found to be distributed differently between healthy and diseased sites on teeth (105–109). There is some evidence for racial differences in periodontal pathogens; *P. gingivalis* and *P. anaerobius* were more significantly associated with black subjects in the adult periodontitis group, while *F. nucleatum* was associated with white subjects in both the adult periodontitis and early onset periodontitis groups (110).

Oral prophylaxis and periodontal treatment in three clinical trials demonstrated a 57% reduction in preterm low birth weight (pooled RR 0.43; 95% CI 0.24-0.78) and a 50% reduction in preterm births (RR 0.5; 95% CI 0.20-1.30) (111) but results of other studies show little or no effect (112). A recent meta analysis of periodontal treatment on PTB reported a significant effect of root planning and scaling on PTB in the absence of history of PTB (OR, 0.48; 95% CI, 0.29-0.77; $P = .003$). The authors also reported that treatment effect on PTB was more in patients with less severe disease as defined by probing depth and bleeding on probing (OR, 0.49; 95% CI, 0.28-0.87 and OR, 0.37; 95% CI, 0.14- 0.95 respectively) (113). Specific microbes are both positively or negatively associated with increased risk of PTB: in a case control study of 53 Turkish women with preterm low birth weight babies and 128 women with term babies, *P. micros* and *C. rectus* significantly

increased and *P. nigrescens* and *A. actinomycetemcomitans* significantly decreased risk of preterm delivery of low birth weight babies (114). A study among 161 Hungarian women found higher levels of periodontal pathogens, *P. gingivalis*, *P. nigrescens*, *T.forsythensis*, *A. actinomycetemcomitans*, *F. nucleatum*, *T.denticola*, *M. micros*, *C. rectus*, *E. corrodens*, *E. nodatum*, and *S. intermedius* in the PTB cases than controls (115). However, a recent study in the USA did not show significant differences between periodontal pathogens in preterm and term births (116).

Host immune response to oral pathogens appears to modify the risk of PTB; both maternal and fetal immunity appears to play an important role in determining PTB risk. In a study of 812 births, maternal immunoglobulin G (IgG) antibody to oral organisms was associated with a decreased rate of preterm delivery and an increase in birth weight, and therefore, provided protection to mothers and fetuses from exposure to bacterial pathogens (117). In contrast, in a predominantly African American group of 448 women, women with elevated second trimester serum IgG levels against *P. gingivalis* were more likely to give birth to a preterm low birth weight infant compared to those with lower serum values (118). In a predominantly Hispanic population (N= 203) there was no association of PTB with IgG levels against specific oral pathogens (119). While the host immune response appears to depend on race and ethnicity; the extent of this association with risk of PTB is not known.

Host genetics and PTB

A familial component to preterm birth has been established (120, 121) and includes an increased risk to PTB if the mother was premature herself (122), if the sister of the mother had a premature child (123) and if there is a sibling born from a previous spontaneous preterm delivery (124). A history of one previous preterm birth is associated with a recurrence risk, i.e., an odds ratio (OR) of 4.58 with a 95% confidence interval (CI) of 4.40-4.78 for 16 to 36 week gestation infants. Recurrence risk alone, however, may be explained by persistence of environmental risk factors and is not necessarily explained by genetic factors. Other studies provide more specific support for the role of genes in the causation of preterm birth. Ward showed a 50-fold increase in the coefficient of kinship for grandparents of preterm infants (121). Using a national cohort of female twin pairs in Sweden (2089 pairs) a significant genetic component was identified for PTB with a heritability of 0.36 (125). Treloar showed heritability of 0.27 in a large twin study of preterm labor in Australia (126). Overall, there is strong support for the role of genes present in the mother and/or fetus in PTB (127).

