Metagenomic Analysis of Oral Microbiome during pregnancy

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INTRODUCTION

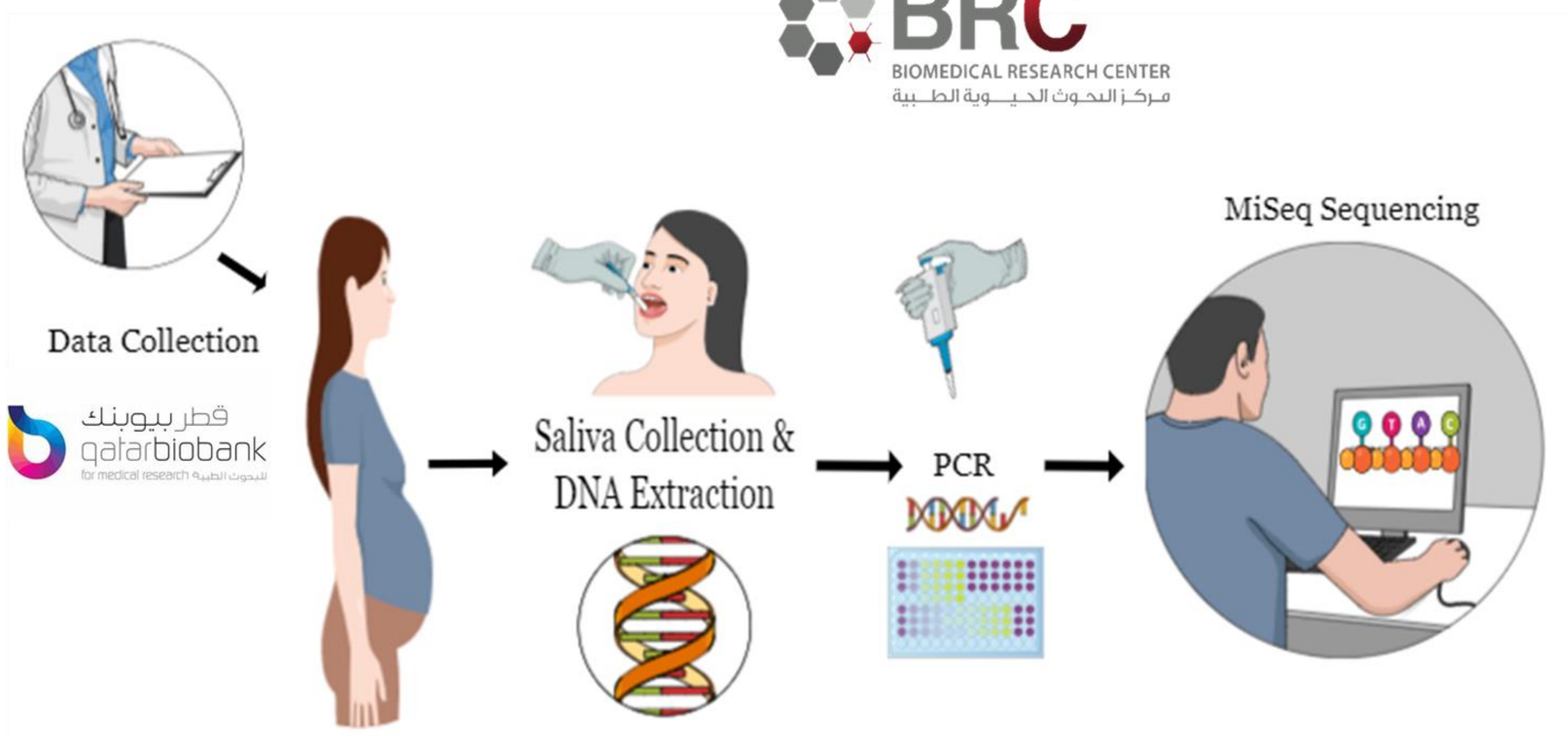
Pregnancy is associated with several hormonal, immunological and metabolic changes that are necessary to support the growing fetus. The pathological and physiological changes in pregnancy are greatly affected by the maternal microbiota [1]. During pregnancy, the composition of the maternal microbiota can change dramatically with fluctuations in certain bacteria's richness. The maternal oral cavity and gut incorporate diverse microbiota that play significant roles in preventing diseases, protecting the health of the oral cavity and maintaining oral hemostasis [2]. However, the specific roles that the oral microbiome plays during pregnancy are yet to be fully discovered [3].

