Moitinho R¹, Barretto L¹, Bertolla R¹, Bertuccez F¹, Camargo M¹, Souza G², Silva C¹, Almeida F¹

1. Universidade Federal de São Paulo - UNIFESP - Escola Paulista de Medicina, 2. Waters Corporation - MS Applications and Development Laboratory, Barueri, Brasil

WHAT CAN URINE TELL US ABOUT INTERSTICIAL CYSTITIS/PAINFUL BLADDER SYNDROME? PRELIMIMARY DATA FROM PROTEOMIC COMPARATIVE STUDY.

Hypothesis / aims of study

The interstitial cystitis/painful bladder syndrome (IC/PBS) has a large spectrum clinical presentation and sometimes the diagnosis is not an easy task. All guidelines regard IC/PBS based the diagnosis in exclusion criteria. Thus, there are several patients that suffers for long periods without properly diagnosis. The main problem is the lack of reliable marker or test that could help clinicians to identify the disease.

In the present study, we performed a shotgun proteomics study to show the difference between the urinary protein profile in control subjects and patients with IC/PBS to identify possible specific proteins and networks associated with IC/PBS.

Study design, materials and methods

We collected 50mL of urine from mid stream first urine in the morning from 5 normal women (control) and from 5 women with IC/PBS. The urine was processed and the protein was quantified for each sample using a BCA protein assay (Sigma-Aldrich, Saint Louis, USA). Pools were prepared normalizing the protein content, using a same amount of protein for each group (control and IC/PBS). After trypsin digestion, the MS^E analysis the NanoUPLC tandem nanoESI acquisition was performed in a Xevo G2 Qtof (Waters, UK) in alternate low (precursor ion scan) and high collision energy (fragment ion scan) from *m/z* 50-2000. The protein identification was performed using ProteinLynxGlobalServer (PLGS) with Identity^E software, searched against the Uniprot databank, version 2012_01, human, with manually revised proteins (UniProtKB/Swiss-Prot). The Statistical analysis was performed using PASW 18.0 for Windows.

Results

We identified 528 proteins in the IC/PBS group and 743 proteins in the control group. Out of the 528 proteins in IC/PBS group, 32 were exclusive, 78 were up-regulated. Out of the 743 proteins in the control group, 247 were exclusive and 16 up-regulated. There was 402 proteins that were similarly distributed in both groups. When we analyzed individually the 110 exclusive and up-regulated proteins in IC/PBS urinary sample, the following protein functions were highlighted: cell death, acute phase and apoptosis. Table 1 shows the main protein identified. In the Control group the exclusive proteins were mainly associated with cell proliferation, glycosaminoglycan biosynthesis process and cell adhesion (Table 2).

The difference in protein expression was investigated for novel protein-protein interactions. In the graph of biological function proteins form urinary samples of IC/PBS patients present negative regulation for cell adhesion and up-regulation for acute inflammatory response.

Interpretation of results

This preliminary study demonstrated that urinary proteomic could help to identify significant difference in urinary proteins. It allows us to determine that IC/PBS patients present an absence of some proteins related to cell proliferation, glycosaminoglycan biosynthesis and cell adhesion. Furthermore, the IC/PBS women presented increase proteins related to acute phase and apoptosis. These findings are clearly associated with pathological events previously described in IC/PBS etiology and could be used as future markers in clinical diagnosis.

Concluding message

This preliminary study indicates a significant qualitative and quantitative difference in urinary proteins between women with and without IC/PBS. In a near future, it may be applied as a new technology to determine biomarkers and help understanding the IC/PBS physiophatology.

Table 1. Exclusive and up-regulated proteins in urinary sample of IC/PBS women.

