

# European Helicobacter and Microbiota Study Group

## XXIXth International Workshop on Helicobacter & Microbiota in Inflammation & Cancer

WILEY **Helicobacter**

Magdeburg, Germany  
15-17 September 2016

### Accepted Abstracts

#### Disclaimer

This abstract supplement has been produced using author-supplied copy. Editing has been restricted to some corrections of spelling and style where appropriate. No responsibility is assumed for any claims, instructions, methods or drug dosages contained in the abstracts; it is recommended that these are verified independently. This abstract book was correct at the time of printing and therefore does not reflect any programme changes after the date of printing.

## The European Helicobacter and Microbiota Study Group

**President**

Peter Malfertheiner, Germany

**Members**

Leif P. Andersen, Denmark  
 Anthony Axon, United Kingdom  
 Lars Engstrand, Sweden  
 Bram Flahou, Belgium  
 Antonio Gasbarrini, Italy  
 Javier P. Gisbert, Spain  
 Ernst Kuipers, The Netherlands  
 Marcis Leja, Latvia  
 José C. Machado, Portugal  
 Francis Mégraud, France  
 Colm A. O'Morain, Ireland  
 Ari P. Ristimäki, Finland  
 Theodore Rokkas, Greece

**Emeritus Members**

Michel A.L. Deltenre, Belgium  
 Giovanni Gasbarrini, Italy  
 Alexander M. Hirschl, Austria  
 Pierre Michetti, Switzerland

José M. Pajares Garcia, Spain  
 Ashley B. Price, United Kingdom  
 Mario G. Quina, Portugal  
 Erik A.J. Rauws, The Netherlands  
 Pentti I. Sipponen, Finland  
 Torkel M. Wadström, Sweden

**Honorary Members**

Franco Bazzoli, Italy  
 James G. Fox, United States  
 David Y. Graham, United States  
 Adrian Lee, Australia  
 Barry Marshall, Australia  
 Guido N.J. Tytgat, The Netherlands

**Corresponding Fellows**

Niyaz Ahmed, India  
 Dmitry Bordin, Russia  
 Luis G. Vaz Coelho, Brazil  
 Toshio Fujioka, Japan  
 Hyun Chae Jung, Korea  
 Varocha Mahachai, Thailand

Yaron Niv, Israel  
 Shu Dong Xiao<sup>†</sup>, China

**Local Organising Committee**

Peter Malfertheiner, Germany  
 Marino Venerito, Germany  
 Christian Schulz, Germany  
 Daniela Deutschländer, Germany

**Scientific Committee**

Steffen Backert, Germany  
 Wolfgang Fischbach, Germany  
 Rainer Haas, Germany  
 Sibylle Koletzko, Germany  
 Joachim Labenz, Germany  
 Julia Mayerle, Germany  
 Thomas Meyer, Germany  
 Michael Naumann, Germany  
 Michael Selgrad, Germany  
 Sebastian Suerbaum, Germany  
 Michael Vieth, Germany

**Table of contents****Plenary Workshops**

|     |                                |    |
|-----|--------------------------------|----|
| PW1 | Plenary Workshop 1             | 71 |
| PW2 | Plenary Workshop 2             | 73 |
| PW3 | Plenary Workshop 3: Microbiota | 74 |

**Parallel Workshops**

|    |  |    |
|----|--|----|
| W1 | Diagnosis, Epidemiology & Pediatrics               | 76 |
| W2 | Inflammation, Immunity, Vaccines, Host interaction | 79 |
| W3 | Treatment & Drug Resistance                        | 81 |
| W4 | Virulence Factors, Pathogenesis and Genomics       | 84 |
| W5 | Gastric Cancer and Carcinogenesis                  | 86 |
| W6 | Helicobacters and Extragastric Diseases            | 89 |

**Posters**

|               |  |     |
|---------------|--|-----|
| P01           | Diagnosis of Helicobacter infection                          | 92  |
| P02           | Epidemiology   | 92  |
| P03           | Paediatrics  | 102 |
| P04           | Virulence factors and pathogenesis of Helicobacter infection | 112 |
| P05           | Microbiology and genomics of Helicobacter                    | 115 |
| P06           | Gastric cancer and cancerogenesis                            | 125 |
| P07           | Treatment of Helicobacter infection                          | 126 |
| P08           | Drug resistance and clinical issues                          | 137 |
| P09           | Inflammation, immunity, vaccines and host interaction        | 155 |
| P10           | Helicobacter and extragastric disease                        | 160 |
| P11           | Microbiota 1   | 164 |
| P12           | Microbiota 2   | 168 |
| Author Index  |  | 173 |
| Keyword Index |  | 178 |

<sup>†</sup>Deceased

**Conclusions:** *Helicobacter pylori vacA* polymorphism strongly correlates with the serological CagA-response to *H. pylori cagA* strains. Furthermore, *vacA* genotype was the main determinant of inflammatory potential in ex vivo and in vivo settings.

