# Community-driven genomics of Helicobacter pylori in Arctic Indigenous communities unravels global signals of circulating strains.

# A community-driven genomic investigation of Helicobacter pylori in Arctic Indigenous communities.

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# Background<sup>1</sup>



Helicobacter pylori is a leading cause of stomach



Prevalence is a sign of inequity.

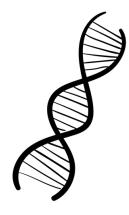


Infections and gastric disease are more common and severe in Arctic Indigenous communities.

# Objectives



Determine the phylogeny of Arctic, Manitoban, and global *Helicobacter pylori* based on genomic similarity.



Investigate if circulating Arctic Helicobacter pylori strains have unique genetic features, for example in key virulence factors like the cag pathogenicity island.

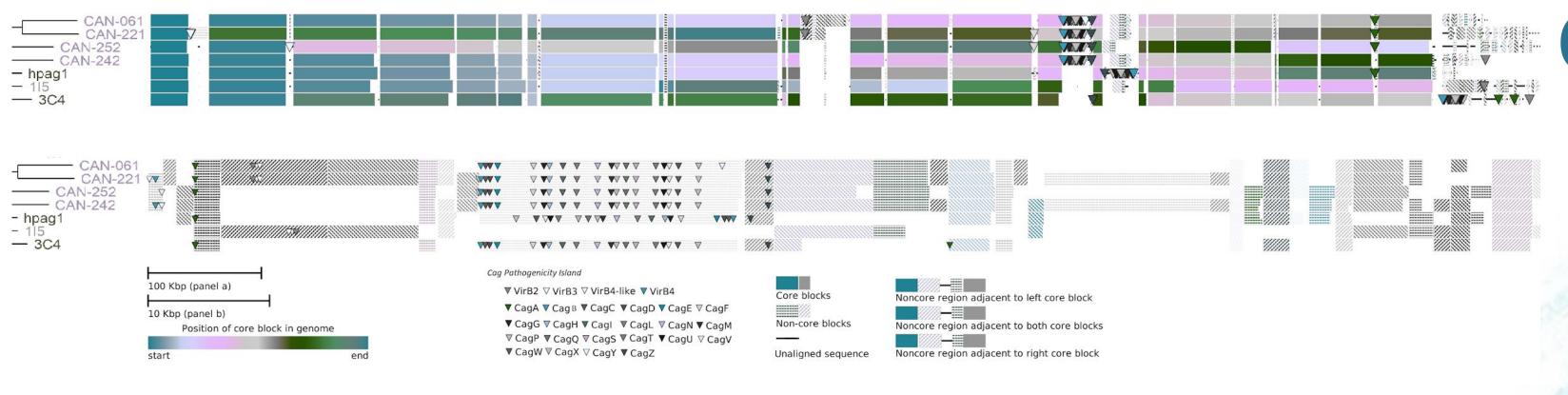
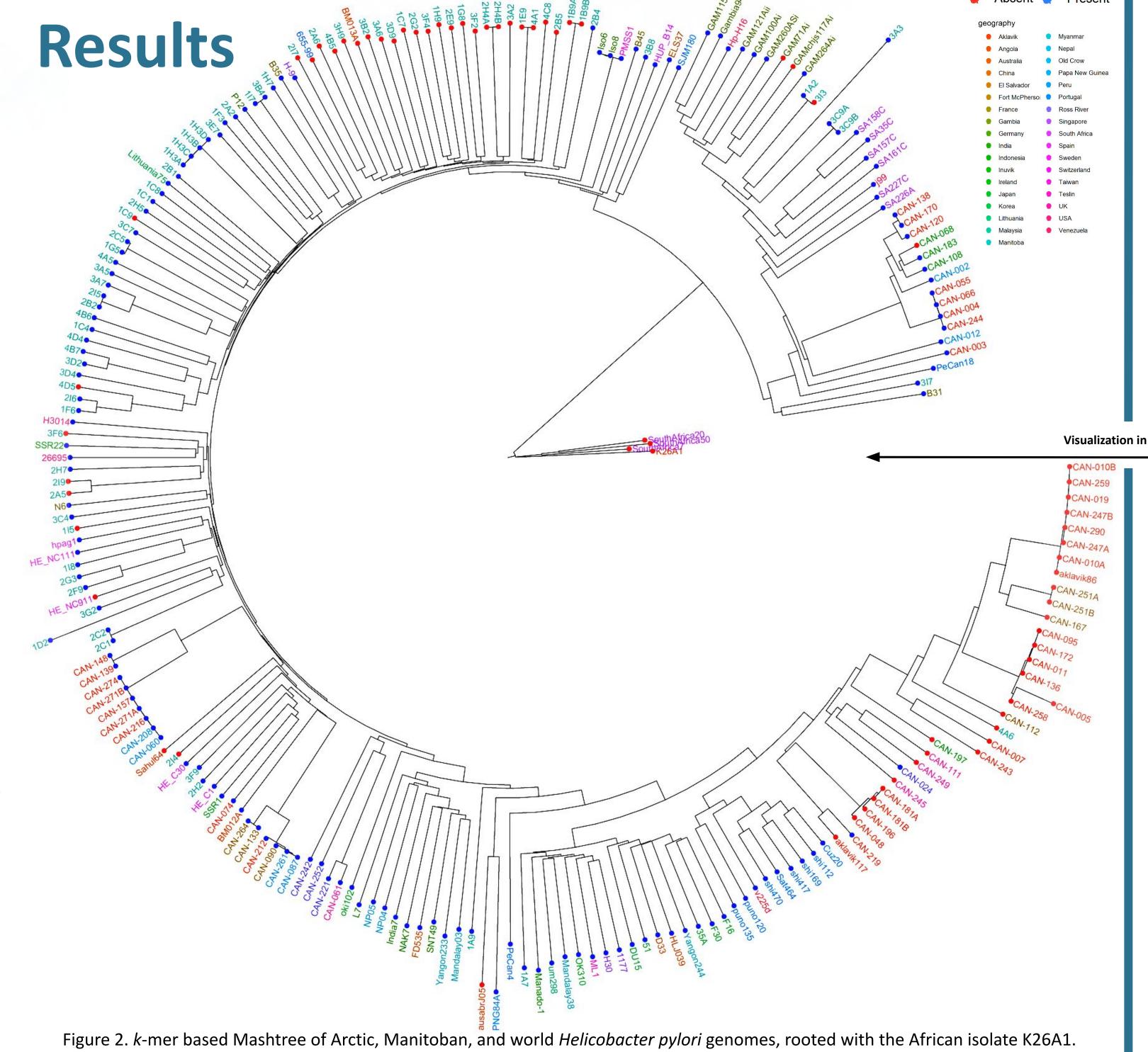