Although both periodontitis and bacterial vaginosis have a strong bacterial etiology, it is clear that in addition to environmental factors, genetic predisposition plays an important role in these diseases. A number of human gene polymorphisms studied to date for periodontal disease and bacterial vaginosis are involved in maternal and fetal inflammatory pathways and have been reviewed elsewhere (128, reviewed in 129, 130–134). These genetic polymorphisms likely result in functional changes (for eg increased expression of pro inflammatory factors), although this has not been demonstrated for all the gene polymorphisms studied to date (135, 136). Most of the research to date has focused on gene variations in pro- and anti-inflammatory cytokine genes and their respective receptors

because these cytokines increase expression of matrix degrading metalloproteinases. A recent study determine increased levels of IL-2, IL-4, IL-5, IL-8, IL-10, monocyte chemoattractant protein 1, macrophage inflammatory protein -alpha, MIP-1 β , soluble IL-6 receptor α , TNF α , soluble TNFR I, and TREM-1 (triggering receptor expressed on myeloid cells) were associated with PTB, while levels of IL-1 β , IL-18, matrix metalloproteinase 9, and neurotrophin 3 decreased in PTB (137). Increased expression of matrix metalloproteinases results in degradation of the extracellular matrix and contributes to cervical ripening and labor (138). Both periodontitis and bacterial vaginosis share a common association with a number of alleles of inflammation-associated genes; some of these have also been implicated in PTB (Table 5). Genetic polymorphisms in these host immune factors that result in increased production of inflammatory cytokines TNF α and IL-6 and decreased production of IL-10 are associated with increased risk of PTB (27). Recent studies imply that some of these differences are race-specific; levels of IL-6 (measured shortly before birth) were found to be higher in PTB (defined as < 35 weeks gestation) in Caucasian women ($p < 0.0003$) compared to African American women ($p < 0.6$), suggesting that elevated IL-6 concentrations are associated with preterm birth in Caucasians but not African Americans (139). In the same population levels of IL-8 were higher in PTB in Caucasians and IL-1 β levels were higher in African American PTB cases (140). It is not known to what extent gene-gene or gene-environment interactions play a role in racial differences seen in cytokine levels between Caucasians and African Americans. A recent study of PTB risk in African Americans suggests a strong role for maternal IL-12 and fetal IL-12RB, indicating that fetal and maternal factors may together contribute to genetic risks for PTB (141).

TNF α is involved in remodeling the cervix and fetal membranes by promoting production of collagen-degrading matrix metalloproteinases (MMPs), including MMP1 and MMP9 and levels of MMPs are higher in PTB and PPROM (142) (138, 143). TNF polymorphisms are not significantly associated with periodontitis; however plasma concentration and gingival cervical fluid levels of TNF α are higher in patients with aggressive periodontitis, which causes more severe inflammation in periodontitis lesions (144, 145).

Bacterial endotoxin and LPS produced by periodontitis and BV organisms activate pattern recognition molecules TLR2 and TLR4 on host cell surfaces and stimulate increased levels of TNF- α and matrix metalloproteinase's (146–148). In a murine model for pregnancy, oral infection with periodontal pathogen *C. rectus* resulted in increased levels of placental TLR4 levels (149). Gene environment interactions are likely to be important; carriers of TNF-2 allele were at a significantly increased risk of spontaneous preterm birth in a case-control study of 375 pregnant women (OR 2.7, 95% CI 1.7-4.5] and this risk was increased significantly when the women also had BV (OR 6.1, 95% CI 1.9-21.0) (150). Interactions between candidate genes in PTB outcome are also significant; a study demonstrating multilocus interaction between SNPs -3448 of TNF α , -7227 of IL-6, and 33314 of IL-6R was successful in predicting low risk of PTB genotypes in European-American women (RR 3.50, 95% CI 2.52-4.87) (151).

The increased risk of PTB due to exposure to bacterial factors is modified by the host's genetic background indicating that successful prevention of PTB may require antibiotic therapy to eradicate the bacterial organisms as well as immunomodulators to decrease the

levels of pro inflammatory immune factors that trigger processes leading to PTB. Studies on non human, primate models of PTB support the notion of preventing PTB by treating both the infection and the associated inflammation; administration of ampicillin together with dexamethasone/indomethacin delayed preterm birth induced by intraamniotic infection by group B *Streptococcus* ($P = .004$) (152).

Hypothesis : Oral-Vaginal Health Interaction

In the past decade there has been an explosion in non-culture based molecular methods to defining the microflora of the oral and vaginal sites; some of the newly discovered bacteria are not amenable to culture such as those belonging to the *Clostridiales* order, others are very fastidious such as *Atopobium*. The discovery of these non cultivable organisms has enabled molecular biologists to study archived tissues from studies and attempt to classify the breadth of bacterial diversity present in the oral and vaginal sites. As we begin to apply these methods to understand the complex microflora involved in bacterial vaginosis and periodontitis there is preliminary evidence pointing to subsets of bacterial organisms that can colonize both the vaginal and oral cavity and that increase risk of PTB (Table 3).

