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ORIGINAL RESEARCH

Does urinary peptide content differ between COPD patients with and without inherited alpha-1 antitrypsin deficiency?

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Abstract: Differentiating between chronic obstructive pulmonary disease (COPD) patients with normal (PiMM) or deficient (PiZZ) genetic variants of alpha-1 antitrypsin (A1AT) is important not only for understanding the pathobiology of disease progression but also for improving personalized therapies. This pilot study aimed to investigate whether urinary peptides reflect the A1AT-related phenotypes of COPD. Urine samples from 19 clinically stable COPD cases (7 PiMM and 12 PiZZ A1AT) were analyzed by capillary electrophoresis coupled to mass spectrometry. We identified 66 peptides (corresponding to 36 unique proteins) that differed between PiZZ and PiMM COPD. Among these, peptides from the collagen family were the most abundant and divergent. A logistic regression model based on COL1A1 or COL5A3 peptides enabled differentiation between PiMM and PiZZ groups, with a sensitivity of 100% and specificity of 85.71% for COL1A1 and a sensitivity of 91.67% and specificity of 85.71% for COL5A3. Furthermore, patients with PiZZ presented low levels of urinary peptides involved in lipoproteins/lipids and retinoic acid metabolism, such as apolipoprotein A-I and C4, retinol-binding protein 4 and prostaglandin-H2 D-isomerase. However, peptides of MDS1 and EVII complex locus, gelsolin and hemoglobin alpha were found in the urine of COPD cases with PiZZ, but not with PiMM. These capillary electrophoresis coupled to mass spectrometry-based results provide the first evidence that urinary peptide content differs between PiMM and PiZZ patients with COPD.

Keywords: alpha-1 antitrypsin, alpha-1 antitrypsin deficiency, COPD, urine, peptidomics, capillary electrophoresis coupled to mass spectrometry, phenotypes, peptides, biomarkers, collagen

Introduction

Chronic obstructive pulmonary disease (COPD), characterized by the chronic and progressive obstruction of lung airflow,[1] is the fourth leading cause of mortality and morbidity worldwide.[2] COPD is a highly heterogeneous disorder resulting from gene–environment interactions. Even in patients with similar limitations in airflow, the clinical, physiologic and radiologic presentation of COPD can vary significantly from patient to patient. Therefore, to improve the management of COPD, it is important to identify clinically significant subgroups of COPD or "COPD phenotypes".[3] A fraction of patients with COPD has inherited PiZZ (Glu342Lys) alpha-1 antitrypsin deficiency (A1ATD), a major genetic determinant influencing the development of early-onset COPD with emphysema, especially in cigarette smokers.[4] The identification of biomarkers that can distinguish between A1ATD-PiZZ and non-A1ATD-PiMM COPD phenotypes could improve our understanding of the disease-driving mechanisms.

The use of proteomics is a growing trend in the search for new biomarkers of COPD. The advantage of this method is that it prompts various hypothesis-generating

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models, but not necessarily hypothesis-driven results. Current proteomic screenings in patients with COPD have involved mostly samples from the respiratory system, including bronchoalveolar lavage fluid, lung tissue, epithelial lining fluid and induced sputum. Several studies have investigated potential protein biomarkers in plasma and serum,[5] and proteomic analyses have implicated proteins involved in the regulation of inflammation, oxidative stress, immune responses and structural proteins.[6–9]

Urine is one of the frequently used biofluids in clinical studies because it is easy to obtain in large quantities and it contains proteins and peptides, which are quite stable and less complex than in plasma.[10] For these reasons, urine is an excellent reservoir of biomarkers (peptides, proteins and metabolites) for many diseases.[11] For example, the levels of elastin degradation products, such as desmosine/isodesmosine, have been investigated in the urine of COPD patients with and without A1ATD.[12] However, urinary desmosine levels are variable and raise during exacerbations of COPD, limiting the application of this measurement in a clinical setting.[13,14]

A novel approach for identifying urinary biomarkers employs capillary electrophoresis (CE) coupled to mass spectrometry (MS). Previously, this method was rarely used, owing to the limitations associated with coupling CE to the MS instrument and the restricted loading capacity of CE capillaries. However, the significantly increased sensitivity of modern MS and optimized methods for coupling CE to MS have transformed CE–MS into an appropriate tool for profiling disease-associated metabolites in body fluid samples such as urine. CE–MS enables simultaneous quantification of hundreds of peptides in a urine sample, which can then be incorporated into a diagnostic or prognostic score.[15] This method has enabled the identification of urinary biomarker classifiers that are highly specific for the diagnosis of various human diseases.[10,16,17] Therefore, we hypothesized that urinary peptidome analysis using CE–MS may help to identify specific peptide profiles in PiZZ and PiMM patients with COPD.

