AUTHORS’ CORRECTIONS

cagA-Positive Helicobacter pylori Populations in China and The Netherlands Are Distinct

ARIE VAN DER ENDE, ZHI-JUN PAN, ALDERT BART, RENÉ W. M. VAN DER HULST, MONIQUE FELLER, SHU-DONG XIAO, GUIDO N. J. TYTGAT, AND JACOB DANKERT

Departments of Medical Microbiology and Gastroenterology, Academic Medical Center, University of Amsterdam, Amsterdam, The Netherlands, and Shanghai Institute of Digestive Disease, Shanghai Second Medical University, Shanghai, People’s Republic of China

Volume 66, no. 5, p. 1822–1826, 1998. Page 1823, column 2: The following paragraph should be inserted at the end of Materials and Methods:

Nucleotide sequence accession numbers. The nucleotide sequences of cagA and glmM have been deposited in the GenBank database under accession no. AJ252963 to AJ252986 and AJ252987 to AJ253010, respectively.

Genomic Analysis Reveals Variation between Mycobacterium tuberculosis H37Rv and the Attenuated M. tuberculosis H37Ra Strain

ROLAND BROSCH, WOLFGANG J. PHILLIPP, EVANGELOS STAVROPOULOS, M. JOSEPH COLSTON, STEWART T. COLE, AND STEPHEN V. GORDON

Unité de Génétique Moléculaire Bactérienne, Institut Pasteur, 75724 Paris Cedex 15, France, and Division of Mycobacterial Research, National Institute for Medical Research, London NW7 1AA, United Kingdom

Volume 67, no. 11, p. 5768–5774, 1999. Page 5773, column 2, “Acknowledgments”: Because of an administrative error, the second paragraph was incomplete and should read as follows:

“Financial support for this work was provided by the Wellcome Trust, the Biomed Program of the European Community (grant BMH4/CT97/2277), the Institut Pasteur, and l’Association Française Raoul Follereau. S. V. Gordon was the recipient of a Wellcome Trust International Travelling fellowship.”