#### W4.5 | Genomes of *Helicobacter pylori* prophages

F. F. Vale<sup>\*</sup>; A. Nunes<sup>†</sup>; M. Oleastro<sup>‡</sup>; J. P. Gomes<sup>†</sup>; D. A. Sampaio<sup>§</sup>; R. Rocha<sup>‡</sup>; J. Vitor<sup>¶</sup>; L. Engstrand<sup>\*\*</sup>; B. Pascoe<sup>††</sup>; E. Berthenet<sup>††</sup>; S. Sheppard<sup>††</sup>; M. D. Hitchings<sup>††</sup>; F. Mégraud<sup>‡‡</sup>; J. Vadivedu<sup>§§</sup>; P. Lehours<sup>‡‡,¶¶</sup>

<sup>\*</sup>Host-Pathogen Interactions Unit, Research Institute for Medicines (iMed-ULisboa), Instituto de Medicina Molecular, Faculdade de Farmácia da Universidade de Lisboa, Lisboa, Portugal

<sup>†</sup>Bioinformatics Unit, Department of Infectious Diseases, National Institute of Health, Lisboa, Portugal

<sup>‡</sup>National Reference Laboratory of Gastrointestinal Infections, Department of Infectious Diseases, National Institute of Health, Lisboa, Portugal

<sup>§</sup>Innovation and Technology Unit, Department of Human Genetics, National Institute of Health, Lisboa, Portugal

<sup>¶</sup>Faculdade de Farmácia, Universidade de Lisboa, Lisboa, Portugal

<sup>\*\*</sup>Department of Microbiology, Tumor and Cell Biology, Karolinska Institute, Stockholm, Sweden

<sup>††</sup>College of Medicine, Swansea University, Institute of Life Science, Swansea, UK, Swansea, UK

<sup>‡‡</sup>Université de Bordeaux, Centre National de Référence des *Campylobacters* et *Helicobacters*, Bordeaux, France

<sup>§§</sup>UM Marshall Centre and Dep of Medical Microbiology, University of Malaysia, Kuala Lumpur, Malaysia

<sup>¶¶</sup>INSERM U1053, Bordeaux, France

Nearly 20% of the *Helicobacter pylori* genomes carry prophages genes. Recently we were able to clearly differentiate four populations of prophages according to geographical origin of host strain. Interestingly we were able to discriminate between Northern Europe and Southern Europe using a phage sequence typing based on 2 prophage genes of *H. pylori* (integrase and holin) but present in only a minority of strains. We hypothesize that strains carrying these genes, located towards the 5' and 3' end of the prophage genome, would have an intact prophage. For this, we used Miseq from Illumina to sequence 28 *H. pylori* clinical isolates from distinct diseases and geographic origins, spreading from gastritis to gastric cancer and covering most continents. We were able to find prophages in all these sequenced genomes, presumably 82% of them are intact prophages, suggesting that integrase and holin genes are good markers for the presence of intact prophages. Prophage genome size ranged in length from 22.6 to 33.0 Kbp and consisted of 27–39 open reading frames. A 36.6% GC percentage was found in prophages in opposition to 39% in *H. pylori* genome. The phage insertion site was found to be

relatively conserved. Furthermore, prophage genomes presented a strong phylogeographic pattern, evidencing four distinctive clusters, comprising one African, one Asian and two European prophage populations.

#### W4.6 | Genome dynamics and functional molecular infection epidemiology of multidrug resistant *Helicobacter pullorum* isolated from retail wet market poultry in India

S. Kumar; M. Majid; N. Ahmed

University of Hyderabad, Hyderabad, India

Chicken are a known source of some of the life threatening food borne and zoonotic infections. Inappropriate and indiscriminate use of antimicrobials in livestock feed has increased prevalence of multidrug resistant bacteria of epidemic potentials. We present whole genome based molecular epidemiological analyses entailing phenotypic as well as genomic characteristics of eleven *H. pullorum* strains isolated from broiler and free range chicken from retail wet markets of Hyderabad city in India. Antimicrobial susceptibility tests revealed all isolates to be resistant to various antibiotic classes such as fluoroquinolones, cephalosporins, sulfonamides and macrolides, irrespective of their isolation sources. All isolates were also found to be 100% ESBL producers and were resistant to beta lactamase inhibitor, clavulanate. Whole genome sequencing and comparative genomic analysis of all the 11 isolates revealed presence of five to six well characterized antimicrobial resistance genes including those encoding RND efflux pump(s). Phylogeny when combined with pan genome dynamics revealed a remarkable degree of genetic diversity among isolates from free range chicken, whereas, a high degree of clonality was observed among broiler chicken isolates. Analyses of all the available *H. pullorum* genomes including our isolates ( $n = 16$ ), identified a number of important virulence genes and revealed some important genetic traits of *H. pullorum* such as its core gene pool characteristics, inventory of prophages and abundance of genomic islands etc. These observations would be able to strengthen functional molecular infection epidemiology of non-pyloric *Helicobacters* such as *H. pullorum* by unraveling their evolution and acquisition in chicken and possible transmissibility to humans.

### W5 GASTRIC CANCER AND CARCINOGENESIS

#### W5.1 | Activation of the Hippo/YAP signaling pathway in gastric epithelial cells in response to *Helicobacter pylori* infection

S. Molina-Castro<sup>\*</sup>; C. Staedel<sup>†</sup>; S. Fernandez<sup>\*</sup>; J. Giraud<sup>\*</sup>; E. Bessède<sup>\*</sup>; P. Lehours<sup>\*</sup>; F. Mégraud<sup>\*</sup>; C. Varon<sup>\*</sup>