

***HELICOBACTER PYLORI AND CRYPTOSPORIDIUM* CO-INFECTION IN DIARRHEIC IMMUNOCOMPROMISED EGYPTIAN CHILDREN AND ESTIMATED RISK FACTORS**

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Background & Objectives: The pathogenic bacterium *Helicobacter pylori* (*H. Pylori*) and *Cryptosporidium* spp are well-known for their high prevalence in immunocompromised pediatric patients worldwide especially in developing countries like Egypt. Associations between both infectious agents due to sharing the same mode of infection estimated risks and predictive factors for susceptibility to co-infection. This study conducted to determine the prevalence of *H. pylori* and *Cryptosporidium* spp co-infection in diarrheic Egyptian children by copro PCR restriction fragment length polymorphism (PCR-RFLP) and immunochromatography test studying their estimated risk.

Methodology: Fecal samples were collected from 100 immuno-compromised pediatric patients. All samples were submitted to coproscopic examination for detection of intestinal parasites before and after concentration, acid-fast stain for coccidian parasites detection such as *Cryptosporidium* and copro-PCR-RFLP targeting *Cryptosporidium* oocyst wall protein (COWP) gene for *Cryptosporidium* and urease subunit alpha (Urea) gene targeted for *H. pylori*. Immunochromatography tests (ICT) were performed for detection of *Cryptosporidium* copro-antigen and *H. pylori* Hsp antigen as a rapid diagnostic test.

Results: Among the studied population, positive cases for cryptosporidiosis by PCR (58%) also were co-infected with *H. pylori*. Additionally among the studied variables only gender, weight loss and polyparasitism were significantly associated (P 0.01) with detection of *H. pylori* by using multivariate analysis using logistic regression.

Conclusion: Our data shed some light on the fundamental role of *Cryptosporidium*, and it's co-infection with *H. pylori*. The potential contribution of *H. pylori* as a favourable condition for intestinal parasites is not completely known yet and its role in determining correlation with gut micro biomes remains to be fully elucidated, therefore, further investigations are warranted.

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