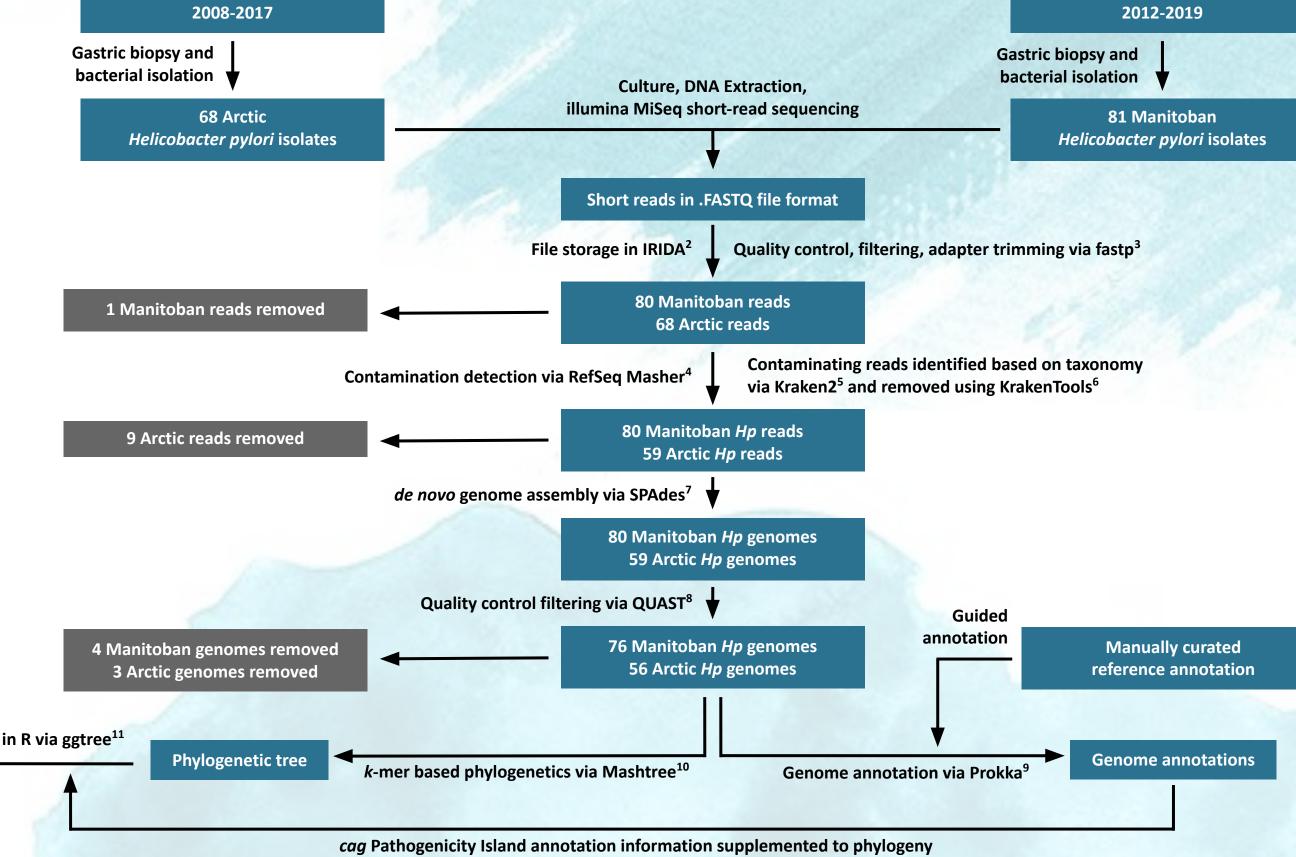
Figure 1. Presence and absence of the cag pathogenicity island within a clade of Helicobacter pylori genomes.



