Benign, potentially malignant & malignant oral lesions; an analysis of oral and gut microbiota

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Introduction:
The oral microbiota is known to have a role in the diseases affecting both the hard and soft tissues of the oral cavity. The gut microbiota is known to have a role with conditions affecting the bowel including colorectal cancer. It is already known that certain pre-dominantly oral microorganisms can be found in the gut; and have a role in the development of colorectal cancers. Understanding oral and gut microbiota profiles could aid with cancer screening by the development of an identifier profile for the detection of oral cancer.This study aims to: 1. Assess the gut and oral microbiota between patients with benign, pre-malignant and malignant oral lesions. 2. Determine if gut and oral microbiota profiles can be used as biomarkers for oral cancer. 3. Investigate the relationship of diet, BMI, smoking and alcohol on the gut and oral microbiota.

Methods:
Participants for this study will be patients that require an oral biopsy. A dataset for each participant has five components; two written forms and three microbiome samples. Written data consists of a demographics form and a Food Frequency Questionnaire (FFQ). The three microbiome samples are of saliva, oral biopsy tissue and stool. Participants will be grouped into three histological groups: benign, potentially malignant, and malignant. Samples will be stored at -20°C initially and then transferred to Teagasc for storage at -80°C. Following DNA preparation, the samples will undergo 16S rRNA MiSeq sequencing using protocol set by illumia (Illumina, Inc.). Microbiota analysis will be carried out to investigate if there is a relationship between gut and oral microbiota and its effect on oral malignancy. The demographics and food frequency data collected will be analyzed to investigate the relationship of diet, BMI, smoking and alcohol on the gut and oral microbiota.

Results:
Target sample size is 30 participants divided evenly across the three histological groups. Currently 27 participants have been screened and 20 recruited. 16 participants have a full dataset while 4 have a partial dataset.

Conclusions:
Conclusions to be made once all results are collected and analysed as described in the methods.