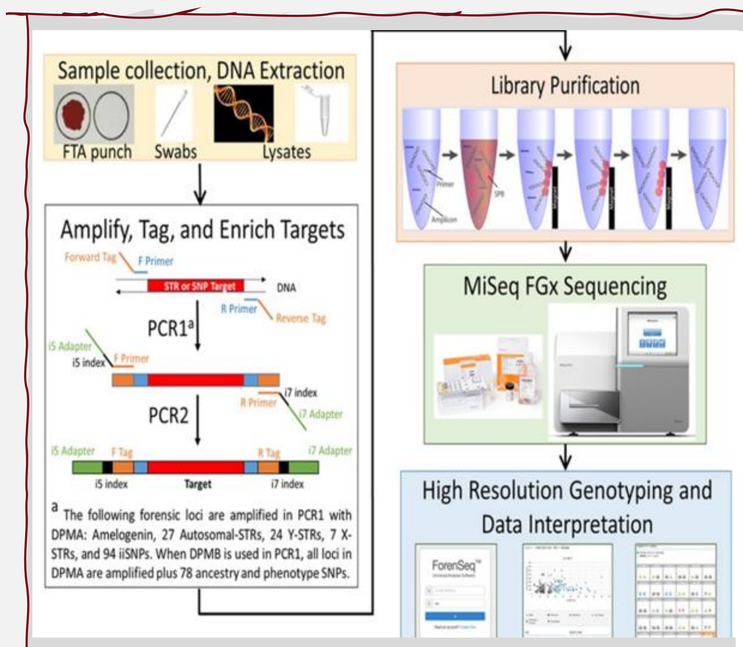
OBJECTIVES

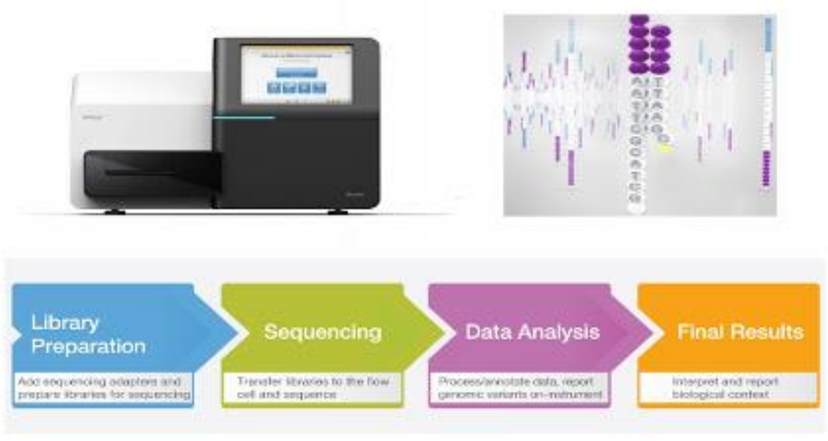
The role of oral microbiota during pregnancy is not well understood and has not been intensely studied. This study aim to analyze changes in the salivary microbiome in healthy pregnant women enrolled in the Qatari Birth Cohort (QbiC) and delineate oral microbiome markers characteristic of pregnancy..

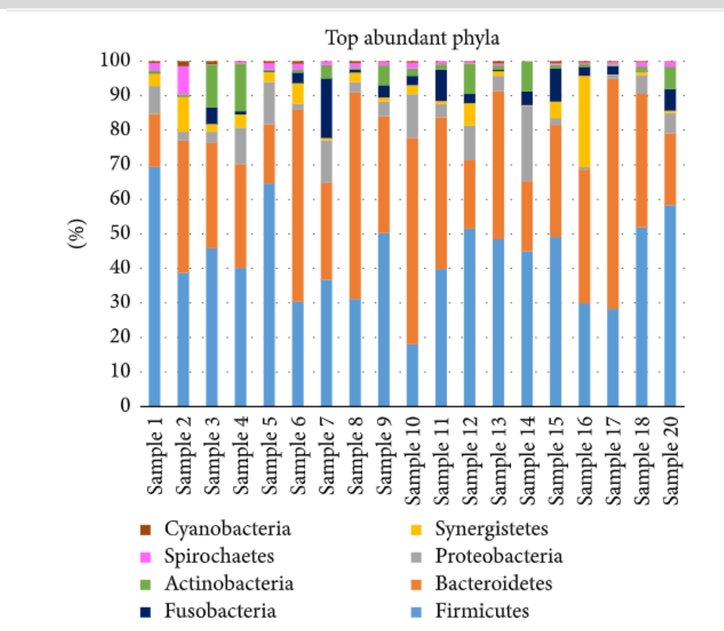
METHODOLOGY

1. Participant's data collection from QBB.
2. Saliva samples collection and DNA extraction.
3. DNA amplification using PCR.
4. MiSeq Sequencing for sample richness and diversity analysis.









Summary of anticipated benefit of the project

It is an epidemiological study that aims to assess the synergetic role of environmental exposure and genetic factors in the development of chronic disease. It monitors the health of women throughout their pregnancy and after birth. The present study is designed to explore changes in salivary microbiome, using high throughput sequencing during pregnancy and to explore key microbial clades involved in pregnancy.

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