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Serum amyloid A1 and plasminogen as predictive proteins to monitor the progression of preleukemic diseases towards acute lymphoblastic leukaemia†

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Acute lymphoblastic leukaemia (ALL) is a type of cancer and is the most common form of leukaemia in children. It also occurs in adults around the age of 50 at a low incidence rate. Aplastic anaemia (APA) and myelodysplastic syndrome (MDS), two preleukemic diseases, have been reported to convert into ALL in some case studies. To obtain molecular insight into this progression and identify the proteomic molecules that can associate these preleukemic diseases to ALL, this study is focused on the comparative proteomic profiling of ALL, APA, MDS and the healthy control. A multi-fractionation approach was used for the fractionation of pooled plasma samples of all study groups. Up- and down-fold changes in the concentration of proteins were observed in two-dimensional gel electrophoresis (2D-GE) gels of diseases compared to the healthy group. Among the 34 identified proteins, the eight proteins that were significantly deregulated included serum amyloid A-1 (SAA1), haptoglobin (HPT), C4b-binding protein alpha chain, complement factor 7, apolipoprotein E (ApoE), plasminogen, prothrombin, and complement factor H (CFH), and their links to important cell signalling pathways were found. Validation through enzyme-linked immunosorbent assay (ELISA) showed that SAA1 and plasminogen may be considered as potential molecules that link ALL with APA and MDS.

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Introduction

Acute lymphoblastic leukaemia (ALL) is a heterogeneous disease, and numerous genetic mutations lead toward its development. It is the most common cancer in children and is caused by the accumulation of multiple consecutive genetic mutations in the early hematopoietic cells.¹ In adults, the incidence peak of ALL is around the age of 50 and although a complete remission is achieved in the children, only 30–40% of the adults can expect a cure from ALL.² It could be either without signs and symptoms or with life threatening infections, respiratory suffering or haemorrhage.

MDS is a group of heterogeneous malignancy of the hematopoietic stem cell, characterized by bone marrow hypercellularity, cytopenias, and increased risk of transformation to acute leukaemia. Usually, one third of the MDS cases transform into acute leukaemia, mainly acute myeloblastic leukaemia (AML). Although conversion to ALL is quite rare, some case studies have been reported in the literature, where MDS has

transformed into ALL. This shows that the origin of this disorder is at the same level as a common progenitor cell, which gives rise to both hematopoietic as well as lymphoid origin cells.^{3–9}

The APA is a hematological illness, and the molecular mechanism behind this abnormal immune system and insufficiencies in hematopoietic cells is genetic, namely mutations in repairing genes of the telomeres and the dysregulated pathways of T-cell stimulation.¹⁰ Some case studies have reported this type of conversion of APA to ALL.^{11–19}

Currently, molecular genetics, cytogenetics, and morphologic, biochemical and immunologic characteristics of lymphoblasts are needed to make the correct diagnosis and classification,²⁰ and to perform all these tests, a bone marrow puncture is required, which is quite painful and invasive, particularly for children. Therefore, diagnostic procedures need to be improved for timely diagnosis using minimal invasive tests.²¹ Proteomic analysis provides information about the proteome's dynamicity and rapid changes towards illness and assesses the consequences of diseases using the powerful tool of proteomics.^{22–24} Our aim in this study is to obtain, for the first time, some proteomic molecules that may determine the relationship of ALL with preleukemic diseases such as APA and MDS using a multidimensional protein fractionation strategy, *i.e.* fast protein liquid chromatography (FPLC), ZOOM isoelectric focusing (IEF), 2D-GE, and matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) analysis.

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Experimental

Sample collection and characterization methodology

We selected ALL, APA, MDS and healthy samples for this study. Blood samples were collected from the National Institute of Blood Diseases and Bone Marrow Transplantation (NIBD), Pakistan, after the written informed consent of the participants, in accordance with the ethical standards in the Helsinki declaration. The study was approved by the Ethics Committee of the hospital as per ICH GCP guidelines as well as by the Independent Ethics Committee (IEC) (-022-HB-2017) of the principal investigating institute. All experiments were performed in compliance with the relevant laws and institutional guidelines, and a detailed questionnaire was filled in by every patient and healthy volunteers, which was accepted by the institutional human research ethics committee. Disease samples were classified according to the World Health Organisation (WHO) guidelines. The samples were processed according to the standard protocol of the human proteome organization (HUPO).²⁵ Furthermore, 5 mL whole blood was taken into vacutainers containing K2 ethylene diamine tetra-acetic acid (EDTA) as an anticoagulant. Whole blood was centrifuged at $2200 \times g$ for 10 min at 4 °C to separate the plasma, followed by aliquoting and storage at -80 °C. Equal amount of individual healthy plasma were mixed to obtain the Pakistani pooled plasma of healthy control group, and same strategy was used for the pooling of disease samples.

