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Circulating level of interleukin (IL)-18 in Helicobacter pylori-infected patients, and its associations with bacterial CagA and VacA virulence factors

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Background: We analyzed the impact of Interleukin (IL)-18 promoter polymorphisms on IL-18 serum levels in H. pylori-infected duodenal ulcer (DU) patients and healthy asymptomatic (AS) carriers. We also aimed to determine the association of the H. pylori virulence factors, CagA and VacA antibodies with serum concentrations of IL-18 as to elucidate any correlation between them.

Methods: Three groups including DU patients (67 individuals), AS carriers (48 individuals), and H. pylori-negative subjects (26 individuals) were enrolled. Serum concentrations of IL-18 were determined by ELISA. Patient sera were tested by Western blot method to determine the presence of serum antibodies to bacterial CagA, VacA. Genotyping of IL-18 promoter polymorphisms at positions -137 G/C and -607 C/A were performed by Allele-Specific Primer PCR protocol.

Results: Our study revealed that serum IL-18 levels are positively influenced by CagA-positive H. pylori strains, so that maximum levels of IL-18 were detected in DU patients with the CagA+ phenotype, regardless of the presence of the anti-VacA antibody. Regarding IL-18 promoter polymorphisms, the AA genotype and A allele at position −607 C/A found to be significantly lower in DU patients than in AS carriers and H. pylori-negative subjects (P=0.032 and 0.043, respectively).

Conclusions: IL-18 -607 C variant was associated with higher levels of serum IL-18 and increased risk of DU. Moreover, our findings indicated that serum concentrations of IL-18 were influenced by CagA factor, irrespective of the VacA status, suggesting that high levels of IL-18 in CagA positive subjects are predisposed to susceptibility to DU.

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