Protein	Description	Gene	Score	p-Value	Fold Change	Function
Q13510	Acid ceramidase	ASAH1	1334,356	,0495	1,7	Cell death
P07339	Cathepsin D	CTSD	5513,86	,0495	1,5	Cell death
P06865	Beta-hexosaminidase subunit alpha	HEXA	213,7733	,0495	2,2	Cell death.
P07686	Beta-hexosaminidase subunit beta	HEXB	296,7381	,0495	2,8	Cell death.
P19652	Alpha-1-acid glycoprotein 2	ORM2	6037,606	,0495	2,5	Acute phase/ inflammatory immune response
P01009	Alpha-1-antitrypsin	SERPINA1	8327,304	,0495	1,6	Acute phase/ inflammatory immune response
P01011	Alpha-1-antichymotrypsin	SERPINA3	1971,545	,0495	1,8	Acute phase/ inflammatory immune response
P00738	Haptoglobin	HP	4194,774	,0495	2,8	Acute phase/ inflammatory immune response

P00734	Prothrombin	F2	4163,33	,0495	1,3	Acute phase/ inflammatory immune response
Q7Z4R8	UPF0669 protein C6orf120	C6orf120	298,9371	only in cystitis		Apoptosis
Q9BRT3	Migration and invasion enhancer 1	MIEN1	1332,216	only in cystitis		Apoptosis.
P12830	Cadherin-1	CDH1	703,5341	,0495	2,7	Apoptosis
P06396	Gelsolin	GSN	2094,463	,0495	1,3	Apoptosis.
P80188	Neutrophil gelatinase- associated lipocalin	LCN2	11728,19	,0495	1,8	Apoptosis.

Table 2. Exclusive proteins in control group.

	Liciusive proteins in control group					1
		_			Fold	
Protein	Description	Gene	Score	p-Value	Change	Function
P08779	Keratin, type I cytoskeletal 16	KRT16	591,5092	only in co	ntrol	Positive regulation of cell proliferation
	Ras-related C3 botulinum toxin					
P15153	substrate 2	RAC2	482,9939	only in co	ntrol	Positive regulation of cell proliferation
	Ciliary neurotrophic factor					
P26992	receptor subunit alpha	CNTFR	192,7764	only in co	ntrol	Positive regulation of cell proliferation
Q16610	Extracellular matrix protein 1	ECM1	482,093	only in co	ntrol	Positive regulation of cell proliferation
	Tumor necrosis factor receptor					
P25942	superfamily member 5	CD40	289,8728	only in co	ntrol	Positive regulation of cell proliferation
P31431	Syndecan-4	SDC4	744,3799	only in co	ntrol	Glycosaminoglycan biosynthetic process
P35052	Glypican-1	GPC1	502,2459	only in co	ntrol	Glycosaminoglycan biosynthetic process
P51654	Glypican-3	GPC3	210,9776	only in co	ntrol	Glycosaminoglycan biosynthetic process
O75487	Glypican-4	GPC4	717,5419	only in co	ntrol	Glycosaminoglycan biosynthetic process
505050	Insulin-like growth factor-	10.541.0	101 1100			
P35858	binding protein complex acid	IGFALS	131,1168	only in co	ntrol	Cell adhesion
DOFOOR	Sodium/potassium-transporting ATPase subunit beta-1	ATD4D4	222 2074	anh in aa	ntral	Call adhasian
P05026	Neural cell adhesion molecule	ATP1B1	332,3071	only in co	ntroi	Cell adhesion
O00533	L1-like protein	CHL1	327,8996	only in co	ntrol	Cell adhesion
P29279	Connective tissue growth factor	CTGF	404,955	only in co	ntrol	Cell adhesion
Q14393	Growth arrest-specific protein6	GAS6	369,4051	only in co		Cell adhesion
P11047	Laminin subunit gamma-1	LAMC1	256,402	only in co	ntrol	Cell adhesion

<u>Disclosures</u> **Funding:** None **Clinical Trial:** No **Subjects:** HUMAN **Ethics Committee:** CEP **Helsinki:** Yes **Informed Consent:** Yes