Materials and methods

Patients

Nineteen clinically stable patients with COPD (10 females and 9 males; 16 ex-smokers and 3 never-smokers) were enrolled for urine analysis at the National Institute of Tuberculosis and Lung Diseases in Warsaw and at the Regional Centre of Pulmonology in Bydgoszcz. The Ethics Committee at the National Institute of Tuberculosis and Lung Diseases in Warsaw approved the study (KB-170/2011), and all subjects signed an informed consent form. Patients were subdivided according to their A1AT genotype: 7 with PiMM and 12 with PiZZ. Pulmonary function tests were performed according to the American Thoracic Society/European Respiratory Society criteria. Plasma levels of A1AT and other variables were analyzed at the clinical center in Warsaw.

Urine samples

Midstream morning urine was collected in sterile containers and stored at −80°C prior to analysis, as recommended by the European Kidney and Urine Proteomics and Human Kidney and Urine Proteome Project and described previously.[18] For analysis, urine was diluted in a solution containing 2 M urea, 10 mM NH_4OH and 0.02% (w/v) sodium dodecyl sulfate. To remove higher molecular mass proteins, such as albumin and immunoglobulin G, each sample was ultrafiltered using a Centrisart ultracentrifugation filter device (20 kDa cutoff Vivaspin; Sartorius, Goettingen, Germany) at 3,000× *g* until 1.1 mL of filtrate was obtained. To remove urea, electrolytes and salts and to enrich polypeptides, the filtrate was then applied to a PD-10 desalting column (GE Healthcare Bio-Sciences AB, Uppsala, Sweden) equilibrated with 0.01% NH_4OH in high-performance liquid chromatography grade water (Roth, Bavaria, Germany). Finally, the samples were lyophilized and stored at 4°C. Shortly before CE–MS analyses, the samples were dissolved in high-performance liquid chromatography grade water, as described elsewhere.[19]

CE–MS analyses

For analysis, the sample resuspension volume was adjusted to yield 0.8 µg/µL protein as measured by the BCA assay (Pierce Biotechnology, Rockford, IL, USA). CE–MS analyses were performed using a CE system (Beckman Coulter, Fullerton, CA, USA) coupled to a micrOTOF II MS (Bruker Daltonic, Bremen, Germany) by Mosaiques Diagnostics GmbH (Hannover, Germany), and the analyses passed all quality control criteria. Validation experiments were performed, and the reference signals of 1770 urinary polypeptides were used for CE–MS calibration.[20] For normalization of the dilution variances, signal intensities were normalized to 29 housekeeping peptides.[21] The obtained peaks indicated the molecular mass of each polypetide, the normalized CE migration (minutes) and the normalized signal intensities. Accuracy, precision, selectivity, sensitivity, reproducibility and stability of the CE–MS measurements were demonstrated elsewhere.[22] All detected peptides were deposited, matched and annotated in a Microsoft SQL database to enable further statistical analyses.[21] STATISTICA 8.0 (StatSoft Inc., Tulsa,

OK, USA) was used for the data calculations. Functional analysis was performed using Gene Group Functional Profiling, g:Profiler (http://biit.cs.ut.ee/gprofiler/).[23]

Results

Patient characteristics

General patient characteristics are summarized in Table 1. Our cohort included patients having different severity of COPD: five PiZZ cases and one PiMM case were categorized as very severe (forced expiratory volume in 1 second [FEV_1] <35%), seven PiZZ and five PiMM cases as severe (35%< FEV_1<49%) and one PiMM case as moderate (50%< FEV_1<79%). As expected, the patients with PiZZ were younger than those with PiMM (mean [standard deviation {SD}]: 54.67±9.03 vs 65.71±6.27 years, respectively, $P<0.05$) and had lower plasma levels of A1AT (mean [SD]: PiZZ 22.52±5.43 mg/dL vs PiMM 166.29±22.89 mg/dL, $P<0.0001$). The patient groups did not differ statistically in terms of the pulmonary function tests, anthropometric measures and other serum parameters (Table 1).

