UMP. 042

CagA gene carriage impact on intrahost dynamics of antimicrobial resistance to Helicobacter pylori

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Background: Treatment of gastroduodenal diseases is usually challenged by the virulence and antimicrobial resistance (AMR) of *H. pylori*. Global data on AMR profile is required to develop comprehensive treatment strategies. In addition, the precise role of *H. pylori* virulence and fitness on acquisition of resistance is uncertain. This study presents AMR profiles of *H. pylori* in Pakistan and describes the relatedness of cagA gene with acquisition of metronidazole and ofloxacin resistance.

Methods & Materials: A total of 178 strains of *H. pylori* were subjected for AMR determination against first and second-line antibiotics. Trends of resistance were analyzed in relation to gastric conditions of the patients and *cagA* gene carriage. The effect of *cagA* gene on the acquisition of resistance was investigated by mutant selection assay.

Results: AMR profiles indicated 89% resistance for metronidazole, 36% clarithormycin, 37% amoxicillin, 18.5% ofloxacin and 12% tetracycline. Clarithormycin resistance was on the rise from 2005 to 2008 (32% vs 38%, *P* 0.004) and significantly observed in non-ulcerative dyspepsia compared to gastritis, gastric ulcer and duodenal ulcer cases (53% vs 20%, 18%, 19%, *P* 0.000) while metronidazole and ofloxacin resistance were more common in gastritis cases. Distribution analysis in patients and in vitro assay correlated the absence of *cagA* gene with metronidazole and ofloxacin resistance.

Conclusion: The study presents the high magnitude of AMR in *H. pylori* in Pakistan. We further describe that the degrees of gastric inflammation and cagA gene are independently implicated in the development of resistance but cagA gene is directly linked with metronidazole and quinolone resistance. The study reaffirms the need for continuous AMR surveillance programs at national and regional levels.

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UMP. 043

Mutations in the 23S rRNA genes of Helicobacter pylori mediate resistance to clarithromycin (A preliminary study)

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Background: Background

Helicobacter pylori(H.pylori) is a bacterium that can colonize in the gastric mucosa. Different antibiotic regimens have been developed in the treatment of H.pylori infections. In recent years it has been suggested that resistance is responsible for reducing the rate of resistant H.pylori eradication caused by mutations developed in different gene regions against antibiotics such as clarithromycin, metronidazole. In this study, we aimed to determine the resistance of clarithromycin in H.pylori strains isolated from gastric biopsy specimens by phenotypic tests and molecular methods and to determine the mutations responsible for resistance.

Methods & Materials: Methods & Materials

Antrum and corpus biopsy specimens from 48 patients with dyspeptic complaints were cultured at Heliocobacter agar(microaerophilic, 3-10 days, at 37 °C). Colonies were identified as H.pylori by testing for Gram stain, urease, catalase and oxidase. Minimum inhibitory concentrations were determined using clarithromycin E-tests(MIC S≤0.25-R≥0.5 mg/L). To investigate the resistance of clarithromycin, 23S rRNA gene region of H.pylori was amplified by PCR. A2143G and A2144G point mutations which are most frequently responsible in addition with less frequent point mutations A2115G, G2141A, A2142G/C, T2182C, T2190C and C2195T for clarithromycin resistance were investigated by sequencing to the obtained products.

Results: Results

Phenotypic resistance to the clarithromycin was detected in 18/48(37.5%) strains(MIC ≥0.5 mg/L). According to the results of the sequencing, 18(37.5%) resistant strains were detected. Point mutations were detected in all of the 18 isolates. These mutations were identified as A2142G/C(8.3%) in 4 samples, A2143G(16.6%) in 8 samples, T2182C(8.3%) in 4 samples, A2144G(2.1%) in 1 sample and G2141A, A2142G/C, A2144G, A2115G(2.1%) multiple mutation in 1 sample. T2190C and C2195T were not detected.

Conclusion: Conclusion

The resistance development problem during the treatment regimens and the search for solutions with the recommended treatment regimens continues increasingly. It was observed that the resistance rate of 37.5% for clarithromycin is slightly higher than that of 36.7%, which we have previously(year2014) identified in our region. Therefore, we suggest that the eradication problem will continue as new treatment alternatives are not developed in our country and in the world due to these resistance rates, which do not decrease in our country yet.