Although there are several reports on the associations of PTB independently with perturbed oral flora (periodontitis) and perturbed vaginal flora (BV), little is known about the combined effects of altered vaginal and oral health on PTB. We found only one report that studied both BV and gingivitis which reported that women with BV were more likely to have gingivitis and the bacterial loads of women with BV and gingivitis were higher than in women with BV alone (153). In women with BV and gingivitis, the vaginal samples had higher counts of bacteria commonly associated with periodontal disease including: *A. actinomycetemcomitans*, *Fusobacterium* sp., *P. micro*, *P. intermedia*, *P. gingivalis*, and *T. forsythia* in comparison with those with BV but not gingivitis, suggesting that oral disease may exacerbate the level of bacterial perturbations associated with BV. The association of BV and gingivitis with PTB was not reported.

The multifactorial etiology of periodontitis and BV are strikingly similar. Both BV and periodontitis are characterized by dynamic colonization by a number of opportunistic bacterial pathogens on squamous epithelial cells in the oral or vaginal cavities. Health behaviors and socioeconomic risk factors are similar between the two conditions (Table 4). Oral pathogens can spread to the vaginal cavity within the female host via the gastrointestinal tract; alternatively there may be transmission between individuals via oro-genital contact. Oral sex has been associated with gum disease (154). Dixon et al reported the isolation of *C. sputigena* and *F. nucleatum* from the amniotic cavity in a single case of PTB with clinical chorioamnionitis; a temporal relation was noted between orogenital contact with the male partner with periodontitis and the onset of clinical infection (155), suggesting exchange of PTB related microflora between oral and genital sites. Thus vaginal and oral cavities possibly share a subset of microbes, making the origin of bacteria isolated from PTB potentially hard to establish. The methodological differences in studies included use bacterial identification at different resolutions; while some studies report genus level identification of bacteria, others classify bacteria at the species level. A systematic analysis of bacterial diversity at oral and vaginal sites at the same taxonomic resolution will allow us to determine the extent of shared bacteria between oral and vaginal sites and its association

with PTB. Establishing the interaction of host genotype in modulating the combined risk of BV and periodontitis to PTB will help identify the subset of women who are at most risk of PTB and who are most likely to benefit from clinical interventions to prevent PTB.

Conclusion

Perturbations in bacterial flora resulting in both BV and periodontitis are potentially related to infection associated PTB. To date, infection associated PTB has been studied in a reductionist framework: oral and vaginal health are treated as being independent of each other. The combined effect of exposure to bacteria that are shared between the oral and vaginal sites and the modifying effect of host genetics on their association with PTB has yet to be studied. Normal bacterial flora represents a dynamic equilibrium of commensal bacteria and opportunistic pathogens. Host genetics and host behaviors modify the bacterial ecology of the vaginal and oral environments and host genetics. Further, there are striking similarities between host genetic factors that predispose to BV, periodontitis and PTB. Newer studies on infection associated PTB will benefit from recognizing the interrelationships between bacterial populations at vaginal and oral sites.

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Abbreviations

PTB	Preterm Birth
PPROM	Preterm premature rupture of membranes
BV	Bacterial vaginosis
RR	Risk ratio
IgG	Immunoglobulin
MMP	matrix metalloproteinases
TNF	Tumor necrosis factor