Table 1 Characteristics of COPD patients

Variables	A1AT genotype		Mann–Whitney test	
	PiZZ (n=12)	PiMM (n=7)	*P*-value	*Z*-adjusted
Age (years)	54.7 (9)	65.7 (6.3)	1.21E-02	−2.51
Gender, M/F	5/7	4/3		
Smoking history, never/ex-smokers	1/11	2/5		
Pack-years	19.2 (11)	32.9 (26)	ns	−1.84
FEV_1%	37.6 (13.8)	43.7 (11.2)	ns	−0.63
FEV_1 (l)	1.1 (0.4)	1.1 (0.6)	ns	0.08
FEV_1%/FVC	37 (10.2)	47.3 (12.5)	ns	−1.14
FVC (l)	3 (0.9)	2.5 (1.2)	ns	0.78
FVC%	78.1 (15.8)	77.5 (12.7)	ns	0.21
VC (l)	3.2 (0.8)	1.4 (0.3)	4.13E-02	2.04
VC%	84.8 (14.8)	75.4 (16.1)	ns	0.75
PEF (l)	3.1 (0.8)	1.8 (0.3)	ns	1.83
PEF%	41.8 (11.4)	38.5 (6.5)	ns	0.43
A1AT (mg/dL)	22.5 (5.4)	166.3 (22.9)	4.53E-04	−3.51
hsCRP (mg/dL)	0.8 (1.4)	0.9 (0.7)	ns	−0.47
ALT (U/L)	28.8 (14.9)	17.6 (3.3)	ns	1.77
AST (U/L)	26.5 (9)	19 (3)	ns	0.94
Leukocytosis (10^9/L)	9.5 (3.5)	8.1 (1.5)	ns	0.49
Neutrophils (10^9/L)	6.1 (2.7)	5.6 (2.1)	ns	0.14
Neutrophils (%)	63 (6.4)	60.8 (5.2)	ns	0.64
Lymphocytes (10^9/L)	2.3 (0.5)	2.5 (0.6)	ns	−0.49
Lymphocytes %	26.2 (7.8)	28.3 (3.5)	ns	−0.21
Monocytes (10^9/L)	0.8 (0.5)	0.8 (0.1)	ns	−1.34
Monocytes %	8.1 (2.5)	9.6 (1.1)	ns	−0.78
Eosinophils (10^9/L)	0.3 (0.4)	0.1 (0.1)	ns	1.01
Eosinophils %	2.8 (3.3)	1.1 (0.8)	ns	0.93
pO_2 (Torr)	60.3 (8.5)	52.9 (11.4)	ns	0.85
pCO_2 (Torr)	38.2 (7)	43.8 (6.3)	ns	−0.76
SO_2%	91.6 (3.5)	86.3 (5.4)	ns	1.04
pH	7.5 (0.03)	7.4 (0.03)	ns	1.43
HCO_3^- (mmol/L)	25.6 (3.7)	27.1 (2.8)	ns	−0.66
BE (mmol/L)	1.7 (3.4)	2.6 (2.6)	ns	−0.66

Note: All data are presented as mean (standard deviation).

Abbreviations: A1AT, α1-antitrypsin; ALT, alanine transaminase; AST, aspartate transaminase; BE, base excess/deficit; ECM, extracellular matrix; FEV_1, forced expiratory volume in 1 second; FVC, forced vital capacity; HCO_3, hydrogen carbonate; hsCRP, high-sensitive C-reactive protein; pCO_2, partial pressure of carbon dioxide; PEF, peak expiratory flow; pO_2, partial pressure of oxygen; SO_2, oxygen saturation; VC, vital capacity.

Functional clustering analysis

We identified over 4200 peptides in each urine sample; however, only 66 peptides (corresponding to 36 unique proteins) differed between the PiMM and PiZZ COPD cases. We used the web server g:Profiler to predict the function of 36 proteins (http://biit.cs.ut.ee/gprofiler/).[23] Functional analysis revealed that the differentially expressed peptides were clustered in significant gene ontology categories related to biologic processes, cellular components, molecular functions and biologic pathways. As shown in Table 2, most of the peptides are related to the regulation of immune processes, collagen catabolism and biosynthesis, endoplasmic reticulum, protein digestion, the PI3K-Akt pathway and scavenging by class A receptor, among others.

Urinary peptides distinguish PiZZ and PiMM COPD cases

Urinary peptides from the collagen family were the most abundant and divergent in our patient cohort. Specifically, COL4A5, COL5A3, COL7A1, COL8A2, COL9A3, COL11A1 and COL23A1 were more frequent in the COPD cases with PiMM, whereas COL4A1 and COL4A3 were more frequent in the COPD cases with PiZZ. Further analysis revealed that COL1A1 (number 15, Table 3; 100% sensitivity, 85.71% specificity, $P<0.005$) and both COL5A3 and COL3A1 (numbers 52 and 62, Table 3; 91.67% sensitivity, 85.71% specificity, $P<0.005$) were useful for discriminating between the PiZZ and PiMM groups.

