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P0828 Genetic determinants and prediction of antibiotic resistance phenotypes in *Helicobacter pylori*

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Background: *Helicobacter pylori* is a major human pathogen, and infection can lead to severe gastroduodenal diseases like ulcers, metaplasia and adenocarcinoma. Diagnosis of *H. pylori* infection and determination of its antibiotic susceptibility still mainly rely on culture and phenotypic drug susceptibility testing (DST) that is time-consuming and laborious for fastidious bacterial pathogens like *H. pylori*. Whole genome sequencing (WGS) has recently emerged as a reliable diagnostic tool in diagnostic microbiology laboratories to detect drug resistant bacterial pathogens within a clinically relevant timeframe. The aim of this study was to compare phenotypic DST results with the predictions based on the presence of genetic determinants identified in the *H. pylori* genome using WGS.

Materials/methods: Phenotypic resistance to clarithromycin, metronidazole, tetracycline, levofloxacin and rifampicin was determined in 140 clinical *H. pylori* isolates by E-Test®, and its association with the occurrence of certain single nucleotide polymorphisms (SNPs) in target genes was assessed by WGS.

Results: Overall, there was high congruence >99% between phenotypic DST results for clarithromycin, levofloxacin and rifampicin and nucleotide substitutions identified in the 23S rRNA, *gyrA* and *rpoB* gene. However, it was not possible to infer a resistance phenotype for metronidazole based on the occurrence of distinct point mutations in *frxA* and *rdxA*. All 140 *H. pylori* isolates analysed in this study were susceptible to tetracycline, which was in accordance with the absence of double or triple nucleotide substitutions in the 16S rRNA gene.

Conclusions: Clarithromycin, levofloxacin and rifampicin resistance in *H. pylori* seems to be confined to a set of well-defined point mutations. This allows the use of WGS for the reliable prediction of phenotypic antimicrobial susceptibility in *H. pylori*, which in turn results in rapid initiation of an effective antimicrobial therapy and improved patient management.