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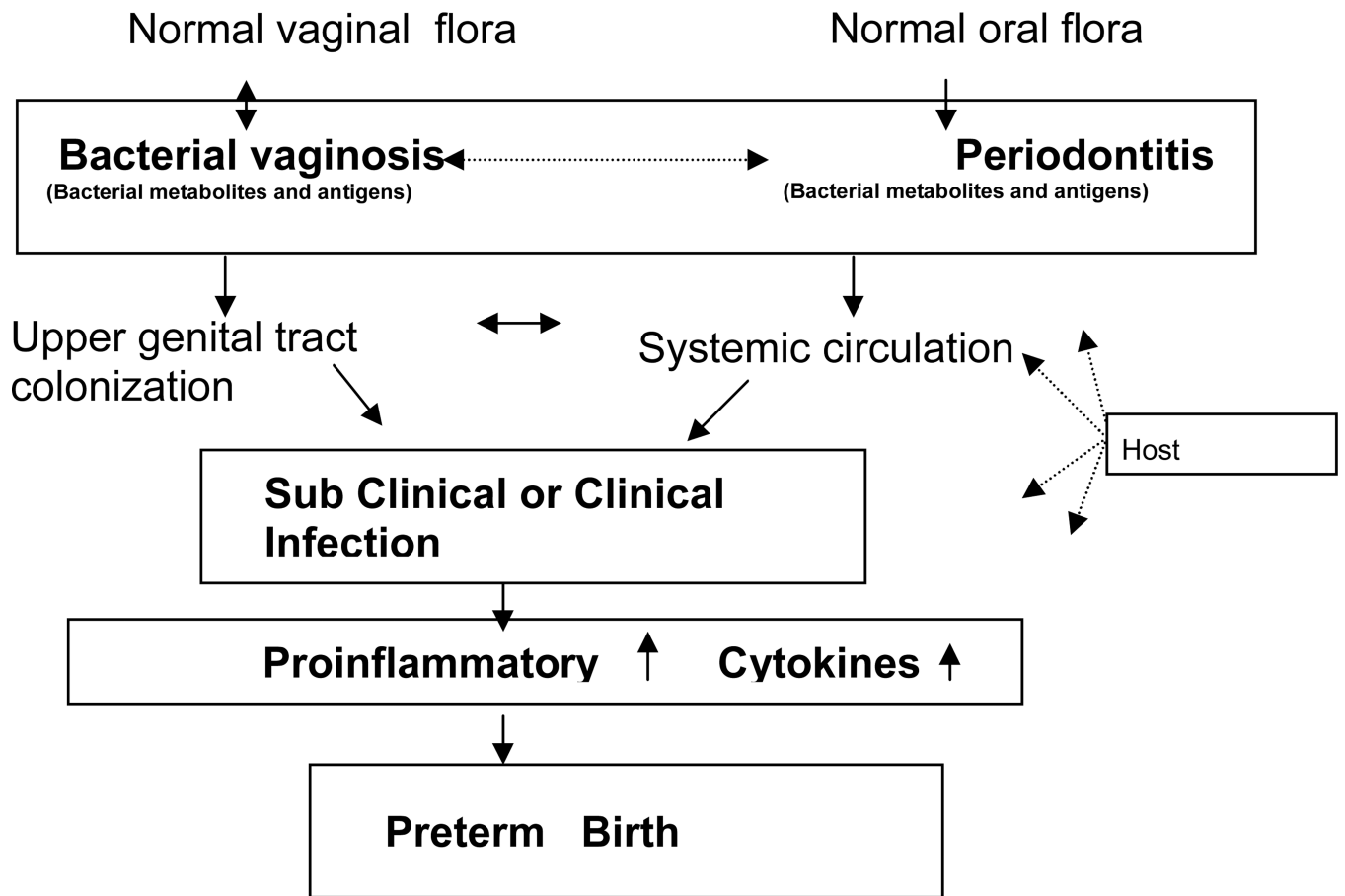


Figure 1.
Hypothesized parallel potential pathways for vaginal and oral flora leading to preterm birth

