Rwanda, a landlocked African nation located at the east of Lake Kivu, struggles with widespread malaria with the prevalence reaching 42.3% in 2- to 10-year-olds ($\text{PPR}_{2\text{-}10}$). Our study focuses on the R561H mutation of *Plasmodium falciparum* which is a marker for possible antimalarial resistance (Uwimana et al., 2020). This work builds upon a previously developed model of malaria transmission and we explore 561H frequency prediction for the next twenty years.

**OBJECTIVES**

1. Comparing simulated $\text{PPR}_{2\text{-}10}$ with reference $\text{PPR}_{2\text{-}10}$ and verifying that the model we used is good for projecting future outcomes.

2. Running replicates for 561H frequency projection with different mutation rates and analyzing the trend of 561H frequency.

**RESULTS**

1. The frequency of 561H is likely to increase over the next 20 years regardless of the mutation rate.

2. All regions in Rwanda have a similar 561H frequency initially. However, starting from 2035, low prevalence regions and high prevalence regions have slightly higher 561H frequency than other regions while 561H frequency remains high in all regions of Rwanda.

3. Since 561H’s frequency will continue growing swiftly, we believe that it is important to take immediate actions to prevent this situation from happening.

**CONCLUSIONS AND FUTURE WORK**

1. Based on our research, the future situation of 561H in Rwanda is likely to lead to increased antimalarial resistance over the next 20 years.

2. We believe that 561H should be closely monitored and immediate actions are needed to prevent bad things from happening.

3. Continued improvements to the simulation will allow for improvements in accuracy and projected outcomes.

**REFERENCES**

