

# Investigating the Influence of Phage Resistance Evolution on the Rhizobia Genome

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## Abstract:

Rhizobia is a soil bacteria that fixes the nitrogen levels inside nodules. During the course of my highly engaging research lab, we studied the interactions of each stage that rhizobia goes through to do this task and how it affects new hosts. My role in the research lab was to assemble not just one but two distinct rhizobia strains and then characterized the genomic changes. As part of this work, I also compared two genome assemblers. I used Canu and Flye to assemble reads from Nanopore. After the reads were assembled, the computer language Linux was used to code to get ancestral and evolved reads. This involved mapping, using methods like snippy, to get the evolved genomes back to the ancestral genome. Once the mapping process was done, a small amount of Python was used to get the results of how the evolution of phage resistance impacts the rhizobia genome. we can see that there 101 different changes that happened for H3C1 and there were 112 changes that happened for H3C2.

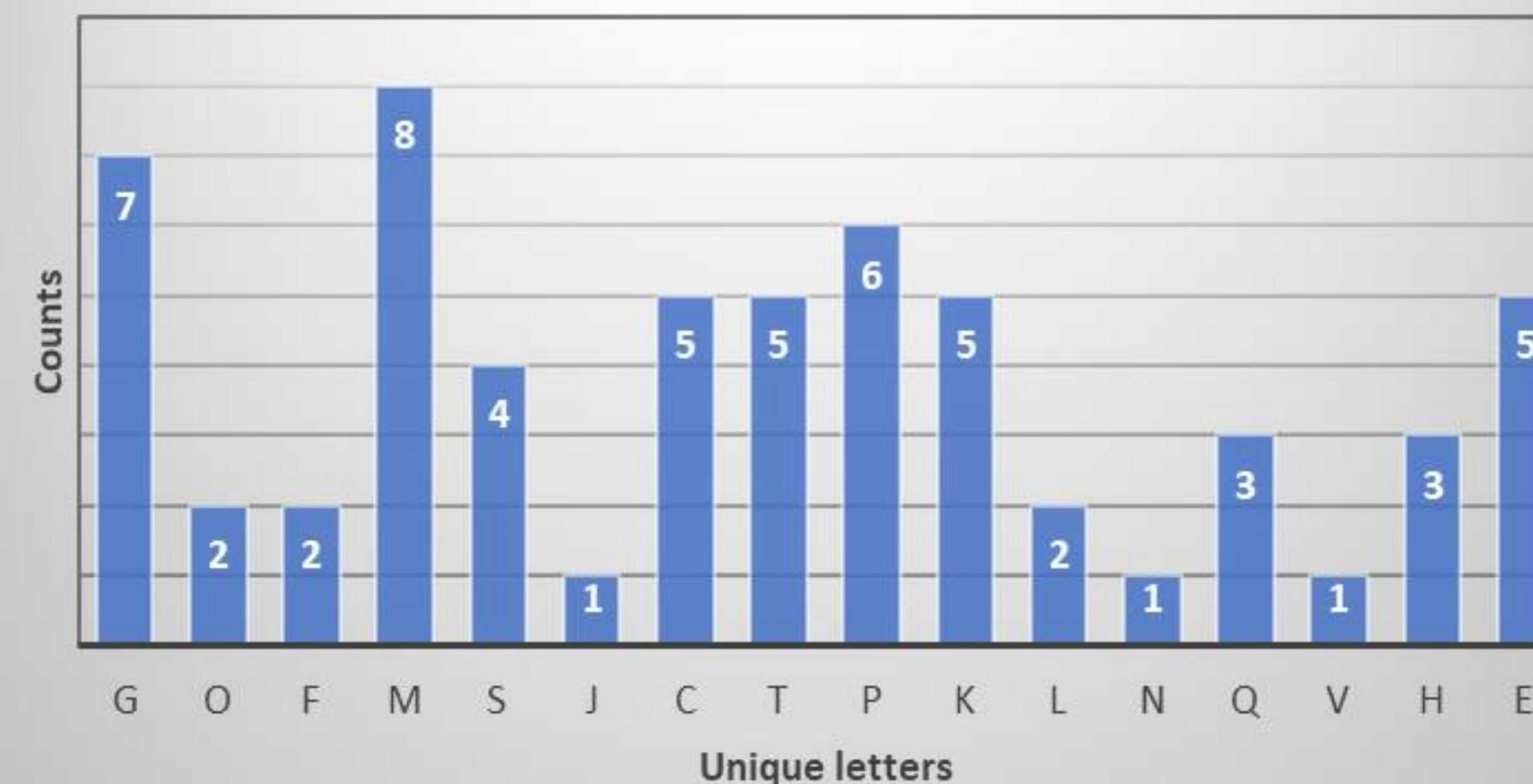
## Question

- How does the evolution of phage resistance impact the rhizobia genome?

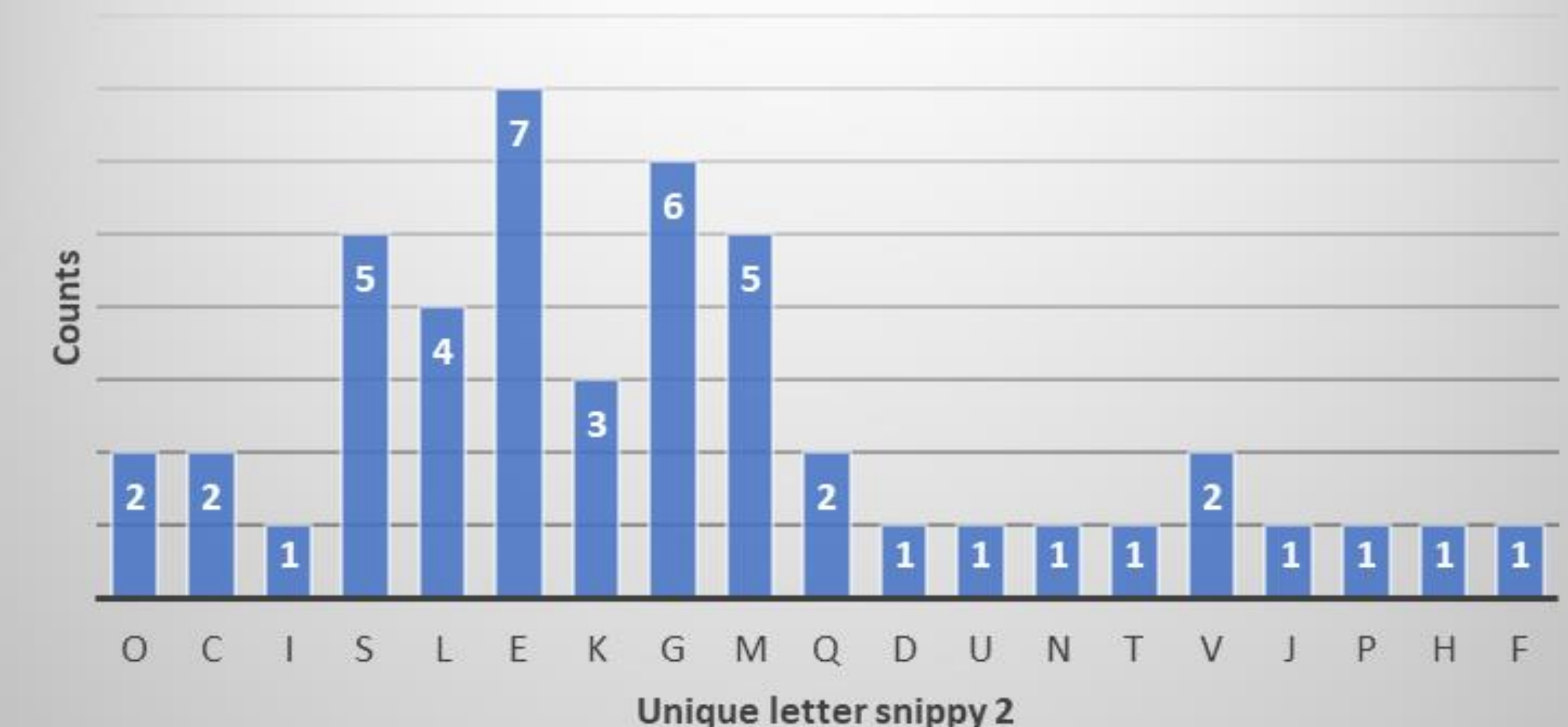
## Methods:

- **Canu** - The software tool is used for genome assembly, which is the process of reconstructing complete genomes from fragmented DNA sequences.
- **Breseq** - a computational tool used for analyzing microbial genome evolution and mutations.
- **Snippy** - Snippy is a bioinformatics tool used for rapid and accurate variant calling in bacterial genomes.

