In order to investigate the reason(s) for the high prevalence of *H. pylori* infection and gastric cancer in Turkey, the *cagA*, *vacA* and *iceA* genes were used as molecular markers to characterise isolates from patients infected with *H. pylori*. In total, 87 isolates of *H. pylori* from adult patients were investigated. Antral gastric biopsy samples taken from patients were cultured using standard methods [3]. The presence of the *cagA* gene, the mid-region of the *vacA* gene, the signal sequences of the *vacA* gene, and the *iceA* genotype were determined by PCR as described previously [4–6]. For *vacA*, the most common genotype was *vacA* m2s2, followed by *vacA* m2s1a. In total, 40 (46%) isolates were *cagA*-positive, and 62 (71.3%) isolates were *iceA* positive. Of these, 28 were positive for *iceA*1 only, 12 for *iceA*2 only, and 22 for both *iceA*1 and *iceA*2.

The fact that 37% and 33% of the isolates, respectively, belonged to the *s1* and *s2* genotypes, and that 46% of the isolates were *cagA*-positive, suggests a strong similarity to the Middle Eastern genotypes [7]. Moreover, the *iceA*1 subtype was twice as common as the *iceA*2 subtype in the present study, and a significant number of isolates possessed both *iceA*1 and *iceA*2, which also indicates that Turkish isolates of *H. pylori* are similar to the Middle Eastern types.

Only a few samples were found which contained multiple genotypes, which implies that most infections in Turkey are caused by single genotypes of *H. pylori*. Twelve isolates were *vacA* s1 *cagA*+ *iceA*1 (11 patients with functional dyspepsia and one with duodenal ulcer), which are considered to be the most pathogenic strains. Only five isolates were vacAs2m2 *iceA* (cagA-negative), which are considered to be the least pathogenic strains [8].

The present study failed to determine the genotypes of several isolates, indicating that mutation had occurred at the primer-binding sites of the genes investigated. *H. pylori* is one of the most genetically diverse bacterial species, and this mutational diversity has been enhanced by extensive inter-strain gene transfer and recombination [9]. Therefore, it is probable that evolution has selected the *H. pylori* strains that are best able to colonise the population of Turkey. Future studies should focus on determining the genetic sequences of these strains.

**REFERENCES**


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**Turkish isolates of *Helicobacter pylori* belong to the Middle Eastern genotypes**

We were interested to read the recent accounts in CMI regarding the distribution of *Helicobacter pylori* genotypes in Mexico and Argentina [1,2]. Epidemiological studies suggest that the prevalence of *H. pylori* infection varies between developed and developing countries, as well as according to ethnicity, place of birth and socioeconomic factors, even among people living in the same country. Molecular epidemiological studies are important in order to elucidate the circulating genotypes.
REFERENCES