Interestingly, cases with PiZZ COPD presented low levels of urinary peptides involved in lipoproteins/lipids and retinoic acid metabolism, such as apolipoprotein A-I and C4, retinol-binding protein 4 and prostaglandin-H2 D-isomerase. In particular, peptides of apolipoprotein C4 (number 60, Table 3) discriminated PiZZ from PiMM cases with a sensitivity of 91.67% and a specificity of 85.71% ($P<0.005$). However, peptides of MDS1 and EVI1 complex locus, gelsolin and hemoglobin alpha, were found in the urine of PiZZ, but not PiMM cases (Table 3). We identified two

Table 2 The 36 proteins functionally clustered by g:Profiler

Biologic process	Count	*P*-value	Genes
Collagen catabolic process	11	4e-16	*COL11A1, COL5A3, COL1A1, COL7A1, COL2A1, COL1A2, COL3A1, COL4A3, COL8A2, COL4A1, COL4A5*
ECM organization	13	2e-11	*COL11A1, COL5A3, COL9A3, COL1A1, COL7A1, COL2A1, GSN, COL1A2, COL3A1, COL4A3, COL8A2, COL4A1, COL4A5*
Collagen fibril organization	6	1e-07	*COL11A1, COL5A3, COL1A1, COL2A1, COL1A2, COL3A1*
Anatomic structure morphogenesis	17	4e-04	*COL11A1, COL1A1, COL7A1, APOA1, ANXA1, RBP4, COL2A1, GSN, RUNX1, MYL3, COL1A2, COL3A1, COL4A3, KRT13, COL8A2, BCL9L, COL4A1*
Collagen-activated tyrosine kinase receptor signaling pathway	3	5e-04	*COL4A3, COL4A1, COL4A5*
Animal organ development	19	5e-04	*COL11A1, COL5A3, COL9A3, COL1A1, APOA1, ANXA1, RBP4, COL2A1, RUNX1, MYL3, COL1A2, B2M, COL3A1, COL4A3, KRT13, COL8A2, BCL9L, KRT10, COL4A1*
Circulatory system development	11	1e-03	*COL11A1, COL1A1, RBP4, COL2A1, RUNX1, MYL3, COL1A2, COL3A1, COL4A3, COL8A2, COL4A1*
Cellular response to amino acid stimulus	4	8e-03	*COL1A1, COL1A2, COL3A1, COL4A1*
Sensory perception of sound	5	1e-02	*COL11A1, COL1A1, COL2A1, COL4A3, ESPN*
Tissue development	13	2e-02	*COL11A1, COL1A1, COL7A1, ANXA1, RBP4, COL2A1, GSN, RUNX1, MYL3, COL3A1, BCL9L, KRT10, COL4A1*
Receptor-mediated endocytosis	6	2e-02	*UNC119, APOA1, SNX9, B2M, HBA1, HBB*
Response to wounding	8	4e-02	*COL1A1, APOA1, ANXA1, GSN, COL1A2, COL3A1, SERPINA1, HBB*
Regulation of immune system process	11	5e-02	*COL1A1, APOA1, IRAK2, ANXA1, RBP4, COL2A1, GSN, RUNX1, COL1A2, B2M, COL3A1*
Cellular component			
Endoplasmic reticulum lumen	16	9e-20	*COL23A1, COL11A1, COL5A3, COL9A3, COL1A1, COL7A1, APOA1, COL2A1, COL1A2, B2M, COL3A1, COL4A3, COL8A2, COL4A1, COL4A5, SERPINA1*
Complex of collagen trimers	10	3e-19	*COL11A1, COL5A3, COL1A1, COL7A1, COL2A1, COL1A2, COL3A1, COL4A3, COL4A1, COL4A5*
Endocytic vesicle lumen	3	9e-03	*APOA1, HBA1, HBB*
Vesicle	19	2e-02	*COL5A3, CHGB, PTGDS, COL1A1, COL7A1, APOA1, SNX9, IRAK2, ANXA1, FXYD2, RBP4, GSN, COL1A2, B2M, KRT13, KRT10, SERPINA1, HBA1, HBB*
Molecular function			
ECM structural constituent	11	2e-15	*COL11A1, COL5A3, COL9A3, COL1A1, COL2A1, COL1A2, COL3A1, COL4A3, COL8A2, COL4A1, COL4A5*
Platelet-derived growth factor binding	5	2e-08	*COL1A1, COL2A1, COL1A2, COL3A1, COL4A1*
Haptoglobin binding	2	2e-02	*HBA1, HBB*
Biologic pathway (KEGG)			
Protein digestion and absorption	12	5e-16	*COL11A1, COL5A3, COL9A3, COL1A1, COL7A1, FXYD2, COL2A1, COL1A2, COL3A1, COL4A3, COL4A1, COL4A5*
ECM–receptor interaction	7	2e-07	*COL9A3, COL1A1, COL2A1, COL1A2, COL4A3, COL4A1, COL4A5*
Amebiasis	6	3e-05	*COL1A1, COL1A2, COL3A1, COL4A3, COL4A1, COL4A5*
AGE–RAGE signaling pathway in diabetic complications	6	3e-05	*COL1A1, COL1A2, COL3A1, COL4A3, COL4A1, COL4A5*
Focal adhesion	7	1e-04	*COL9A3, COL1A1, COL2A1, COL1A2, COL4A3, COL4A1, COL4A5*
PI3K/Akt signaling pathway	7	4e-03	*COL9A3, COL1A1, COL2A1, COL1A2, COL4A3, COL4A1, COL4A5*
African trypanosomiasis	3	8e-03	*APOA1, HBA1, HBB*
Biologic pathway (reactome)			
Collagen biosynthesis and modifying enzymes	13	7e-19	*COL23A1, COL11A1, COL5A3, COL9A3, COL1A1, COL7A1, COL2A1, COL1A2, COL3A1, COL4A3, COL8A2, COL4A1, COL4A5*
Scavenging by Class A receptors	5	6e-07	*COL1A1, APOA1, COL1A2, COL3A1, COL4A1*
NCAM1 interactions	4	1e-03	*COL9A3, COL4A3, COL4A1, COL4A5*

