Title
Genome Sequences of Three Colombian Helicobacter pylori Strains Isolated from Tolimense Patients.

Permalink
https://escholarship.org/uc/item/70f1s0r3

Journal
Microbiology resource announcements, 9(18)

ISSN
2576-098X

Authors
Guevara, Alix A
Torres, Roberto C
Suárez, John J
et al.

Publication Date
2020-04-30

DOI
10.1128/mra.00117-20

Peer reviewed
ABSTRACT  We present the complete genome sequences of three *Helicobacter pylori* strains isolated from patients who resided in Tolima Department, Colombia, diagnosed with chronic gastritis. The genomes present an average length of 1.6 Mbp and 1,546 genes and correspond to different *H. pylori* subpopulations.

*Helicobacter pylori* colonizes over 50% of the human population, and it is estimated that in Colombia, 70 to 80% of the adult population is infected (1). Although colonization of the gastric mucosa with *H. pylori* is the main known risk factor for gastric cancer, just a small percentage of infected people develop disease (2). Altered coevolution of the human host and its infecting *H. pylori* strain is associated with increased risk for premalignant gastric lesions (3). In Colombia, genomic studies of infecting *H. pylori* have shown a mixed ancestry between the European, African, and Asian origins, and some isolates diverge from the reported populations and constitute a different subgroup (4–6). We are still learning about the structure of *H. pylori* populations in Colombia, and isolates from more regions need to be studied. This report presents the draft genome sequences of three *H. pylori* strains isolated from patients with gastritis in the department of Tolima.

This study was approved by the Tolima University Bioethics Committee (act number 02 of 31 July 2018). Informed consent and histopathological diagnosis were recorded for all participants. Gastric biopsy specimens were collected from patients at Javeriana Clinic during upper gastrointestinal endoscopy as part of the treatment of dyspepsia. The gastric biopsy specimens were grown on blood agar supplemented with sodium carbonate, hydrolyzed casein, tryptone, activated carbon, 10% fresh horse blood serum, and 1% Vitox and *Campylobacter* selective supplements (Oxoid, Basingstoke, UK) at 37°C for 3 to 15 days under microaerophilic conditions. Each isolate was obtained from a single colony that was grown under the same conditions for 3 days, and genomic DNA was obtained from established growth using a DNeasy blood and tissue kit (Qiagen). Sequencing libraries were prepared with a TruSeq Nano DNA kit (Illumina), and genomes were sequenced using the 2 × 150 paired-end protocol of the Illumina NovaSeq platform (Macrogen, South Korea). Read data sets were trimmed to improve quality with the software package Trimomatic version 0.39 (7). The genomes were assembled de novo with SPAdes version 3.13.1 (8) and annotated with Prokka version 1.12 (9). Ancestry of the samples was determined using fineSTRUCTURE version 4 (10) and ChromoPainter version 2 (11) based on the single nucleotide polymorphisms (SNPs) present in the core genome and using the default parameters. To calculate the


Editor  Julie C. Dunning Hotopp, University of Maryland School of Medicine

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Address correspondence to Mabel E. Bohórquez, mbohorquez@ut.edu.co.

Received 28 February 2020

Accepted 13 April 2020

Published 30 April 2020
# TABLE 1 Summary of genome sequences reported

<table>
<thead>
<tr>
<th>Strain</th>
<th>BioSample accession no.</th>
<th>GenBank accession no.</th>
<th>SRA accession no.</th>
<th>Diagnosis</th>
<th>Host origin in Colombia</th>
<th>No. of contigs &gt;0 bp</th>
<th>No. of contigs &gt;1,000 bp</th>
<th>Genome size (bp)</th>
<th>Coverage (x)</th>
<th>GC content (%)</th>
<th>N50 (bp)</th>
<th>No. of genes</th>
<th>Population</th>
</tr>
</thead>
<tbody>
<tr>
<td>GCT27</td>
<td>SAMN1 3950472</td>
<td>CP048601</td>
<td>SRR1 1183158</td>
<td>Chronic active gastritis</td>
<td>Valle del Cauca</td>
<td>57</td>
<td>32</td>
<td>1,643,791</td>
<td>102</td>
<td>39.000</td>
<td>110,298</td>
<td>1,559</td>
<td>hspAfrica1WAfricaNAmerica</td>
</tr>
<tr>
<td>GCT43</td>
<td>SAMN1 3950473</td>
<td>CP048600</td>
<td>SRR1 1183157</td>
<td>Chronic active gastritis</td>
<td>Risaralda</td>
<td>68</td>
<td>35</td>
<td>1,642,398</td>
<td>102</td>
<td>39.046</td>
<td>98,340</td>
<td>1,566</td>
<td>hspAfrica1SAfricaMiscAmerica</td>
</tr>
<tr>
<td>GCT97</td>
<td>SAMN1 3950474</td>
<td>CP048599</td>
<td>SRR1 1183156</td>
<td>Chronic active gastritis</td>
<td>Tolima</td>
<td>60</td>
<td>40</td>
<td>1,656,586</td>
<td>103</td>
<td>38.847</td>
<td>94,297</td>
<td>1,569</td>
<td>hspSWEuropeColombia</td>
</tr>
</tbody>
</table>

*a* Including contigs of ≥0 bp.  
*b* Based on contigs of ≥500 bp.
population, we included as donors all those genomes included by Thorell et al. (5), Gutiérrez-Escobar et al. (4), and Muñoz-Ramírez et al. (6).

On average, the genomes have 39% GC content, 1.6 Mbp size, and 1,564 genes. Although the strains are from patients who reside in the same department, the population of each strain was different (Table 1); the GCT27 strain corresponds to a North American subpopulation with African ancestry, the strain GCT43 corresponds to a subpopulation including strains from different regions of Latin America with African ancestry, and the GCT97 strain corresponds to a Colombian subpopulation with European ancestry. These genomes provide information on the genetic population structure and the evolution of Colombian *H. pylori*.

**Data availability.** The sequence read files and the genome sequences of the strains have been deposited in the GenBank database under the accession numbers shown in Table 1. These sequences represent the first described versions (CP048601.1, CP048600.1, and CP048599.1).

**ACKNOWLEDGMENTS**

This study was supported by the Research Group in Cytogenetic Phylogeny and Evolution of Populations of Tolima University, Infectious Diseases Research Unit of the Instituto Mexicano del Seguro Social, and by the program for the formation of high-level human capital for the Department of Tolima of Colciencias and Tolima governorate (755-2016).

**REFERENCES**