

2D protein maps of mucosal biopsies in patients with ileal pouch-anal anastomosis

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A group of researchers headed by Professors Patrizia Brigidi and Massimo Campieri utilized a comparative proteomic approach to profile protein expression in mucosal biopsies from patients with chronic refractory pouchitis following antibiotic or probiotic treatment.

Total proctocolectomy with ileal J-pouch-anal anastomosis (IPAA) is the surgical treatment of choice for patients with refractory ulcerative colitis (UC). Although the surgery generally cures UC allowing a significant improvement of health-related quality of life, complications can occur after IPAA. The most common complication of this surgery is pouchitis, a non-specific [inflammatory condition](#) at the ileal pouch reservoir occurring in up to 50% of patients, with 10% of these patients becoming chronic sufferers.

Although the etiology and pathogenesis of pouchitis are still not entirely clear, the bulk of the evidence points towards an abnormal mucosal immune response to altered microbiota patterns. The management of pouchitis is largely empirical and only a few small placebo-controlled clinical trials have been conducted. Although antibiotics represent the mainstay of treatment, probiotics have recently gained more attention as an effective therapeutic option for pouchitis management. However, little is known about the molecular mechanisms underlying the protective effects of probiotics against pouchitis onset.

A research article to be published on January 7, 2010 in the [World Journal of Gastroenterology](#) addresses this question. A study group led

by Dr. Patrizia Brigidi from Italy, profiled [protein expression](#) in mucosal biopsies from patients with chronic refractory pouchitis following antibiotic or probiotic treatment, using a comparative proteomic approach. For the first time, 2D protein maps of mucosal biopsy samples from patients who underwent IPAA are provided. In the first set of 2D gels, 26 different proteins with at least 2-fold changes in their expression levels between the pouchitis condition and antibiotic-induced remission were identified. In the second set of analysis, the comparison between mucosal biopsies proteomes in the normal and probiotic-treated pouch resulted in 17 significantly differently expressed proteins. Of these, 8 exhibited the same pattern of deregulation as in the pouchitis/pouch remission group.

After classifying the identified proteins on the basis of the biological functions, the authors give an overall theoretical analysis. Their findings suggest the involvement of enterocyte mitochondrial dysfunction and perturbed cytoskeletal structure into pouchitis pathophysiology. The modulation of metabolic pathways and the effects on cell integrity and morphology in response to probiotic administration, provide new insights into the molecular interaction between [probiotics](#) and the altered host intestinal ecosystem in IPAA.

The proteomic technologies could play a major role in unraveling the mystery of immunopathogenic mechanisms of pouchitis and in discovering novel biomarkers for disease activity, diagnosis and prognosis.

More information: Turrone S, Vitali B, Candela M, Gionchetti P, Rizzello F, Campieri M, Brigidi P. Antibiotics and probiotics in chronic pouchitis: A comparative proteomic approach. World J Gastroenterol 2010; 16(1): 30-41 www.wjgnet.com/1007-9327/16/30.asp

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