**Mycoplasma Multiplex PCR Analysis of Ocular Surface Squamous Neoplasia**

Introduction

**Ocular Surface Squamous Neoplasia (OSSN) is a form of ocular cancer**. In Zambia, ocular cancers are the 5th most common cancer (Kalubula et al). In Sub-Saharan Africa, rates of OSSN are more than double the rates of OSSN in the United States (Hossain and McKlelvie; Sayed-Ahmed; Simbiri and Robertson; Hollhumer). Recently, **OSSN has increased in prevalence in** individuals who are **immunocompromised** (specifically HIV positive) (Simbiri and Robertson). Diagnoses range from increased proliferation of the basal layer of epithelial cells of the ocular surface, to malignant cancer that envelopes the entire layer of epithelium.

An initial study conducted in Zambia recruited over 300 patients. Clinical and sociodemographic data was collected. From a subsection of these patients, the tumor removed was large enough to obtain for laboratory analysis. These **tumors were DNA extracted**. With these DNA extractions, we have **run multiplex PCR for a set of four bacterium** (Ureaplasma *spp*., Mycoplasma *hominis*, Mycoplasma *genitalium*, and Lactobacillus *iners*. These were qualitative measures to identify if any of the four bacterial species are present.

Objectives

Analysis of the multiplex PCR has yet to be performed. These results can be compared with other clinical data collected or sociodemographic data collected. The goal then is to determine if there is any association between OSSN clinical/sociodemographic data and the bacteria tested for in the multiplex PCR.

This will be completed through statistical analysis of select relationships (ie- HIV Status vs Mycoplasma Species), and graphical representation of the relationships. Additionally, I plan to build a function to filter out “NA” results by each specific factor. This may change as I move through the semester and learn more about code optimization and better ways to do the filtering.

For example, in my metadata, two of the important factors I want to consider are `HIV Status` and `Diagnosis`. When I filter out any samples that produced an “NA” with `HIV Status`, I do not want to lose samples that have a result in `Diagnosis`. So currently, I have done the following:

HIV\_meta\_wo\_NA <- meta %>% filter(HIV.STATUS=="POS"|HIV.STATUS=="NEG")

Diagnosis\_meta\_wo\_NA <- meta %>% filter(Diagnosis != "NA")

This is relatively easy, but I think there could be a better solution.

Methods

*Sociodemographic data*:

This data was collected by a paper questionnaire that was filled out by medical staff at the time of surgery/sample collection. It was then transposed into an excel document.

*Clinical data*:

Samples have been processed for a number of clinical tests, such as testing CD4+ T cell counts, HIV Viral Loads, and the presence of multiple oncogenic viruses. This data was recorded in excel.

*Mycoplasma Multiplex PCR*:

Samples were analyzed by PCR, then ran on an agarose gel. This was then interpreted as a positive or negative, and recorded in excel.

*Current Metadata*:

Excel sheets were combined into one excel document.

References

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