Opinion

The contagious environment of the oral cavity supports a complex microbial community. Accordingly, the oral cavity harbours the second most diverse microbial community in the body (being second only to the gut) with around 1000 species and many of them are uncultivated bacteria [1]. Humans depend on commensal bacteria for nutritive, immune modulation and maintaining health [2]. An array of physiological and pathological status such as the obesity and metabolic syndrome has been implicated for microbial changes in body sites termed as ‘dysbiosis’. Moreover, microbial changes could result in several body habitats such as the gut, oral cavity and vagina due to alterations in diet, environment, weight and hormones. Hence, significant microbial changes occur with regard to aforementioned body habitats as well as in placenta, during pregnancy which denotes a unique milestone in a woman’s life demonstrating weight gain, metabolic changes, endocrinal and immunological changes [3]. A growing body of research evidence substantiates the influential role of human microbiome, as characterized by next generation sequencing technologies in maternal and child health outcomes including preterm birth, cardio-metabolic complications of pregnancy such as pre eclampsia and gestational weight gain [3]. Nevertheless, microbial changes occurring in pregnancy could be considered as a natural consequence of a healthy pregnancy as well [4]. However, it is not so with mothers’ poor oral health status which provides the possible link between maternal periodontitis and increased risk of adverse pregnancy outcomes such as low birth weight, pre-term birth weight, pre-eclampsia [5-7]. This brief description provides some updated evidence-based insights in this regard.

As 35-50% of the oral microbiome is uncultivable, the array of culture-independent laboratory techniques including next generation sequencing (NGS), bacterial microarrays, DNA hybridization, PCR and quantitative PCR have dramatically improved appreciation of the diversity and characterization of the oral microbiome in [8]. Accordingly, recent developments in technology of molecular biology have significantly contributed to compositional analysis of oral bacteriome.

A significant body of research evidence supported an association between periodontal pathogenic bacteria and preterm birth and preeclampsia mediated via periodontopathic bacteria [5,6], for example, Fusobacterium nucleatum Porphyromonas gingivalis, Campylobacter rectus. Several pathways have been propose in this regard such as hematogenous spread (bacteremia) of periodontal pathogens, hematogenous spread of multiple mediators of inflammation that are generated by the host and/or fetal immune response to pathogenic bacteria as well as the possibility of oral microbial pathogen transmission resulting from sexual practices [6]. There is an upsurge of research evidence on the striking resemblance of the placental microbiome with maternal oral microbiome [9,10] there by providing the plausible mechanism between maternal periodontitis and adverse pregnancy outcomes.

Periodontal disease increases the risk for pre-term birth but treatment for this condition may not reduce the risk as reported by a large scale multi-centre randomized clinical trial conducted in USA [11], because causation and treatment efficacy could be interrelated or they could function independently. The classic example to support this notion is bacterial vaginosis, which is considered to be a contributory factor among other factors for preterm births, yet antibiotic treatment for bacterial vaginosis has not reduced the risk for pre-term births in controlled clinical trials [12]. Nevertheless, prevention and control of maternal periodontitis by appropriate public health interventions targeting women prior to getting pregnant and during early and late stages of pregnancy by
maintaining optimal oral hygiene status would be a cost-effective strategy to reduce the risk of adverse pregnancy outcomes. Further research is warranted in this regard.

References