Abbreviations: RAGE, receptor for advanced glycation endproduct; AGE, advanced glycation endproduct; NCAM1, neural cell adhesion molecule 1; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix.

Table 3 Urinary peptides distinguish PiZZ and PiMM COPD cases

Pep	Protein name	UniProt AC	Exp Mass	Peptide sequence	Intensity, mean (SD)		Z-adjusted	FDR
					PiZZ	PiMM		
1	Hemoglobin subunit β	P68871	2,659	FESFGDLSTPDAVMGNPKVKAHGKK	148 (191)	519 (379)	2.1*	2E-03
2	β-2-Microglobulin	P61769	1,077	IVKWDRDM	16 (37)	127 (121)	2.9**	2E-03
3	MDS1 and EVI1 complex locus protein MDS1	Q13465	1,140	TSHSSSNVWH	3,724 (4,315)	0 (0)	−2.6**	3E-03
4	Collagen α-1(I) chain	P02452	1,900	SPGRDGSPGAKGDRGETGPA	12 (41)	259 (261)	2.5*	1E-03
5	Collagen α-1(III) chain	P02461	1,354	KGEPGGPGADGVPGK	592 (389)	1,100 (551)	2*	8E-03
6	Collagen α-1(III) chain	P02461	2,154	NGEPGGKGERGAPGEKGEGGPPG	92 (142)	205 (82)	2.1*	3E-03
7	Retinol-binding protein 4	P02753	1,439	LQKGNDDHWIVD	242 (623)	390 (243)	2.2*	5E-03
8	Collagen α-1(I) chain	P02452	1,355	GQPGAKGEPGDAGAK	46 (43)	108 (69)	2*	8E-03
9	Collagen α-l(I) chain	P02452	1,877	DDGEAGKPGRPGERGPPGP	1,985 (715)	3,634 (1,405)	2.1*	3E-03
10	Gelsolin	P06396	2,232	DEELGGTPVQSRVVQGKEPAH	120 (176)	0 (0)	−2.2*	2E-03
11	Hemoglobin subunit α	P69905	2,021	AAHLPAEFTPAVHASLDKF	21 (25)	0 (0)	−2.2*	3E-03
12	Keratin; type I cytoskeletal 13	PI3646	1,361	EKITMQNLNDR	214 (464)	389 (246)	2*	9E-03
13	Apolipoprotein A-I	P02647	1,524	SALEEYTKKLNTQ	0 (0)	179 (425)	2.4*	2E-03
14	Ig λ-2 chain C regions	P0CG05	3,202	WKADSSPVKAGVETTTPS KQSNNKYAASSY	44 (125)	98 (66)	2.5*	6E-04
15	Collagen α-1(I) chain	P02452	858	SPGEAGRPG	410 (227)	134 (130)	−3**	1E-02
16	Collagen α-1(VII) chain	Q02388	2,410	GLKGDRGDPGPQGPPGLALGERGPP	60 (200)	111 (113)	2*	3E-03
17	Prostaglandin-H2 D-isomerase	P41222	1,843	YSQGSKGPGEDFRMATL	20 (40)	61 (63)	2.2*	3E-03
18	Annexin AI	P04083	2,057	FIENEEQEYVQTVKSSK	0 (0)	34 (62)	2.4*	1E-03
19	α-1-antitrypsin	P01009	1,943	EAIPMSIPPEVKFNKPFV	0 (0)	16,167 (39,363)	2.4*	1E-03
20	Myosin light chain 3	P08590	1,739	PAPAPPPEPERPKEVE	362 (216)	587 (265)	2*	4E-03
21	α-1-antitrypsin	P01009	2,042	EAIPMSIPPEVKFNKPFV	0 (0)	9,238 (22,506)	2.4*	1E-03