One-dimensional gel electrophoresis

One-dimensional sodium dodecyl sulfate-polyacrylamide gel electrophoresis (1D SDS-PAGE) was performed on an X Cell SureLock system (Invitrogen, USA). Chemicals and reagents were purchased from Invitrogen (USA), containing Precast NuPAGE® bis-tris mini gels 12%, NuPAGE® 2-(*N*-morpholino-ethanesulfonic acid) MES SDS running buffer 20×, NuPAGE® MOPS SDS running buffer, protein ladder, and colloidal Coomassie staining kit. β -Mercaptoethanol, sucrose, and Tris HCl were purchased from Sigma Aldrich (USA).

Depletion of abundant proteins

Immunodepletion of the top-7 most abundant proteins was performed using the Multiple Affinity Removal Column (MARS) Hu-7 (4.6 × 50 mm) purchased from Agilent (USA) on an ÄKTA™ Purifier FPLC system, GE Healthcare (Sweden). Protease inhibitors EDTA, leupeptin, pepstatin-A and phenylmethanesulfonyl fluoride (PMSF) were purchased from Sigma Chemicals (USA). A 500 mL Vacuum Filter/Storage Bottle System was purchased from Corning (USA). A total of 300 μ L of the plasma was depleted according to the manufacturer's protocol, followed by 1D SDS-PAGE to check the sample recovery.

The pooled unbound fraction was enriched through a 5 kDa molecular weight cut-off (MWCO) filter tubes according to the kit protocol. The enrichment efficiency was checked through 1D SDS-PAGE analysis by loading the volume of fractions equivalent to 0.1 μ L of the original plasma (before and after concentration).

Proteins in the unbound portion were reduced and alkylated according to a standard protocol with minor modifications.²⁶ Urea, tris, dichlorodiphenyltrichloroethane (DTT), and iodoacetamide (IAM) were purchased from Invitrogen (USA), Boehringer Mannheim (Germany), and SERVA (Germany), respectively. Acetone and trichloroacetic acid (TCA) were purchased from Fisher Scientific (UK) and Scharlau (Spain), respectively. The protein precipitation was performed using the TCA/acetone protocol²⁷ with some minor modifications.

Microscale isoelectric focusing

The ZOOM IEF Fractionator Combo Kit comprising a ZOOM IEF Fractionator was purchased from Invitrogen (USA). The sample pellet was dissolved in the ZOOM buffer along with the addition of 26 μ L of the ZOOM carrier ampholytes (pH 3–10) and a small amount of bromophenol blue (BPB). The fractionation of the each pooled unbound fraction was carried out using established protocols.²⁸ The 1D SDS-PAGE analysis of all the five ZOOM fractions of different pH ranges was performed to check the efficiency of IEF and compare the disease samples to the healthy control.

2D gel electrophoresis

The proteins from the ZOOM fractions were precipitated according to the above mentioned protocol. The 2D-GE was performed on a Bio-Rad PROTEAN IEF cell (USA). The Ready-Prep 2-D Starter Kit, ReadyStrip IPG Strips, 7 cm, pH 4–7, Ready Gel Precast Gel, mineral oil, and 10× Tris/glycine/SDS buffer were all purchased from Bio-Rad (USA). The entire procedure was performed according to the kit protocol provided by the manufacturer.

The gel images were taken through the Gel DOC 800 system Bio-Rad (USA). Analysis was performed in Bio-Rad PDQuest version 8.0.1. Bio-Rad (USA). The images were cropped to the area containing the spots of interest. A master gel was created and the healthy plasma pool was considered as the control. Spot detection, spot matching, and semi-quantitative statistical analysis were performed. The *t*-test was used to study the differential expression, with the *p* value < 0.05. Two analysis sets were created, one with a 4× quantity difference and the other with a significance level \geq 95%; using these analysis sets numerous other Boolean union/intersect analysis sets were created among the gels of the study groups. Some detected spots were manually edited for greater accuracy. The protein spots of interest were extracted using the manual cutting procedure.

