

PROTEOMICS OF KETAMINE CYSTITIS AND INTERSTITIAL CYSTITIS – A WAY TO SEARCH FOR DIFFERENT PATHOPHYSIOLOGY BETWEEN DISEASES WITH SIMILAR BLADDER SYMPTOMS

Hypothesis / aims of study

Although similar suburothelial inflammation and histological symptoms in interstitial cystitis/painful bladder syndrome (IC/PBS) and ketamine cystitis (KC) were found, the level of urothelial dysfunction and apoptosis are different. More severe urothelial dysfunction and increased apoptosis, which correlated with more severe clinical symptoms, was found in KC. Besides, some KC progressed into the end-stage bladder manifested with contracted bladder and bilateral obstructive uropathy which were rarely observed in IC/PBS. This study was designed to identify significantly differentially expressed proteins between patients with IC/PBS and KC with the use of proteomic techniques.

Study design, materials and methods

Three patients each with KC and IC/PBS undergoing partial cystectomy and augmentation enterocystoplasty were enrolled consecutively. In the same time, 3 patients with bladder cancer or prostate cancer undergoing radical surgery who never had episode of urinary tract infection or irritative bladder symptoms were also included and serve as controls. The bladder wall specimens obtained during partial cystectomy and augmentation enterocystoplasty (IC/PBS and KC) or radical operations (radical cystectomy or radical prostatectomy, AC) was harvested and sent for pathological examination and urological laboratory for investigations. A proteomic approach was used to study the proteins associated with KC and IC/PBS and bioinformatics was used to construct the protein protein network.

Results

A total of 62 proteins were significantly different between IC/PBS and KC bladders (Table 1 and Fig. 1) and these proteins were connected by protein-protein interaction network (Fig. 2). 27 of these proteins were up-regulated in KC and 35 of these proteins were down-regulated in KC. From the protein-protein interaction network, CFL1, GSN, Lmna, MYL, and CNN1 are associated with caspase 3 which is an apoptosis associated protein. Furthermore, CNN1 is also associated with necrosis and leads to inflammation.

Interpretation of results

This study demonstrated that the etiology of IC/PBS and KC might be mediated by multiple signalling pathways. The identified proteins contributing to the spectrum of IC/PBS and KC bladders may be used to elucidate the etiology of IC/PBS and KC and as candidate biomarkers for diagnostic test.

Concluding message

The etiology of IC/PBS and KC might be mediated by multiple signalling pathways. The identified proteins contributing to the spectrum of IC/PBS and KC bladders may be used to elucidate the etiology of IC/PBS and KC and as candidate biomarkers for diagnostic test.

Table 1. Differentially expressed proteins in KC bladders (dark blue: up-regulated, light blue: down-regulated)

FLNA	VCL	FGG	ACTN1	SERPINA1	GSN	CCT8	ACTA1
ACTG1	IMMT	ALDH1A2	FGB	WDR1	PHGDH	GAPDH	MYH11
CNN1	CALR	SYNM	TF	ARHGDI1	HSP90AB1	HSPA1A	PGK1
CDKN2A	DDX11	HSD17B4					
C1QBP	IGK@	LDHA	VDAC2	LGALS3	SOD2	CFL1	NME1
ANXA6	CCT4	CCT5	ALDH	TAPBP	P4HB	ANXA5	TPM2
ANXA2	TPI1	LMNA	FES	CAPZB	NDUFS8	DLST	CKB
PCBP1	ACAT1	RNF126	MDH2	HADHA	ETFA	MYH	VDAC2
FBXL19	CA1	ATP5A1					

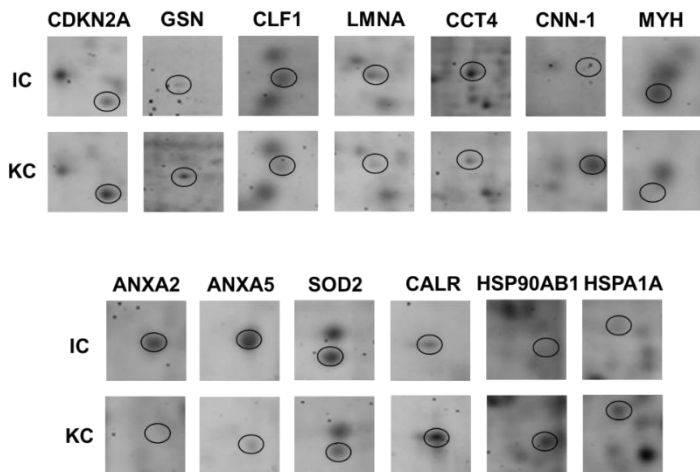


Fig. 1. Selective enlarged 2D gel image of differentially expressed proteins in IC/PBS and KC.

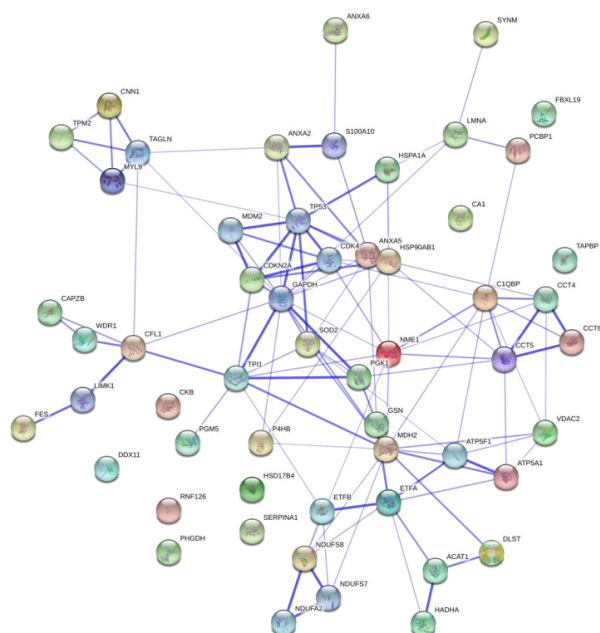


Fig. 2. The protein-protein interaction network of the identified differentially expressed proteins.

Disclosures

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