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UMP. 044

Successfully emerging Acinetobacter baumannii clones from two hospitals in Lima, Perú

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Background: *Acinetobacter baumannii* is an opportunistic nosocomial pathogen responsible for 2–10% of all gram-negative nosocomial infections and is classified in the six most important multidrug-resistant microorganisms in hospitals worldwide. Most frequent and lethal (35-52%) infections include ventilator associated pneumonia and bacteremia. Outbreaks of resistant strains are increasingly reported worldwide, being sustained by similar clusters that successfully spread due to acquisition of antimicrobial resistance genes. These genes include class-D β-lactamases such as bla_{OXA-23}, bla_{OXA-24} and bla_{OXA-58}, among others.

Methods & Materials: This study included 80 non-duplicate clinical samples of *Acinetobacter* spp. collected from inpatients at two tertiary care hospitals in Lima, Perú. Strains were identified as *Acinetobacter baumannii* by Matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS). Antimicrobial susceptibility was assessed with disk diffusion method according to CLSI guidelines. Resistance genes were detected by PCR and DNA sequencing. The clonal relatedness was examined by pulse-field gel electrophoresis (PFGE).

Results: Eighty clinical isolates of *Acinetobacter* spp were identified as *A. baumannii* by MALDI-TOF MS and were also positive for the bla_{OXA-51} by PCR. The majority of isolates (71.43%) were classified as extensive drug-resistant *A. baumannii* (XDRAB). Resistance was elevated for carbapenems (97.5%) and cephalosporins (89.29%). Susceptibility only remained high for colistin (77.38%) and polymyxin B (72.62%). The bla_{OXA-40} was detected in 83.75% of the strains, bla_{OXA-23} in 13.75% and bla_{OXA-58} in 1.25%. Isolates were classified into nine PFGE clusters. Two main clusters, equally present in both hospitals, however, contained 62.5% and 16.25% of all isolates, respectively and were associated with carriage of bla_{OXA-40}.

Conclusion: *Acinetobacter baumannii* strains in this study showed high resistance levels for all antimicrobials. Carbapenem resistance correlate with the presence of bla_{OXA-40}, bla_{OXA-23} and bla_{OXA-58}. Susceptibility is mainly restricted to polymyxins. Carriage of the bla_{OXA-40} gene was associated with two major clones that were endemic in both hospitals and belonged to ST2 and ST79, which constitute epidemic high risk clones that are disseminated worldwide. Interestingly, two smaller clusters carrying the bla_{OXA-23} gene were also reported, the latter belonging to non-epidemic lineages of *A. baumannii.* Healthcare systems need to develop and improve current surveillance and infection control programs to prevent spread such successful clusters.

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UMP. 045

High occurrence blaCTX-M, blaSHV, and blaTEM Genes in Extended-Spectrum β-Lactamase-Positive Strains of Salmonella typhimurium in Nasarawa State: results of a point prevalence survey

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Background: Increasing trend of Extended-Spectrum Beta-Lactamase producing strains of *Salmonella spp* have posed a unique threat to public health.Increasing numbers of ESBL-producing bacterial strains exhibiting multidrug resistance have been observed. The study aimed to evaluate the prevalence of extended spectrum β-Lactamase-producing strains of *Salmonella typhimurium* in Nasarawa State.

Methods & Materials: A retrospective cohort studies were conducted on patients hospitalized from October to September 2017 comparing patients infected by Salmonella strains producer of ESBL (ESBL+) and patients infected by Salmonella strains ESBL (ESBL-) was carried out for fatal outcomes. We performed a Multivariate regression analysis to pinpoint fatal outcomes from risk factors. We also performed a multistate model, and a cost-effectiveness of illness analysis to evaluate the length of stay (LOS) attributed to ESBL positive production

Results: The incidence rate of ESBL- infections was due to Salmonella strains 3 cases/1000 patient-days (95% CI: 1.5–2.6 cases/1000 patient-days). Case fatality rate was higher in ESBL+ than in ESBL- infections (50.2% versus 33.6%, p□=□0.0007). The fatal outcome as a result of risk factors associated with ESBL (OR□=□9.7, 95% CI: 6.7–41.9, p□=□0.020) and being under catheter (OR□=□9.7, 95% CI: 4.8–60.9, p□=□0.041). ESBL positive production increased hospital stay by (+6 days) and reduced the hazard of release significantly after controlling for confounders (HR□=□0.8, 95% CI: 0.4–0.12). Patients suffering from urinary tract infections (UTI) were at-risk for severe outcomes. The extra charges connected with ESBL-production of $ 250 is considerable given to the socioeconomic status in Nigeria.

Conclusion: Our results point out a significant clinical impact of ESBL infections in Nasarawa State. Attention should be placed in adequate infection disease control.

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