Matrix-assisted laser desorption ionization-time-of-flight-mass spectrometry

Analysis was performed using the matrix-assisted laser desorption ionization-time-of-flight-mass spectrometry (MALDI-TOF-MS) (Ultraflex III, Bruker Daltonics Germany). The mass spectrometric profile was obtained using flexAnalysis version 3.0 (Bruker Daltonics). Spot cutting and the in-gel digestion was performed according to the reported protocol.^{29,30} The digested peptides were analysed using a MALDI-TOF mass spectrometer. Briefly, the samples were mixed in equal proportion with freshly prepared α -



cyano-4-hydroxycinnamic acid in acetonitrile (ACN). Instrument calibration was done in a reflector positive mode using a peptide calibrant standard I (Bruker Daltonics). Spectra were obtained over the mass range of 500–3000 m/z with the sum of 2000 laser shots within the same spot (200 shots per position) and an intensity of 20–40%.

The protein mass fingerprinting (PMF) of the mass values obtained from MALDI-TOF was performed using the online MASCOT server with Swiss-Prot and NCBI nr databases; moreover, carbamidomethylation of cysteine as the fixed and the oxidation of methionine as the variable modification were selected. The maximum number of the missed cleavages was set to 0 and 1, peptide tolerance 100 ppm per 1 Da, and $p < 0.05$ was used to find the proteins.

Pathway analysis

Differently expressed proteins were further subjected to Gene Ontology (GO)-based analysis to determine their functions, and

then the connections among the proteins and their connection with the other proteins were assessed using the STRING: EMBL (European Molecular Biology Laboratory) software.³¹

ELISA analysis

ELISA was performed on individual samples for the five proteins SAA1, CFH, complement C7, plasminogen, and ApoE on Thermo Fischer Scientific™ Multiskan™ FC Microplate Photometer (USA). The ELISA kits were purchased from Crystalchem (USA) and Assaypro (USA). Plasma samples of 20 ALL, 15 AA, 15 MDS, and 15 healthy individuals were diluted according to the kit protocol. The entire procedure was performed according to the manufacturer's given methodology, followed by statistical analysis using GraphPad Prism 7.0.

Results

Auxological data

A total of 65 plasma samples of ALL, 41 AA, and 17 MDS were included in this study, while 50 healthy male and 50 female healthy volunteers were selected for the control group. The classification of healthy samples on the basis of age and number of samples are shown in Table 1. All the healthy individuals were free of any hematological diseases at the time of sampling with normal vital signs and with no family history of ALL, AA, and MDS.

Immunodepletion of top-7 abundant proteins

The pool plasma samples were depleted of the top-7 most abundant proteins using a MARS column. The resultant FPLC spectrum showed a clear separation of the unbound and bound proteins, in

Table 1 Statistics and strategy of collecting healthy plasma samples

	Healthy		Number of samples	
			Male	Female
Age group	20–30 years	Group I	20	20
	30–40 years	Group II	10	10
	40–50 years	Group III	10	10
	50–above years	Group IV	10	10
Total number of samples	100			

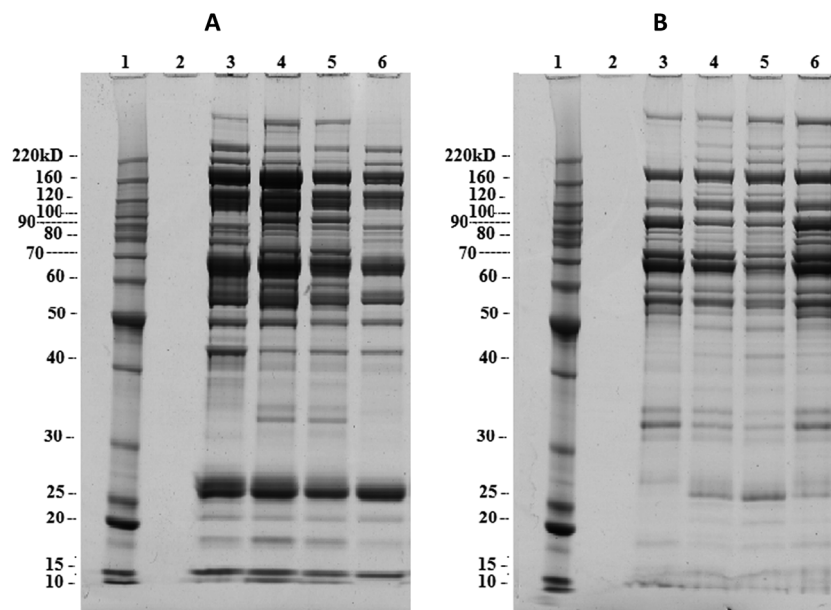


Fig. 1 (A) Comparison of fraction-3 (pH: 5.4–6.2) after ZOOM IEF. (1) Protein ladder, (2) blank, (3) ALL, (4) APA, (5) MDS and (6) healthy. (B) Comparison of fraction-4 (pH: 6.2–7.0) after ZOOM IEF. (1) Protein ladder, (2) blank, (3) ALL, (4) APA, (5) MDS and (6) healthy. The amount of fractions loaded into the gel was equivalent to 3 μL of the original plasma.



