three genomes, comparative genomics and characteristics of the *H. pylori* pan- genome in the aftermath of the three new genomes described herein shall be presented.

Abstract no.: W7.2
Genome rearrangements revealed through comparison of four complete genomes of Japanese *H. pylori*

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A clinical study in Japan strongly suggested that *H. pylori* is responsible for recurrence of gastric cancer. There have been hypotheses linking the genotype of East Asian *H. pylori* to the high incidence of gastric cancer in East Asia. In order to fully understand the East Asian strains, our group determined entire genome sequences of 4 *H. pylori* strains from Japanese patients by Sanger sequencing and compared them with the 6 complete genome sequences. We analyzed ortholog relationships, phylogenies, horizontal transfer, gene gain and loss, and genome rearrangements.

Potential macro-regional genome rearrangements were analyzed and rearrangement pathways were reconstructed by combination of regional inversion events. Even within the closely-related Japanese isolates, many genome inversions have occurred at various positions. Their recombination points were frequently linked to restriction-modification (RM) genes, which suggest their involvement. We also detected RM systems and genomic islands specific to the Asian strains. In a Japanese strain, we found a genomic island with features of putative prophages. This may be the first report of prophage-like region in *H. pylori*. Analysis of the other plastic regions and genes will also be reported.

Abstract no.: W7.3
Bacteriophage and *H. pylori*: an underestimated phenomena

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The recently sequenced strain B45 isolated from a gastric MALT lymphoma patient has a prophage sequence in its genome with 25.4 kb, highly similar to *Helicobacter acinonychis* prophage II. Until now *H. pylori* has been described has a species without prophage with the exception of the strain B38 which contains some prophage remnant sequences. Moreover, the number of reports of *H. pylori* phages is sparse in the literature.

The aim of our study was (1) to test the inducibility of the B45 prophage and using mitomycin C or UV, (2) to investigate the prevalence of *H. pylori*-prophage carrying isolates.

No significant lysis plaque was observed after mitomycin or UV induction. However, phage DNA was recovered after extraction and amplified by PCR. Some phage particles having a structure compatible with the *Siphoviridae* phage family were observed by transmission electron microscopy.

Using a PCR strategy, based on degenerated primers designed on the B38, B45 and *H. acinonychis* prophage II aligned bacteriophage integrase genes, we have screened until now 310 *H. pylori* strains isolated from different geographic regions and pathologies. The prevalence of the integrase sequence was 21.5%, suggesting that this is a much frequent phenomena that initially estimated. Integrase gene prevalence is similar in different pathologies. Phylogenie analysis shows a trend for a geographical distribution. This study shows for the first time that bacteriophage can play a significant role in *H. pylori* genetic diversity. It also opens new exciting ways in the comprehension of the interaction between the bacteria within its environment.

Abstract no.: W7.4
Prophage carriage among *H. pylori* clinical isolates

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Introduction: Prophages are involved in DNA transfer among bacteria. Virulence factors or resistance determinants may be encoded by prohages. Very little is known about prophage carriage among *H. pylori* strains.

Objective: To detect the presence of prophages by the induction of its lytic cycle after culturing clinical isolates in the presence of low concentrations of mitomycin C.

Methods: 17 strains of *H. pylori* were isolated from gastric biopsies by standard culture methods. TIGR 26695 and the 17 clinical isolates were subcultured on recently prepared blood agar plates containing 5 ng/ml Mitomycin C, 10 mg/l vancomycin and 5 mg/l amphotericyn B. Induced phages, that were detected by the presence of inhibition plaques, were extracted by suspension on 3ml of BHI centrifugation and filtration. 10 μl of this extract was tested against the 18 strains cultured on Mitomycin C free blood agar plates.

Results: Inhibition plaques were observed in 6 out of 18 strains (not in TIGR). The extract obtained from these strains produced growth inhibition of different *H. pylori* strains. 1 extract in 15