22	Collagen α-1(II) chain	P02458	2,133	GARGPEGAQGPRGEPGTPGSPGP	1,152 (687)	2,266 (1,111)	2.1*	3E-03
23	Collagen α-2(I) chain	P08123	1,226	GPPGPDGNKGEPG	539 (73)	690 (176)	2.2*	8E-03
24	Collagen α-1(I) chain	P02452	1,211	SPGPDGKTGPPGP	0 (0)	94 (179)	2.4*	5E-03
25	Collagen α-l(I) chain	P02452	1,408	GPPGEAGKPGEQGVP	149 (287)	353 (339)	2.1*	7E-03
26	Hemoglobin subunit β	P68871	2,171	TPEEKSAVTALWGK VNVDEV	0 (0)	341 (469)	2.8**	3E-04
27	Collagen α-l(I) chain	P02452	2,150	DGQPGAKGEPGDAGAKGDAGPPGP	1,774 (913)	3,022 (1,085)	2.6**	7E-04
28	Collagen α-2(I) chain	P08123	1,171	DQGPVGRTGEVG	54 (113)	0 (0)	−2.2*	1E-02
29	Collagen α-1(III) chain	P02461	1,423	GLPGTGGPPGENGKPG	2,341 (1,410)	3,863 (1,416)	2*	7E-03
30	Collagen α-1(I) chain	P02452	2,584	AGPPGADGQPGAKGEPG DAGAKGDAGPPGP	4 (13)	41 (61)	2.2*	2E-03
31	Collagen α-1(II) chain	P02458	1,096	APGEDGRPGPP	0 (0)	12 (18)	2.4*	8E-03
32	Sodium/potassium-transporting ATPase subunit γ	P54710	1,431	LSMDGGGSPKGDVDP	56 (90)	169 (138)	2*	8E-03
33	Collagen α-1(III) chain	P02461	1,660	GPPGPPGTSGHPGSPGSPG	202 (228)	714 (282)	3**	3E-04
34	Collagen α-3(IV) chain	Q01955	1,628	PGPPGPPGPPGHPGPQGP	205 (124)	71 (95)	−2*	6E-03
35	Collagen α-1(IV) chain	P02462	1,717	GPPGPPGPPGPPGEKGQM	127 (412)	50 (47)	2.1*	4E-03
36	Collagen α-1(XXIII) chain	Q86Y22	1,601	DPGPPGQSGRDGYPGP	49 (60)	189 (104)	2.3*	3E-03
37	Collagen α-3(IX) chain	Q14050	3,048	QGDRGDKGAAGAGLDG PEGDQGPQGPQGVPGTS	33 (67)	169 (146)	2.3*	1E-03
38	Sodium/potassium-transporting ATPase subunit γ	P54710	1,504	GLSMDGGGSPKGDVDP	0 (0)	42 (49)	2.4*	2E-03
39	Collagen α-5(IV) chain	P29400	1,627	PGAPGFPGSKGEPGDIL	101 (177)	460 (502)	2*	5E-03
40	Collagen α-1(XI) chain	P12107	1,734	PPGPKGNMGPQGEPGPPG	0 (0)	62 (69)	3.3**	1E-04
41	Collagen α-1(I) chain	P02452	2,946	NSGEPGAPGSKGDTGAKG EPGPVGVQGPPGPAG	4 (8)	31 (34)	2.2*	2E-03
42	Collagen α-1(XI) chain	P12107	1,675	KGENGDVGPMGPPGPPGP	28 (39)	215 (185)	2.1*	4E-03
43	Collagen α-2(VIII) chain	P25067	1,822	GPPGEGRAGEPGTAGPTGPP	314 (378)	848 (304)	2.5*	1E-03
44	Collagen α-1 chain	P02461	1,652	QPGEKGSPGAQGPPGAPG	4 (10)	79 (57)	3.1**	2E-04
45	Prostaglandin-H2 D-isomerase	P41222	1,805	AQVSVQPNFQQDKFLG	0 (0)	32 (46)	2.4*	2E-03
46	Secretogranin-1	P05060	3,202	SSQGGSLPSEEKGHPQEES EESNVSMASLGE	43 (68)	220 (192)	2.3*	1E-03