full agreement with the figure provided in the manufacturer's protocol (Fig. S1†). The depletion efficiency was shown to be effective through the one-dimensional gel electrophoresis (1D-GE) analysis (Fig. S2†). Then, the unbound portions of each group were enriched through 5 kDa MWCO tubes, and the efficiency showed acceptable protein enrichment (Fig. S3†).

Microscale isoelectric focusing

Fractionated proteins were further separated using the ZOOM IEF over a pH range of 3.0–10 into several fractions with different pH ranges; pH: 3.0–4.6, pH: 4.6–5.4, pH: 5.4–6.2, pH: 6.2–7.0, and pH: 7.0–10.0. The 1D-GE results showed that the two fractions of pH: 5.4–6.2 and pH: 6.2–7.0 from all the study groups had a large number of the protein bands (Fig. S4†). The comparison of these two fractions is shown in Fig. 1. These two fractions were pooled to make a single pooled fraction over the pH range from 5.4 to 7.0 from each group, followed by protein precipitation.

2D gel electrophoresis and mass spectrometry

The resultant (2D-GE) maps of all the study groups are shown in Fig. 2. The master gel was used for the comparison of ALL gels

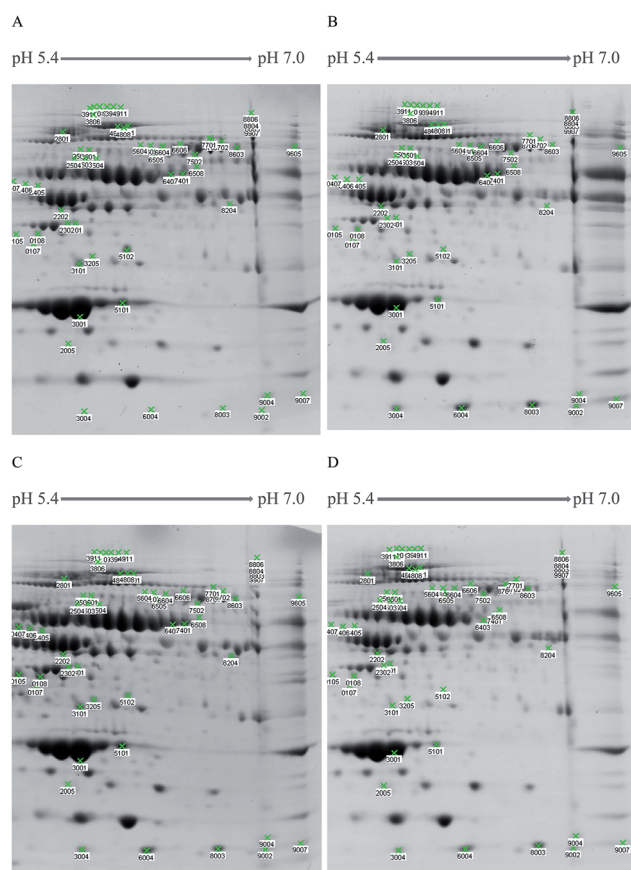


Fig. 2 2D-Gel analysis of the pools. (A) Healthy pool, (B) acute lymphoblastic leukaemia, (C) aplastic anemia and (D) myelodysplastic syndrome. Green crosses are spots that are 95% significant and 4 \times up- or down-regulated.

with the preleukemic and the healthy gel images (Fig. S5†). The ALL pool was compared with the pool of the two preleukemic diseases and with the healthy pool, separately. Boolean intersection sets were created for each comparison separately and their Boolean union was created, which had 56 spots, for a combined comparison. The bar graphs of these 56 spots are shown in Fig. S6.† Among the 56 spots, we chose only those spots that had a pattern of up- or down-regulation in the leukemic and preleukemic diseases compared to the healthy sample.

