Published in final edited form as:

Eur Urol. 2015 December ; 68(6): 1099–1100. doi:10.1016/j.eururo.2015.08.048.

Re: The Relationship Between Irritable Bowel Syndrome, Functional Dyspepsia, Chronic Fatigue and Overactive Bladder Syndrome: A Controlled Study 6 Years After Acute Gastrointestinal Infection

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Experts' summary

Following up patients affected by an outbreak of giardiasis in Bergen, Norway, in 2004, this elegant study identified a higher prevalence of overactive bladder (OAB) after previous confirmed giardiasis compared with matched controls (18.7% [$n = 716$] vs 13.6% [$n = 833$]; $p = 0.007$). The authors also explored interactions between OAB and irritable bowel syndrome, functional dyspepsia, and chronic fatigue. They postulated that the apparent association between OAB and giardiasis can be ascribed to comorbid functional disorders because the prevalence of OAB among exposed versus control participants without comorbid disorders was similar (12.4% vs 10.9%, $p = 0.51$), and the risk of OAB was more than two-fold increased with any functional comorbid disorder.

Experts' comments

Although most management strategies for OAB target the bladder, these authors suggested instead that the observed overlap between OAB and other functional disorders might arise either because of cross-sensitization of common neural pathways between gut and bladder or because of a tendency to overinterpret somatic sensations. We have compelling evidence of an association between affective disorders and lower urinary tract symptoms [1], and this study provides a further reminder of the importance of a holistic approach to OAB.

A second line for future investigation may explore the relationship between *Giardia* infection and the urinary microbiome. *Giardia* infection causes a profound transient shift in the fecal flora, and some changes may persist beyond resolution of clinical infection [2]. The fecal and urinary microbiota are intimately linked [3], and recent research has demonstrated differences in the urinary microbiota of women with and without OAB, using both 16S ribosomal RNA sequencing and expanded quantitative urine culture techniques [4]. In a murine model of *Giardia*, the bacterial strains that penetrated the gut mucosa in the

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Conflicts of interest: The authors have nothing to disclose.

postinfective phase included *Bacillus*, *Lactobacillus*, *Staphylococcus*, and *Phenyllobacterium* [2]. Two of these four bacteria, *Staphylococcus* and *Lactobacillus gasseri*, were identified more frequently in a US study of the urinary microbiome of women with OAB [4]. It is certainly possible that the apparent epidemiologic association between *Giardia* exposure and OAB is mediated only by relationships with other functional disorders, but it is also possible that *Giardia* exposure has a persistent impact on the fecal and urinary microbiota, even 6 yr following exposure. This study provides further support for chronic bacterial infection as one precipitant of OAB, and further research should explore this possibility and its implications for treatment.

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