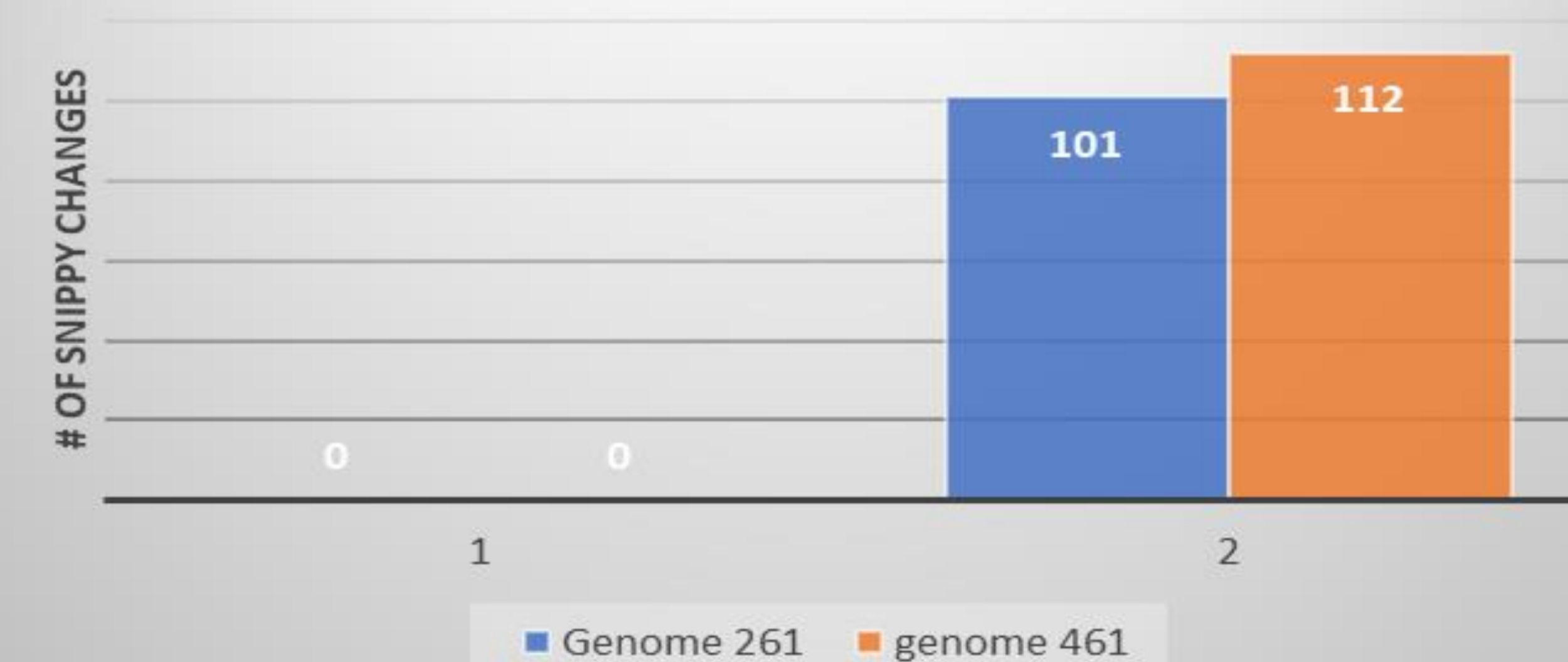
COG unique letters x counts



2nd COG letters x count



THE CHANGES OF SNIPPY CHANGES



## Conclusion:

As shown in the graphs above, the evolution of phage resistance has many impacts on the rhizobia genome. For example, the number of snippy changes that happen to each genome strand and the difference between the two strand Unique COG letters.

## Acknowledgements:

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