

عنوان مقاله:

Prevalence of HopQ gene in patients with gastric ulcer

محل انتشار:

بیستمین کنگره بین المللی میکروب شناسی ایران (سال: 1398)

تعداد صفحات اصل مقاله: 1

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خلاصه مقاله:

Materials & Methods: Biopsy specimens from 100 patients with gastric ulcer *Helicobacter pylori* were collected and separated, different allele hopQ, vacA, cagA was determined by PCR (Polymerase Chain reaction). The relationship between genes the chi-square test and Fisher IBM SPSS Statistics version 21.0 was used for statistical analysis. A value of <0.05 was considered as statistically significant. **Results:** In this study of 100 gastric ulcer alleles HopQ abundant HopQ I 54 (54%) and HopQ II 46 (46%) was also the genes of CagA and VacA s1 / s2 respectively, with frequency 51 (51%), VacA s1 83 (83%) and VacA s2 17 (17%). The relationship between the gene and gene I HopQ with CagA ($P<0.01$), the presence of gene II HopQ with CagA ($P<0.01$), the presence of VacA s1 Gene I HopQ ($P<0.026$) the presence of VacA s1 gene HopQ II ($P<0.026$), gene by gene VacA s2 I HopQ ($P<0.026$) and the presence of VacA s2 with gene HopQ II ($P<0.026$), were statistically significant. Also, the presence of gene VacA s1 with CagA ($P<0.726$) and the presence of the gene VacA s2 ($P<0.726$) CagA statistically significant relationship was not found. **Conclusion:** The results can be HopQ impact on virulence genes and CagA and VacA relationship between gene in patients with peptic ulcer to argue. Further studies in this direction would be to identify strategies for physicians and the anti-peptic ulcer disease, gastritis and gastric cancer to improve.

کلمات کلیدی:

Helicobacter pylori, HopQ gene, Peptic ulcer, outer membrane proteins

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