Altogether, a total of 182 gel spots were analysed using MALDI-TOF MS, which led to the identification of 34 distinct proteins and/or their respective isoforms and subunits (Fig. 3). The list of identified proteins is shown in Table 2. We identified eight proteins that are significant and consistently deregulated: ApoE, complement factor 7, C4b-binding protein alpha chain, plasminogen, prothrombin, SAA1, CFH, and HPT. The former five proteins were found to be down-regulated, while the latter

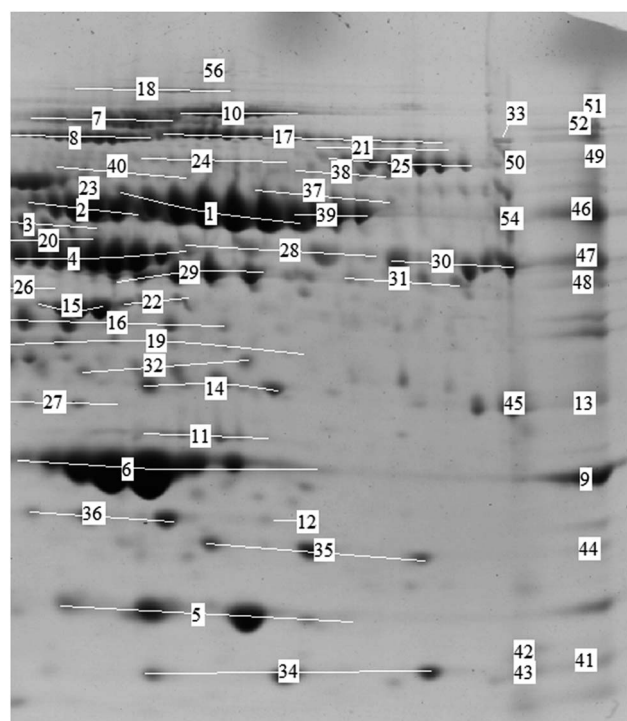


Fig. 3 Identified variants and subunits of proteins in 2-D gel image through MALDI-MS and MASCOT database searching [(1, 39 and 46) hemopexin, (2) alpha-1 β -glycoprotein, (3 and 20) kininogen-1, (4) Vit-D-binding protein, (5) transthyretin, (6 and 9) apolipoprotein A-I, (7, 8 and 52) ceruloplasmin, (10, 51 and 55) complement factor H, (11) human serum amyloid-P component, (12, 13, 14 and 32) apolipoprotein E, (15) apolipoprotein A-IV, (16, 35 and 44) haptoglobin, (17 and 53) alpha 2-macroglobulin, (18) fibronectin, (21) complement factor 7, (22) CD5 antigen-like, (23 and 40) prothrombin, (24) complement C1r-subcomponent, (25) complement factor B, (26) complement C4-A, (27) alpha-1 microglobulin, (28, 29 and 48) fibrinogen gamma chain, (30, 31 and 47) fibrinogen beta chain, (33, 49 and 50) plasminogen, (34, 41 and 43) serum amyloid A-I, (36) retinol-binding protein, (37 and 39) C4b-binding protein alpha chain, (38) gelsolin, (39) human serum albumin, (42) serum amyloid A-IV, (43) hemoglobin β -component, (45) complement C4 and (54) fibrinogen alpha chain].





Table 2 List of 34 identified proteins through mass spectrometry and MASCOT database searching