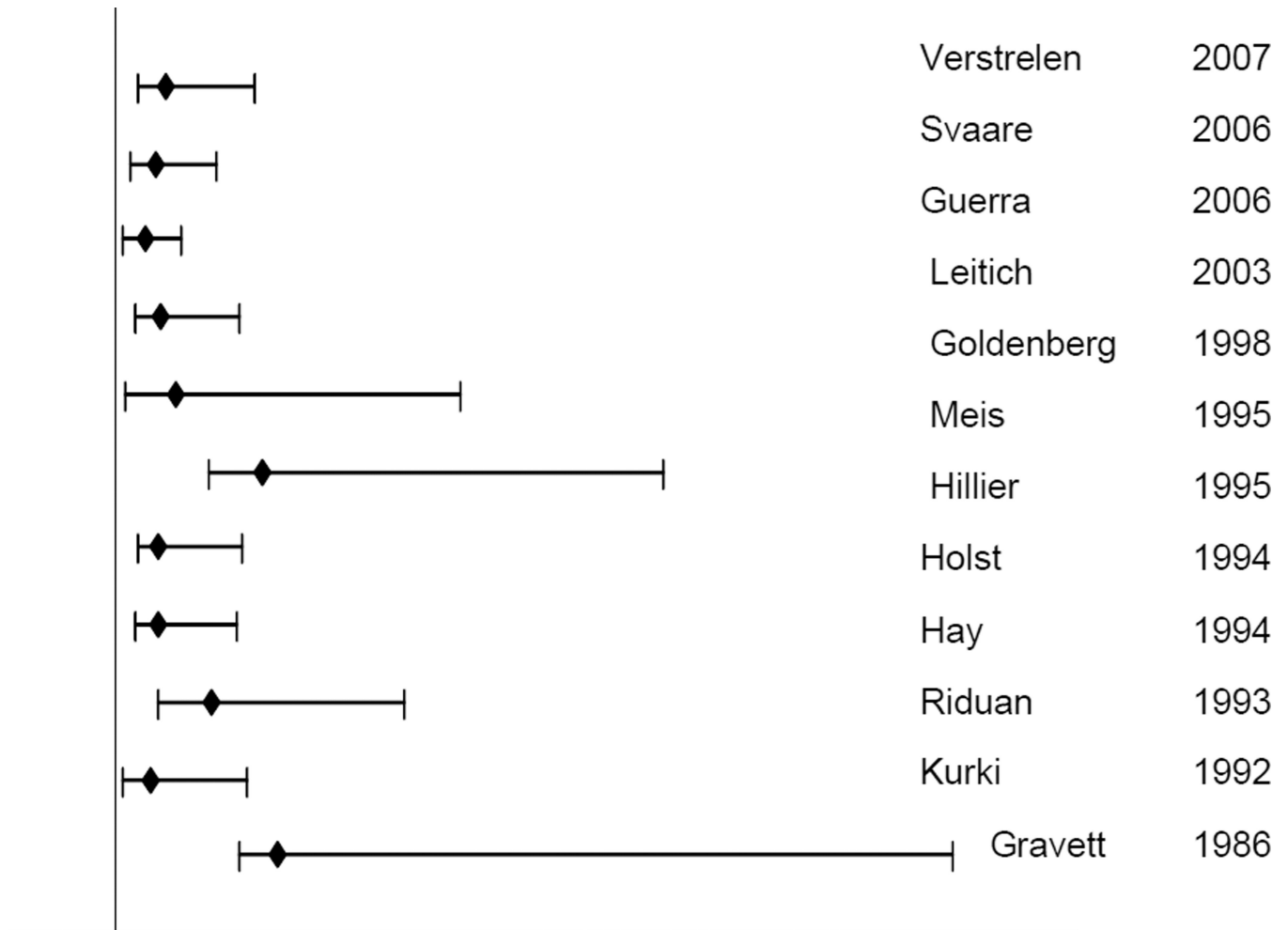


Figure 2. Relative risk of preterm birth with bacterial vaginosis

11 observational studies conducted between 1986 and 2007 on populations varying in sociodemographic variables and sample size were included. Y-axis intersects x-axis at relative risk = 1.

