European Helicobacter and Microbiota Study Group

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WILEY Helicobacter

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Accepted Abstracts

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†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

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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

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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 phenotypi c 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

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