SSP IDs	Protein name	Accession no.	Database	Sequence coverage (%)	M_r	pI	Matched peptides no.	Expect value	Score
3803, 3907-3911, 4801-4804, 4911, 4912, 5701, 5702, 5801, 5802, 6801-6803, 7701, 7801-7803	Alpha-2-macroglobulin	gi 224053	NCBItr	29%	162 072	5.92	38/146	3.1×10^{-7}	120
3804, 3805, 3901, 4807-4809, 4902, 5901	Complement factor H	CFAH_HUMAN	SwissProt	35%	143 680	6.21	45/136	6.4×10^{-11}	145
0701, 0702, 0706, 1601, 1602, 1701, 1801, 1802, 2801-2803	Ceruloplasmin	CERU_HUMAN	SwissProt	26%	122 983	5.44	19/107	1.4×10^{-5}	92
5604, 6601, 6603, 6604, 7601, 7602, 8601, 8602	Complement factor B	CFAB_HUMAN	SwissProt	30%	86 847	6.67	20/90	3.3×10^{-6}	98
2501, 3501, 3503, 4501-4503	Complement C1r subcomponent	C1R_HUMAN	SwissProt	21%	81 606	5.82	16/64	6.7×10^{-4}	75
2503, 2504, 3504	Prothrombin	THRB_HUMAN	SwissProt	34%	71 475	5.64	18/88	6.4×10^{-8}	115
5504, 6404, 6507, 6508, 7402, 6402, 6403, 7401	C4b-binding protein alpha chain	C4BPA_HUMAN	SwissProt	39%	69 042	7.15	19/131	2.5×10^{-7}	109
0401, 0408, 1401, 2401	Alpha-1 β -glycoprotein	A1BG_HUMAN	SwissProt	35%	54 790	5.56	18/125	9.5×10^{-5}	83
0301, 0302, 1201, 2201, 2203, 3301	Vitamin D-binding protein	VTDB_HUMAN	SwissProt	41%	54 526	5.40	15/111	2.5×10^{-4}	79
6402, 6403, 7401, 2402, 3401, 4401, 5401, 5402, 6401	Hemopexin	HEMO_HUMAN	SwissProt	41%	52 385	6.55	19/127	2×10^{-9}	130
2202, 2204, 3201, 3402, 4201, 5201, 5301, 6204, 6208, 6405, 9205	Fibrinogen gamma chain	gi 223170	NCBItr	31%	46 823	5.54	10/66	7.5×10^{-3}	76
0405, 0406	Kininogen 1	gi 37748641	NCBItr	44%	48 954	6.29	17/115	2×10^{-6}	112
0105, 0107, 0108, 2005, 2101, 2103, 3103, 3104, 4002, 4107, 5103, 6001, 8002	Haptoglobin	HPT_HUMAN	SwissProt	36%	45 861	6.13	15/102	8×10^{-8}	114
3806	Fibronectin	FN1_HUMAN	SwissProt	18%	266 052	5.46	43/179	0.0079	64
2301, 2302, 3302	CD5 antigen-like	CD5L_HUMAN	SwissProt	55%	39 603	5.28	17/80	1.3×10^{-7}	112
0101, 0102, 1001, 2001, 3001, 4101, 5101	Chain A, apolipoprotein A-I	gi 90108664	NCBItr	62%	28 061	5.27	15/77	9.9×10^{-9}	135
2106, 3108, 3109, 4106, 5104	Serum amyloid P-component	SAMP_HUMAN	SwissProt	29%	25 485	6.10	9/76	2×10^{-3}	70
0002, 3002, 5001	Chain A, transthyretin	gi 14719497	NCBItr	66%	12 671	5.26	6/81	4.8×10^{-3}	78
0201-0203, 1202	Apolipoprotein A-IV	APOA4_HUMAN	SwissProt	38%	45 371	5.28	15/72	1.1×10^{-5}	92
2105, 3101, 3205, 4102, 4105, 5102, 6102	Apolipoprotein E	APOE_HUMAN	SwissProt	50%	36 246	5.65	16/92	1.3×10^{-7}	112
0002, 3002, 5001	Transthyretin	TTHY_HUMAN	SwissProt	48%	15 991	5.52	4/95	0.04	57
7301, 8201, 8202, 8204, 8301, 8401, 9302, 9303	Fibrinogen beta chain	FIBB_HUMAN	SwissProt	60%	56 577	8.54	28/108	8×10^{-15}	184
6605-6607, 7603, 8701, 8702	Complement component C7	CO7_HUMAN	SwissProt	23%	96 550	9.06	17/91	0.0034	68
9402	Fibrinogen alpha chain precursor	gi 11761629	NCBItr	36%	70 227	8.23	23/147	0.0016	83
9002	Hemoglobin subunit beta	HBB_HUMAN	SwissProt	49%	16 102	6.75	6/78	0.72	44
9004	Serum amyloid A-4	SAA4_HUMAN	SwissProt	40%	14 851	9.17	6/60	0.016	61
8803, 8804, 8806, 9601, 9605, 9907	Plasminogen	PLMN_HUMAN	SwissProt	39%	93 247	7.04	27/112	1×10^{-14}	183
6501, 6505, 7501, 7505	Gelsolin	GELS_HUMAN	SwissProt	17%	86 043	5.90	13/105	0.46	46
3004, 6004, 8003, 9002, 9007	Serum amyloid A-1	SAA1_HUMAN	SwissProt	46%	13 581	6.28	5/70	0.0079	64
0105, 0108, 2101, 3103, 4107	Retinol-binding protein	RET4_HUMAN	SwissProt	51%	23 337	5.76	9/63	0.11	53
2501, 3501, 3503, 4501-4503	Complement C1s subcomponent	C1S_HUMAN	SwissProt	25%	78 174	4.86	18/113	0.29	48
6402, 6403, 7401	Serum albumin	ALBU_HUMAN	SwissProt	39%	71 317	5.92	21/129	7.7×10^{-6}	94

three were up-regulated, as shown in the column graphs (Fig. S6†).