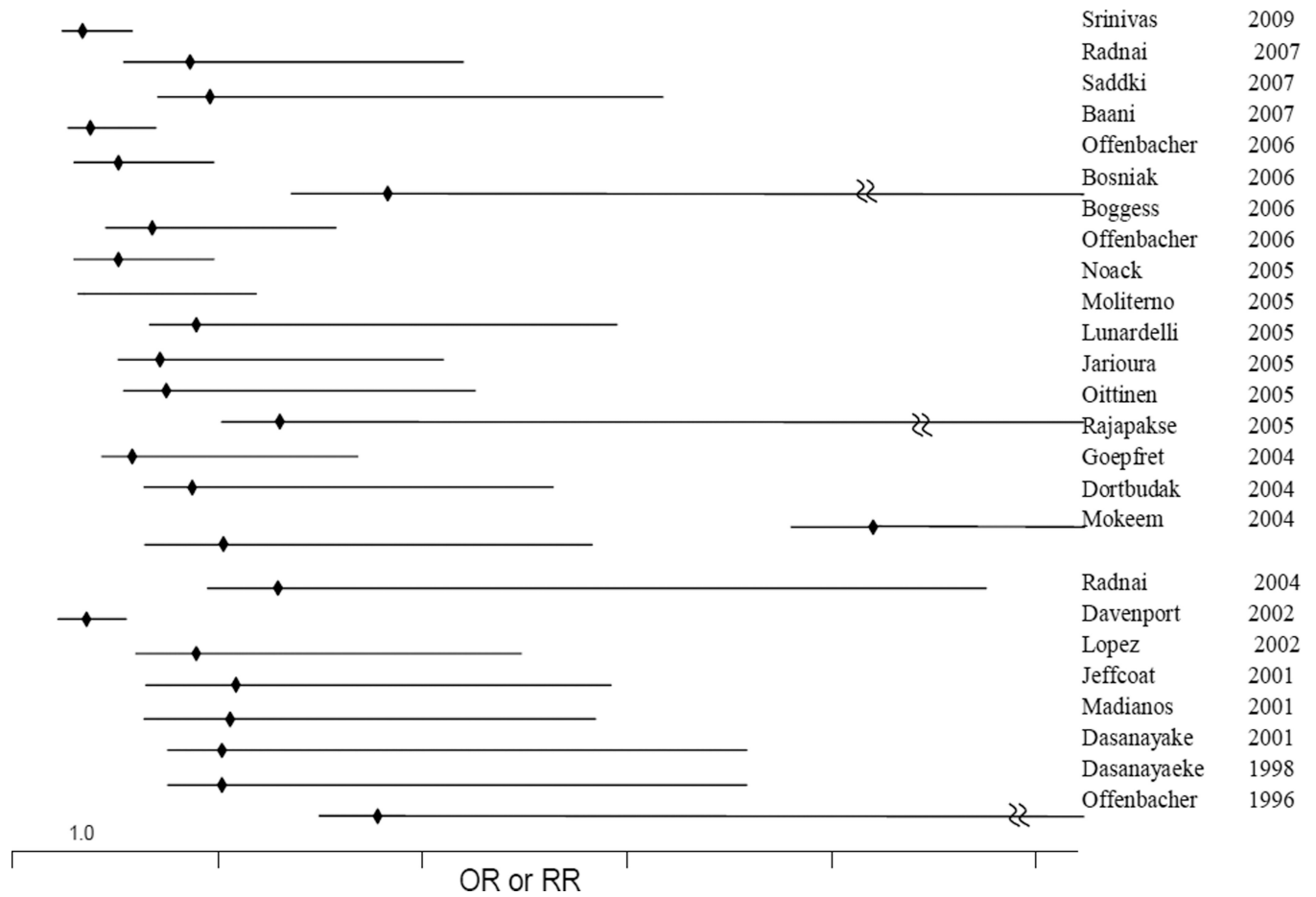


Figure 3. Relative risk of preterm birth associated with periodontitis
 25 observational studies conducted between 1996 and 2009 on populations varying in sociodemographic characteristics and sample sizes were included. Y-axis intersects X-axis at relative risk = 1.

Table 1

Organisms isolated from the amniotic cavity of pregnant women with preterm birth.

Organism	Species	Reference
<i>Acenitobacter</i>		
<i>Bacteroides</i>	<i>B.urealyticus</i>	(46, 73, 156, 157)
<i>Candida</i>		(29, 158)
<i>Capnocytophaga</i>	<i>C.sputigena</i>	(155, 159)
<i>Eikenella</i>	<i>E.corrodens</i>	(160, 161)
<i>Escherichia</i>	<i>E.coli</i>	(2, 45, 46)
<i>Fusobacterium</i>	<i>F.nucleatum</i>	(47, 155, 162)
<i>Gardnerella</i>	<i>G.vaginalis</i>	(73, 157)
<i>Lactobacillus</i>		(73)
<i>Leptotrichia</i>	<i>L.amnionii</i>	(46, 163)
<i>Mobiluncus</i>		(73)
<i>Mycoplasma</i>	<i>M.hominis</i>	(46, 52, 73, 157)
<i>Peptostreptococcus</i>		(73, 164)
<i>Staphylococcus</i>	<i>S.aureus</i>	(164)
<i>Streptococcus</i>	<i>S.agalactiae</i> <i>S.millerii</i> <i>S.acidominus</i> <i>S.intermedius</i> <i>S.constellatus</i> <i>S.sanguis</i> <i>S.mutans</i> <i>S.uberis</i>	(45, 73, 164–166)
<i>Ureaplasma</i>	<i>U.urealyticum</i>	(42)

Table 2
Effect of antibiotic treatment on specific bacterial organisms in preterm birth outcomes in the years 1990–2007.

