Genome-based expression profiles as a single standardized microarray platform for the diagnosis of bladder pain syndrome/interstitial cystitis: an array of 139 genes model

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Abstract

Introduction and hypothesis The aim of the study was to investigate the molecular signatures underlying bladder pain syndrome/interstitial cystitis (BPS/IC) using cDNA microarray. **Methods** Microarray gene expression profiles were studied in a matched case-control study by using a system of conditional regression modeling.

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Results The main findings are summarized as follows: Firstly, a “139-gene” model was discovered to contain high expressions of bladder epithelium, which feature in BPS/IC. Secondly, complex metabolic reactions, including carbohydrate, lipid, cofactors, vitamins, xenobiotics, nucleotide, and amino acid metabolisms, were found to have a strong relationship with bladder smooth muscle contraction through IC status. Thirdly, we found the transcriptional regulations of IC-induced bladder smooth muscle contraction status, including the level of contractile force, tissue homeostasis, energy homeostasis, and the development of the nervous system. In addition, our study suggested the mast-cell activation mediated by the high-affinity receptor of Fc epsilon RI triggering allergic inflammation through IC status. Such genetic changes, jointly termed “bladder remodeling,” can constitute an important long-term consequence of BPS/IC.

Conclusions The success of this innovation has supported the use of microarray-based expression profiling as a single standardized platform for diagnosis of BPS/IC and offers drug discovery.

The abstract of this article contained some errors that were overlooked or introduced while the manuscript was being prepared for publication. The corrected abstract is reproduced here.