ELISA validation

We selected SAA1, ApoE, plasminogen, complement factor 7 and CFH proteins for further validation through ELISA.

Serum amyloid A1

One-way analysis of variance (ANOVA) test showed significant differences among the means of these four groups with a p value < 0.0001 . The mean value was 1.188 ± 0.2694 mg dL⁻¹, 1.238 ± 0.3705 mg dL⁻¹, 1.175 ± 0.3594 mg dL⁻¹ for ALL, APA, and MDS, respectively which are high compared to the healthy group *i.e.*, 0.6953 ± 0.1962 mg dL⁻¹ (Fig. 4). Tukey's multiple comparisons test showed no significant difference among the ALL and preleukemic diseases but showed a significant difference when these three groups were compared to the healthy group (Fig. 4). This protein followed the up-regulated pattern in ALL, APA and MDS compared to the healthy group, which is quite similar to the 2D-GE results.

Apolipoprotein E

The validation results of individual samples through ELISA did not follow the same pattern as expected from the 2D-GE results (down-regulated in all three diseases compared to healthy group), but showed up-regulation in the ALL group compared to the healthy group, while the results of APA and MDS were in accordance with the 2D-GE results. One-way ANOVA test

showed a significant difference among the means of the study groups with a p value of 0.0012. The mean values of the ALL, APA, MDS, and healthy samples were 904 ± 516.8 μg mL⁻¹, 551 ± 358.4 μg mL⁻¹, 443.5 ± 5 μg mL⁻¹, and 504.4 ± 214.2 μg mL⁻¹, respectively. Similarly, Tukey's multiple comparison test showed a significant difference among APA and ALL, MDS and ALL, and healthy and ALL pairs, but no significant difference between MDS and APA, healthy and APA, and healthy and MDS pairs.

Complement factor C7

The results were found to be up-regulated in both the leukemic and preleukemic conditions, opposite to the 2D-GE results (down-regulated in all three diseases compared to the healthy group). One-way ANOVA test showed no significant difference, with a p value of 0.1559, and the mean values were 105.4 ± 27.54 μg mL⁻¹, 100.3 ± 23.03 μg mL⁻¹, 102 ± 37.26 μg mL⁻¹, and 84.62 ± 17.92 μg mL⁻¹ for ALL, APA, MDS, and healthy samples, respectively. Tukey's multiple comparisons test also showed no significant difference.

Complement factor H

These results are not similar to the 2D-GE results (up-regulated). A one-way ANOVA test showed no significant difference among the study groups with a p value of 0.1399. The mean values were 4180 ± 374.5 μg mL⁻¹, 4265 ± 164.6 μg mL⁻¹, 4324 ± 256.3 μg mL⁻¹, and 4381 ± 109.2 μg mL⁻¹ for the ALL,