Organism	Preterm birth Indicators	Association	Treatment Effect	Antibiotic(s) Prescribed	References
<i>S. agalactiae</i>	PTB <37 weeks	1.1 (0.9–1.4)	1.1 (0.8–1.2)	Assorted <i>i</i>	(63)
	LBW	1.3 (1.05–1.7)	1.0 (0.7–1.5)	Erythromycin <i>j</i>	(62)
	Chorioamnionitis	7.2 (2.4–21.2)	1.2 (0.34–4.4)	Not available	(64)
<i>U. urealyticum</i>	LBW <i>b</i>	Not reported	0.70 (0.46–1.07)	Erythromycin	(65)
				Clindamycin <i>a</i>	
<i>C. trachomatis</i>	PTB	9.0, p=0.05		Erythromycin <i>c</i>	(37)
	PPROM	1.3 (1.1–1.5)	0.37, p<0.01	Erythromycin	(84)
	PTB		0.39 (0.14–1.1)	Erythromycin	(67)
<i>T. vaginalis</i>	PTB		1.8 (1.2, 2.7) <i>d, f</i>	Metronidazole	(14, 84)
			1.45 (0.8–2.7)	Metronidazole	(67)
<i>T. vaginalis</i> + BV <i>e</i>		3.3 (1.01–10.7)	0.6 (0.19–1.9)	Clindamycin	(67)
		1.4 (0.4–5.5)			(167)
<i>T. vaginalis</i> + <i>C. trachomatis</i> +BV	PTB <37 weeks	3.6 (1.8–7.5)	0.13 (0.02–1.0)	Clindamycin	(167) <i>g</i>
Asymptomatic bacteriuria <i>E. coli</i> <i>a</i>	LBW	Not reported	0.66 (0.49–0.89)	Assorted <i>k</i>	(168)

a Results of meta analysis

b PTB outcome not measured

c Erythromycin treatment at 26 to 30 weeks. *U. urealyticum* colonization not associated with PTB.

d Metronidazole treatment was not associated with increased risk of PTB at <35 or <32 weeks

- ^e Individual effects not evaluated due to low numbers
- ^f Metronidazole treatment associated with increase in PTB
- ^g Study conducted in african american women
- ^h Heavy colonization, defined as growth of *S.agalactiae* in non-selective media
- ⁱ Antibiotics effective against *S. agalactiae* - penicillins, cephalosporins, erythromycin, clindamycin, trimethoprim-sulfa, sulfisoxazole, and triple sulfa vaginal cream were used in different studies
- ^j Treatment during the third trimester and before 30 weeks and continuing for 10 weeks or until 35 weeks 6 days of pregnancy
- ^k Treatments from different studies with one of the following: nitrofurantoin, sulphadimidine, penicillin and Sulphonamides

Table 3

Genus and species of organisms found in the vaginal and oral cavity and association with preterm birth.

Genus	Species	Found in Vaginal flora <i>b</i>	Found in Oral flora <i>b</i>	Associated with PTB? <i>b</i>	References
Bacteroides	<i>B. forsythus (T.forsythensis)</i>	x	x	x	(47, 169–173)
	<i>B. bivius</i>				
	<i>B. assacharolyticus</i>				
	<i>B. capillosus</i>				
Fusobacterium	<i>F. nucleatum sub nucleatum</i>	x	x	x	(47, 155, 162, 173–175)
	<i>F. nucleatum sub vincentii</i>				
	<i>F. nucleatum var polymorphum</i>				
Gardnerella	<i>G. vaginalis</i>	x		x	
Lactobacillus	<i>L. fermentum</i>	x	x	x	(174, 176–182)
	<i>L. crispatus</i>				
	<i>L. jensenii</i>				
	<i>L. gasseri</i>				
Peptostreptococcus	<i>P. micros</i>	x	x	x	(47, 173–175)
	<i>P. anaerobius</i>				
	<i>P. lacrimalis</i>				
	<i>P. ivoirii</i>				
	<i>P. assacharolyticus</i>				
	<i>P. magnus</i>				
<i>P. prevotii</i>					
Porphyromonas	<i>P. gingivalis</i>	x	x	x	(47, 172–175)
Prevotella	<i>P. intermedia</i>	x	x	x	(172–174, 183–185)
	<i>P. nigrescens</i>				
	<i>P. bivia</i>				
	<i>P. buccalis</i>				

