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MEFV gene polymorphism and gastric microbial diversity among the dyspeptic patients presented to endoscopic clinic Colombo South Teaching Hospital, Sri Lanka

Weerasinghe G.G.Y.H.[1]*, Gunasekara T.D.C.P.[1], Weerasekera M.M.[1], Fernando S.S.N.[1]

[1]*Department of Microbiology, Faculty of Medical Sciences, University of Sri Jayewardenepura, Gangodawila, Nugegoda, Sri Lanka*

MEFV gene encodes a protein called Pyrin and it plays a major role in inflammasome activation. Pyrin is suggested to be associated with dysregulated immune response to microorganisms by generating defective signals on the host-gut microbiota signaling pathways. Thus, it was hypothesized that pyrin gene mutations may influence the gastric microbial diversity. Therefore, present study investigated the association of MEFV gene mutations and gastric microbial diversity among dyspeptic patients. Sixty dyspeptic patients (34 males and 26 females) were enrolled for the study. Biopsy specimens were collected for DNA extraction and biopsy urease test. PCR for yeast species was carried out using NL1/LS2 primers. MEFV gene mutations were determined using commercially available FMF strip assay kit based on DNA hybridization. Interviewer administered questionnaire was used to collect the demographic data. Majority of the patients complained of abdominal pain (93%, n=57), followed by nausea (80%, n=48), belching (40%, n=25), emesis (18%, n=11) and abdominal rumbling (13%, n=9). Eleven patients were positive for *Helicobacter pylori* by biopsy urease test while ten patients were positive for yeast DNA. Among the 60 dyspeptic patients, no homozygous mutations were detected, and three heterozygous mutations were identified, i.e., E148Q (45%), P369Q (5%) and M680I (11.6%). There was no significant association found between these three heterozygous mutations and the presence or absence of yeast species or *H. pylori.* Presence of *H. pylori* and the yeast species provide evidence for a non-sterile stomach. Hence in this population, MEFV gene polymorphisms was not a main contributing factor affecting gastric microbial diversity.

Keywords: Gastric microbiota, *Helicobacter pylori,* MEFV

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* Corresponding author: yashodhayhw@gmail.com