(*Continued*)

Table 3 (*Continued*)

Pep	Protein name	UniProt AC	Exp Mass	Peptide sequence	Intensity, mean (SD)		*Z*-adjusted	FDR
					PiZZ	PiMM		
47	Collagen α-2(I) chain	P08123	1,853	NGAPGEAGRDGNPGNDGPPG	118 (128)	13 (26)	−2.2*	2E-03
48	Collagen α-1(III) chain	P02461	1,860	NPGPPGPSGSPGKDGPPGPAG	282 (201)	81 (101)	−2.5*	1E-03
49	Collagen α-1(II) chain	P02458	3,458	TGPPGPAGFAGPPGADGQP GAKGEQGEAGQKGDAGAPGP	23,598 (6,494)	11,915 (9,047)	−2.3*	1E-03
50	Collagen α-1(I) chain	P02452	1,685	EPGSPGENGAPGQMGPR	0 (0)	395 (953)	2.4*	2E-03
51	Collagen α-1(I) chain	P02452	1,826	GANGAPGNDGAKGDAGAPGAPG	493 (414)	130 (126)	−2.1*	3E-03
52	Collagen α-3(V) chain	P25940	1,699	GIDGSPGEKGDPGDVGGPG	1 (4)	39 (33)	3.4***	8E-05
53	Keratin; type I cytoskeletal 10	P13645	1,737	TQLLNNMRSQYEQL	0 (0)	244 (431)	2.8**	5E-04
54	Collagen α-(I) chain	P02452	1,762	QGPGGPPGPKGNSGEPGAPG	0 (0)	34 (57)	2.4*	2E-03
55	Runt-related transcription factor 1	Q01196	3,443	SISDPRMHYPGAFTYSP TPVTSGIGIGMSAMGSA	3 (9)	81 (74)	2.9**	2E-04
56	Collagen α-1(I) chain	P02452	2,104	GPPGEAGKPGEQGVPGDLGAPGP	1,631 (447)	2,430 (662)	2.6**	7E-04
57	Interleukin-1 receptor-associated kinase-like 2	O43187	2,192	ANGSLQDRLQGQGGSDPLPWP	2 (5)	15 (15)	2.1*	3E-03
58	Collagen α-2(I) chain	P08123	3,633	DQGPVGRTGEVGAVG PPGFAGEKGPSGEAGTAGPPGTPGP	10 (32)	132 (105)	3.2**	7E-05
59	Sorting nexin-9	Q9Y5X1	2,501	ASTAQASSSAASNNHQ VGSGNDPWSA	19 (28)	107 (104)	2.2*	2E-03
60	Apolip oprotein C-IV	P55056	2,418	TQQPQQDEMPSPTFLTQVKES	8 (20)	67 (32)	3.3***	6E-05
61	Collagen α-5(IV) chain	P29400	2,646	GQDGIPGPAGQKGEPG QPGFGNPGPPGL	0 (0)	25 (47)	2.4*	1E-03
62	Collagen α-1(III) chain	P02461	2,854	PQGPPGPTGPGGDKGD TGPPGPQGLQGLPGT	2,570 (2,224)	8,157 (6,403)	2.5*	7E-04
63	Espin	B1AK53	1,005	LPPPPPPPPP	17 (19)	62 (51)	2*	3E-02
64	Collagen α-1(II) chain	P02458	1,594	PGTPGNPGPPGPPGPPGP	110 (187)	8 (21)	−2.2*	4E-03
65	Protein unc-119 homolog A	Q13432	1,247	SESGSESEPDAGP	2 (6)	23 (35)	2.2*	6E-03
66	B-cell CLL/lymphoma 9-like protein	Q86UU0	1,557	PGMGWTEDLPPMGGP	888 (431)	443 (255)	−2.1*	5E-03

Notes: Statistical results based on Mann–Whitney *U*-test and FDR test; Exp Mass (molecular mass of the peptide, kDa), the *Z*-adjusted reported the equivalent *P*-values as follows: *$P<0.05$; **$P<0.01$; ***$P>0.001$.
Abbreviations: CLL, chronic lymphocytic leukemia; FDR, false discovery rate; SD, standard deviation.

peptides of A1AT in the urine of 43% of PiMM cases, but they were absent in PiZZ cases.

Discussion

The increased proteolytic activity and protease–antiprotease imbalance in COPD have been well described. Therefore, many studies have focused on identifying protease-generated peptides in various biologic fluids from patients with COPD.[24] Recently, Wendt et al have used liquid chromatography coupled to MS for metabolomic profiling of bronchial lavage fluid obtained from patients with COPD and further confirmed a significant increase in peptides compared with healthy controls.[25]

PiZZ A1ATD-related COPD is associated with low circulating levels of A1AT (10%–15% of normal levels), which is the main inhibitor of neutrophil proteases. Neutrophils are among the key participants in COPD, and they secrete serine proteases (neutrophil elastase, cathepsin G and proteinase-3) and matrix metalloproteinase (MMP)-8 and MMP-9.[26,27] Active elastase can degrade many extracellular matrix substances, including elastin, collagen types I–IV and fibronectin, and activate MMPs.[28] For example, it has been demonstrated that elastase, cathepsin G and proteinase-3 activate MMP-2, and this activation is blocked by A1AT, but not by an MMP-inhibitor.[29] Macrophages also secrete proteases, including MMP-2, MMP-9 and MMP-12, and cathepsins K, L and S. Macrophages from patients with COPD exhibit greater activation and elastolytic activity that those from non-COPD controls.[28] Careful examination of the data revealed that A1AT deficiency favors proteolysis and tissue destruction, in general. Therefore, patients with COPD who carry inherited PiZZ A1ATD are expected to display higher levels of activated proteolytic enzymes and proteolysis-generated peptides than those with PiMM A1AT. Previous analyses of patients with COPD revealed that the protease caspase-9 is upregulated in the lung tissue of patients with PiZZ, whereas cathepsin B is upregulated in those with PiMM. Moreover, the differences between

PiZZ and PiMM COPD cases were found in processes related to protein biosynthesis, energy pathways and cellular defense response.[30]

COPD is associated with systemic abnormalities, such as renal and hormonal abnormalities, malnutrition, muscle wasting, osteoporosis and others. These systemic abnormalities have been attributed to increased systemic inflammation. Therefore, COPD is considered to have a significant systemic component.[31] Urine is a rich source of biomarkers for a wide range of systemic diseases; therefore, we hypothesized that urinary peptide profiles might differ in patients with PiZZ and PiMM COPD. This is the first study to apply CS–MS for the analysis of urinary peptides in PiMM and PiZZ COPD patients.