Genus	Species	Found in Vaginal flora ^b	Found in Oral flora ^b	Associated with PTF? ^b	References
<i>Actinomyces</i>	<i>A. Actinomycetemcomita</i>		x	x	(178, 186)
	<i>ns A. naeslundii</i>				
<i>Campylobacter</i>	<i>C. gracilis</i>		x	x	(173, 175)
	<i>C. sputorum</i>				
	<i>C. rectus</i>				
	<i>C. showae</i>				
<i>Capnocytophaga</i>	<i>C. sputigena</i>		x	x	(186)
<i>Mobiluncus</i>	<i>M. curtisi</i>	x		x	(174, 182, 187)
	<i>M. mulieris</i>				
<i>Leptotrichia</i>	<i>L. amnionii</i>	x		x	(188, 189)
<i>Atopobium</i>	<i>A. rinae</i>	x	x	?	(175, 181, 182, 190–192)
	<i>A. vaginae</i>				
<i>Megasphaera</i>		x		?	(74, 193)
<i>Veillonella</i>	<i>V. parvula</i>	x	(194)	?	(195)
<i>Clostridiales order</i>	<i>BVAB1, BVAB2, BVAB3 a</i>	x		?	(74)

^a BVAB1-3 are uncultivable phylotypes of unknown genera in the *Clostridiales* order that are found highly associated with BV.

^b Genus but not necessarily all species listed

Table 4

Commonality of sociodemographic and behavioral risk factors for bacterial vaginosis and periodontitis

Bacterial Vaginosis	Periodontitis
Stress (196–198)	Stress (199, 200)
Smoking (201–203)	Smoking (204–209)
Poor nutrition (210, 211)	Poor nutrition (212)
Ethnicity : African Americans at higher risk of BV(213, 214)	Ethnicity; African Americans have a higher risk of periodontitis (215–217)
Microbiology of infection not fully characterized; decreased levels of H ₂ O ₂ producing <i>Lactobacilli</i> (218–220)	Microbiology of infection not fully characterized; decreased levels of H ₂ O ₂ producing <i>Lactobacilli</i> (176, 221, 222)
Invokes local proinflammatory immune response (223–225)	Invokes local and perhaps systemic immune response (226–228)

Table 5

Polymorphisms in host genetic factors that play a role in the inflammatory immune response to bacterial infection

Function	Polymorphism	Bacterial vaginosis association	Periodontitis association	PTB association
Pro and anti-inflammatory cytokines	TNF(-308)	x (229)	ns (230, 231)	x (232) ^c
	TNF-B1(codon 25)	nd	x (233)	nd
	IL-6 (-174)	nd ^b	x (233, 234)	x (235)
	IL-4(-590)	nd	x (236) ^c	nd
	IL1Beta (-511)	x (132) ^b	ns	x
	IL1Beta (+3954)	x (132) ^b	x (237)	nd
	IL-2 (-330)	nd	x (238)	x (239)
	IL-10 (1082)	nd	x (240)	
	IL-10 (819)	nd	x (240)	ns ⁽²⁴¹⁾
	IL-10(-590)	nd	x (240)	
	IL-1RN (VNTR)	x (242) ^a	x (237)	x (242)
	IFN- γ R1	nd	x (243)	nd
	Innate defence against bacteria	Toll like receptors		
TLR4 896		x (244)	x(245)	x (246)
TLR2		nd ^b	nd	x
Metalloproteinase				
MMP1(-1607)			x(247) (248) ^d	x (142)
MMP9(-1562)			x (249, 250)	x (251)
			x (251)	

nd not determined

ns not significant

^a only in African American women.

^b polymorphisms not known but enzymatic levels are higher in BV (252) (253, 254)

^c results in other studies do not show any association (255–258) (259)

^d results in other studies do not show association (260)