**Introduction:** Chronic *Helicobacter pylori* infection is known to be associated with the development of gastritis, peptic ulcers (PUs), gastric cancer and gastric MALT lymphoma. *H. pylori* CagA is the first bacterial oncoprotein to be identified in relation to human cancer. The pathogenic CagA protein contains a highly polymorphic Glu-Pro-Ile-Tyr-Ala (EPIYA) repeat region in the C-terminal part of the molecule. CagA diversity with regard to EPIYA-A, -B, -C, or -D phosphorylation motifs may play an important role in *H. pylori* pathogenesis, and therefore determination of these motifs in *H. pylori* clinical isolates can become a useful prognostic tool.<br/>

**Methods:** *H. pylori* strains were obtained from 149 patients with gastritis and 31 patients with PUs referring to the endoscopy units of several cities in Iran. After DNA extraction, these strains were investigated for the presence of cagA gene and CagA EPIYA motifs using PCR amplification. Multiple Linear and logistic regression models were used for the analysis of data using SPSS software.<br/>

**Results:** A total of 121 isolates were CagA positive and varied according to their C-terminal motif. Five different sizes (bp) were observed for this region by PCR (370/AB, 470/ABC, 500, 570/ABCC, 670/ABCCC). The statistical analysis showed no correlation between these motifs and PUs or gastritis (P> 0.05).<br/>

**Conclusion:** It is proposed that the *H. pylori* CagA EPIYA motifs might not be considered as an important determinant of gastritis or PUs in Iranian population.<br/>

**Keywords:** *H. pylori*, CagA, EPIYA, Peptic ulcer, Gastritis

**Presentation:** Poster