While Helicobacter pylori from Southern Manitoba cluster with isolates from every geography, Arctic isolates (CAN-XXX) have tight clades with African, European, Asian, and Indigenous signal. Indigenous strains in the Arctic lack the cag pathogenicity island, while African, European, and Asian strains maintain it.

The phylogenetic tree is annotated with isolate geographical source and cag pathogenicity island presence or absence.

# Methods



### Further Discussion

The Helicobacter pylori genome has high rates of mutation and recombination. Because of this, various reference-based bioinformatics tools are unsuited for genomic analysis<sup>12</sup>. Phylogenomics was done using a reference-free k-mer based tool, Mashtree<sup>10</sup>. The phylogenetic tree presented in the Results section contains all sequenced Arctic and Manitoban isolates, supplemented with publicly available genomes from across the world.

The scope of this project was unfortunately limited due to the COVID-19 pandemic. The pandemic and associated lockdowns resulted in the loss of a number of Helicobacter pylori isolates, as well as limiting the amount of laboratory work that could be done. Sequencing and conducting genomic analysis on all approximately 280 CANHelp Helicobacter pylori isolates falls outside the scope of my MSc project. Further work by CANHelp students, fellows, and other researchers will build upon the exploratory results of this pilot project.

Work still required for this MSc project includes characterizing the presence of significant genomic features within all isolates including antimicrobial resistance, virulence factor presence and genotyping, and the presence of mobile genetic elements such as transposons, phages, and integrative and conjugative elements.

Phylogenomic data will be overlayed onto geographic maps to better visualize the presence of strains with genetic origin across geographies using GenGIS 2<sup>13</sup>. Investigating genomic admixture and ancestral recombination events will be done using Gubbins<sup>14</sup>, fineSTRUCTURE, and ChromoPainter<sup>15,16</sup>. It is expected that Manitoban genomes will be the product of significant admixture, while Arctic isolates will have less due to their geographic and cultural isolation<sup>17</sup>.

A planned genomics workshop in Inuvik, NT for April 2020 was cancelled due to COVID-19. As a result, community engagement and knowledge exchange activities with CANHelp partner communities were conducted virtually in February and March of 2021.

### Acknowledgements

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