**Genome Sequences of Three *Helicobacter pylori* Strains from Patients with Gastric Mucosa-Associated Lymphoid Tissue Lymphoma**

Hsuan-Chen Wang, a Feng-Chi Cheng, b Ming-Shiang Wu, c Hung-Yu Shu, d H. Sunny Sun, e Yu-Chun Wang, a Ih-Jen Su, a Chi-Jung Wu a

National Institute of Infectious Diseases and Vaccinology a and Institute of Population Health Sciences b, National Health Research Institutes, Miaoli, Taiwan; Department of Internal Medicine, National Taiwan University Hospital, Taipei, Taiwan c; Department of Bioscience Technology, Chang Jung Christian University, Tainan, Taiwan d; Institute of Molecular Medicine, College of Medicine, National Cheng Kung University, Tainan, Taiwan e; Department of Internal Medicine, National Cheng Kung University Hospital, Tainan, Taiwan f

Most of the published complete genome sequences of *Helicobacter pylori* strains are limited to clinical isolates associated with gastritis, peptic ulcers, or gastric cancer. The genome sequences of three *H. pylori* strains isolated from patients with gastric mucosa-associated lymphoid tissue (MALT) lymphoma are presented here to facilitate studies of *H. pylori*-associated MALT lymphomagenesis.

**TABLE 1 Summary of statistics for three sequenced gastric MALT lymphoma *H. pylori* strains**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genome content</th>
<th>Accession no.</th>
<th>Genome length (bp)</th>
<th>Coverage depth (fold)</th>
<th>G+C content (%)</th>
<th>No. of predicted genes</th>
<th>No. of coding sequences</th>
</tr>
</thead>
<tbody>
<tr>
<td>HPML01</td>
<td>Circular chromosome</td>
<td>AP014710</td>
<td>1,629,815</td>
<td>67</td>
<td>38.69</td>
<td>1,707</td>
<td>1,671</td>
</tr>
<tr>
<td>HPML02</td>
<td>Circular chromosome</td>
<td>AP014711</td>
<td>1,562,125</td>
<td>45</td>
<td>38.92</td>
<td>1,751</td>
<td>1,715</td>
</tr>
<tr>
<td>HPML03</td>
<td>Circular chromosome and circular plasmid</td>
<td>AP014712 (chromosome) and AP014713 (plasmid)</td>
<td>1,629,114 and 6,220</td>
<td>60</td>
<td>38.67</td>
<td>1,744</td>
<td>1,708</td>
</tr>
</tbody>
</table>

a Determined by OMIGA.
b Determined by 454 Newbler.
c Determined by CG-Pipeline software.
and HPLM03 that are absent in the five published *H. pylori* strains (namely, 26695 [recovered from a patient with gastritis], HP J99 [duodenal ulcer], HPAG1 [atrophic gastritis], G27 [unspecified], and Shi470 [chronic gastritis]) (7–11), eight of which are hypothetical proteins. HPLM01, HPLM02, and HPLM03 also were found to share many gene substitution, deletion, and insertion sites that are not present in the five published strains. Although the biological significance of this genetic variability needs to be functionally validated, knowledge of the genome sequences of MALT lymphoma *H. pylori* strains opens new avenues for the further genomics-based exploration of virulence determinants contributing to MALT lymphomagenesis.

**Nucleotide sequence accession numbers.** The genome sequences of HPLM01, HPLM02, and HPLM03 were deposited into the whole-genome sequencing (WGS) database of DDBJ/EMBL/GenBank under the accession numbers listed in Table 1. The versions described in this paper are the first versions.

**ACKNOWLEDGMENTS**

This work was supported by an intramural grant from the National Health Research Institutes, Taiwan (IV-101-SP-13). We thank the Center for Genomic Medicine of the National Cheng Kung University for support of this project.

**REFERENCES**