Volume 8, Issue 3, 2019, Pages 149-159

Clarithromycin resistance and genetic pattern of helicobacter pylori in a group of patients with peptic ulcer disease in alexandria, Egypt

Alhammad, M.A.[a], El-Kady, H.[b], Hamed, Y.[c]

[a] Medical Technology Department, Faculty of Public Health, Benghazi University, Libyan Arab Jamahiriya

[b] Medical Laboratory Technology Department, Faculty of Allied Medical Sciences, Pharos University, Alexandria, Egypt

[c] Fundamental and Applied Sciences Department, Universiti Teknologi PETRONAS, Bandar Seri Iskandar, Perak Darul Ridzuan 32610, Malaysia

Abstract:

Clarithromycin resistance is one of the main predictors of eradication treatment failure in Helicobacter pylori (H. pylori) infections. Clarithromycin-based regimens were commonly used as a first-line therapy for H. pylori-positive patients. Lately, cure rates of H. pylori infection are decreasing to as low as 60% and are inversely correlated with antibiotic resistance rates that have crossed the 15-20% threshold. Monitoring of antibiotic susceptibility of H. pylori can be achieved through molecular methods; which stand out as an attractive alternative to conventional culture-based methods. The 23S rRNA Real-time PCR has several advantages in detection of H. pylori resistance to antibiotics; such as short working time, a high specificity up to 100% and low risk of contamination. This study aimed to detect clarithromycin resistance and genetic pattern of H. pylori in a group of 50 patients suffering from symptoms suggestive of gastrointestinal diseases. Gastric biopsy specimens were taken by endoscopy at the Gastroenterology Department of Alexandria Main University Hospital. Genotyping of H. pylori strains using multiplex PCR to detect CagA and VacA genes and detection of point mutations conferring clarithromycin resistance using a 23 S rRNA real time PCR was carried out. The majority (98%) of H. pylori strains detected in patients were CagA positive while only 28/50 (56%) were VacA positive. Most of the strains (67.86%) expressed the s2 (non toxigenic) allele and the most common genotype was VacA s2m1; expressed by 39.3% of strains. All H. pylori strains of the control group were sensitive to clarithromycin while resistance was detected in 26% of strains recovered from cases. The majority (77%) of point mutations responsible for resistance to clarithromycin were due to A-G transition at position 2143 while only 23% of which were due to A-C transition at position 2142.

Volume 8, Issue 3, 2019, Pages 149-159

Reference:

https://08105wt7q-1104-y-https-www-scopus-com.mplbci.ekb.eg/record/display.uri?eid=2-s2.0-85063138741&origin=resultslist&sort=plf-f&src=s&nlo=&nlr=&nls=&sid=3cc007c560e6c15f88e5b16895ea04a4&sot=aff&sdt=cl&cluster=scopubyr%2c%222019%22%2ct%2bscosubjabbr%2c%22ENGI%22%2ct&sl=49&s=AF-ID%28%22Pharos+University+in+Alexandria%22+60011287%29&relpos=7&citeCnt=0&searchTerm=