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Original Article



Detection of clarithromycin-resistant *Helicobacter pylori* strains in a dyspeptic patient population in Sri Lanka by polymerase chain reaction-restriction fragment length polymorphism

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Abstract

Aim: The aim of this study was to investigate the proportion of common clarithromycin-resistant mutation types present in the 23S ribosomal ribonucleic acid (rRNA) gene of *H. pylori* strains in Sri Lanka. Settings and Design: The study was a cross-sectional, descriptive study where 76 dyspeptic patients who were required to undergo endoscopy examination were included. The study was carried out at a Teaching Hospital in Sri Lanka. Subjects and Methods: In-house urease test and polymerase chain reaction (PCR) amplification of the glmM gene of *H. pylori* was performed to confirm the *H. pylori* infection. Analysis of point mutations in 23S rRNA gene strains were performed by PCR-restriction fragment length polymorphism (RFLP). Results: Of the 16 urease-positive biopsies, 94% (n = 15) were positive by PCR using the glmM primer. All *H. pylori* strains yeilded a point mutation at A2142G site of the 23S rRNA gene, while A2143G mutation was not detected. Conclusions: For the first time in Sri Lanka, we reported predominance of A2142G point mutation associated with claritromycin resistance of *H. pylori* in a Sri Lankan population.

Key words: Clarithromycin, Helicobacter pylori, mutation, restriction fragment length polymorphism, 23S ribosomal ribonucleic acid gene