Using CS–MS to analyze urine from patients with COPD, we detected 66 urinary peptides (corresponding to 36 unique proteins) that differed between PiMM and PiZZ cases with COPD. The peptides related to collagen breakdown products, actin organization/vesicle trafficking, lipid metabolism and the PI3K/Akt pathway are interesting candidates for distinguishing COPD with and without inherited A1ATD.

Remarkably, peptides of the MDS1 and EVI1 complex locus protein MDS1, collagen α-2(I) chain, gelsolin and hemoglobin subunit α, were detected in the urine of the PiZZ cases only, whereas peptides of apolipoprotein A-I, A1AT, collagen α-1(I) chain and hemoglobin subunit β, were detected in the urine of the PiMM cases (Table 3). Gelsolin, an actin-binding protein, is a key regulator of actin filament assembly. Caspase-3-mediated gelsolin fragmentation has been proposed to be an apoptotic effector mechanism in COPD pathogenesis and a marker of lung injury.[32] Alterations in gelsolin expression have been associated with cigarette smoking and different pulmonary diseases such as fibrosis; however, little is known about the role of gelsolin in COPD.[32–34] Gelsolin activates PI3K/Akt pathway,[35] which regulates cell growth, proliferation, adhesion, migration and survival. Interestingly, it promotes the differentiation of alveolar epithelial type I and II cells from alveolar epithelial stem cells.[36,37]

COPD cases with PiZZ A1ATD presented low or undetectable levels of peptides associated with lipoproteins/lipids and retinoic acid metabolism, such as apolipoprotein A-I and C4, retinol-binding protein 4 and prostaglandin-H2 D-isomerase. Apolipoprotein A-I is the main component of high-density lipoproteins. Moreover, it has a protective role as an antioxidative, anti-inflammatory and antiapoptotic factor and as an inhibitor of metalloprotease activation in human lungs and cigarette smoke-exposed murine models.[38–40] In addition, reduced levels of apolipoprotein A-I are observed in the lungs of patients with COPD, compared with smoker controls.[38] Apolipoprotein A-I and retinol-binding protein 4 are proposed to be putative biomarkers of COPD severity.[41,42]

A recent review by Bidan et al[43] summarized various studies on lung collagen content in COPD. Despite the fact that many studies have found increased collagen in the lungs of patients with COPD, there are contrasting data about the contribution of individual collagen subtypes. Little is known about the collagen content in urine from patients with COPD.

We identified two peptides of A1AT that were present in the urine of 43% of the PiMM cases, but in none of the PiZZ cases. A1AT and its fragments have been reported to be upregulated in chronic kidney diseases.[44–46] Peptides of A1AT were detected in the urine of patients with kidney diseases and sepsis, and were suggested as putative biomarkers.[47] Thus, increased urinary excretion of fragments of A1AT may reflect chronic renal damage in some COPD cases with PiMM. Further studies are required to investigate this possibility.

Due to the close relationship between the kidneys and urine, most current studies use the CE–MS method of identifying urinary biomarkers in the investigation of kidney diseases.[48] However, only a limited number of urinary biomarker studies in lung diseases have been conducted, likely because the lung and the kidneys are not anatomically related, raising questions about the potential presence of lung disease biomarkers in urine. For example, enzyme-linked immunosorbent assay-based results from a recent study by Cane et al suggest that MMP levels in lung, serum and urine are independent of each other and do not reflect disease severity.[49]

CE–MS technology has certain limitations, as described in our previous publication.[18] The small sample volume (<200 μL) and inability to determine the sequence of some of the biomarker peptides are among the most relevant limitations. However, the advantages of this technology include its robustness, reproducibility and well-characterized platform, resulting in the availability of a database containing over 40,000 highly comparable individual datasets.

Use of the CS–MS method, even in a small cohort, allowed detection of distinct patterns of urinary peptides differing between the PiZZ and PiMM patients with COPD. Our novel and preliminary data suggest a clinical value for urinary peptidomics and encourage further validation of the CS–MS method in COPD patient cohorts of sufficient size for appropriate power analysis.

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Disclosure

The authors report no conflicts of interest in this work.

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