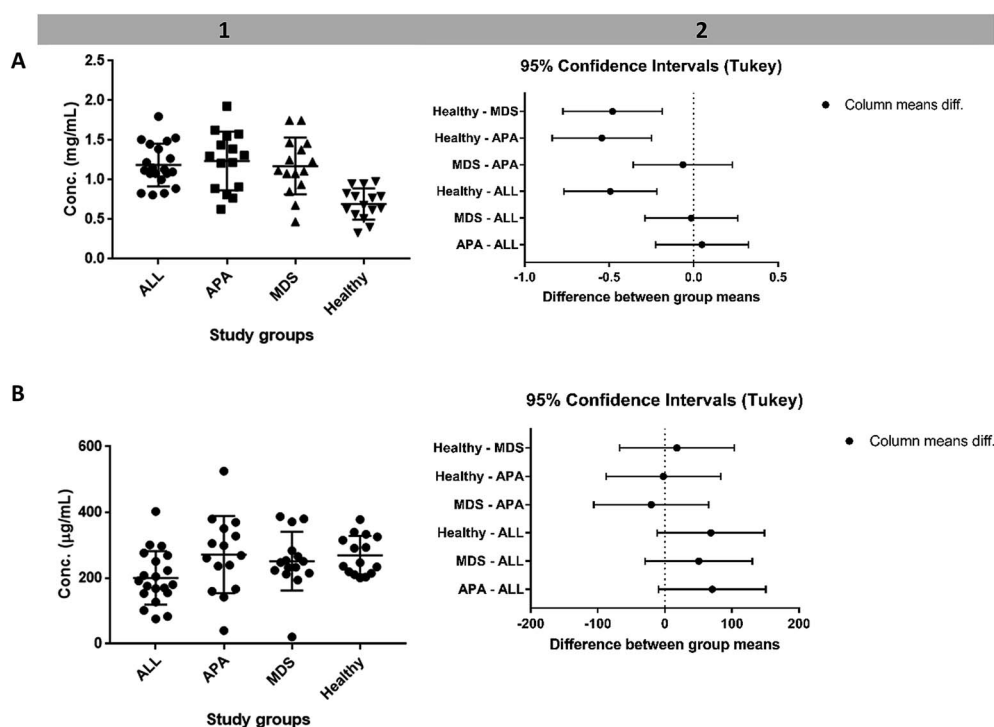


Fig. 4 Left side: Scatter plot with standard deviation achieved through ELISA results of individual samples of healthy, APA, MDS and ALL subjects. (A1) SAA1 protein and (B1) plasminogen. Right side: Confidence intervals (Cis) for graphing ordinary one-way ANOVA. (A2) SAA1 and (B2) plasminogen.



APA, MDS, and healthy samples, respectively. Tukey's multiple comparisons test also showed no significant difference.

Plasminogen

This protein showed a similar behaviour of down-regulation in both leukemic and preleukemic conditions, quite similar to the 2D-GE results (Fig. 4). One-way ANOVA test and Tukey's multiple comparisons test showed no significant difference (Fig. S6†). The mean values of plasminogen were $201 \pm 81.45 \mu\text{g mL}^{-1}$, $271.8 \pm 117.6 \mu\text{g mL}^{-1}$, $251.7 \pm 89.35 \mu\text{g mL}^{-1}$, and $269.8 \pm 58.74 \mu\text{g mL}^{-1}$ of the ALL, APA, MDS, and healthy samples, respectively. All these statistics indicate that the plasminogen protein followed a pattern of down-regulation in ALL and MDS compared to the healthy groups (similar to 2D-GE results), but up-regulation in APA.

Discussion

We have investigated differential protein patterns between leukemic, preleukemic conditions, and the healthy group in order to examine certain proteins or the group of proteins that might act as a useful indicator of the link between ALL and two preleukemic diseases, APA and MDS, when there is a history of progression of these preleukemic diseases towards ALL.

We first depleted the samples from the top-7 most abundant proteins in plasma including albumin, immunoglobulin G (IgG), immunoglobulin A (IgA), fibrinogen, transferrin, anti-trypsin and HPT, followed by 1D-GE. We noticed that the depletion was not 100% because we identified albumin, three chains of fibrinogen ($\alpha\beta\gamma$), and haptoglobin in the unbound fraction (Fig. 3). This issue has also been reported in other studies.³² From the observed 2D-GE images, it was found that several proteins consisted of more than one spot, and their change in pI or the mass shifts between the theoretical and the experimentally calculated values might be because of the post translational modifications (PTMs), particularly glycosylation, affecting the electrophoretic mobility of the proteins, as has already been reported (Fig. 3).³³

According to Gene Ontology, the functions of the total identified proteins could be categorized as 21.24% protein binding, 4.42% antioxidant activity, 2.65% phosphatidylcholine-sterol *O*-acyltransferase activator, 4.42% alcohol binding, 5.31% peptidase regular activity, 8.85% receptor binding, 2.65% cholesterol transport, 4.42% heparin binding, 7.96% enzyme regulator, 4.42% endopeptidase inhibitor, 3.54% steroid binding, 5.31% enzyme inhibitor, 3.54% lipid transport, 1.77% haemoglobin binding, 6.19% lipid binding, 2.65% cholesterol binding, 1.77% complement component C1q binding, 2.65% copper ion binding, 2.65% chaperone binding, 1.77% phosphatidylcholine binding, and 1.77% vitamin transport. To gain an understanding of the biological functions and the interactive links that are most significantly associated with the differentially expressed proteins in the dataset, the STRING software program was used with an interaction score of medium confidence 0.400, using stringent criteria, and only experimental protein-protein interactions and the pathways from the Kyoto Encyclopedia of Genes and Genomes (KEGG)

databases were taken into account. The blue lines show that known interactions are from the KEGG pathways, whereas purple lines designate experimental evidence (Fig. S7†). The pathways involved in these differentially regulated proteins are mentioned in Table S1.†

In a STRING pathway analysis, links were found to the phosphatidylinositol 3'-kinase (PI3K)-Akt, the p53, and Rap1 signalling pathways. The cumulative effects of the three pathways are cell cycle arrest, apoptosis, protein synthesis, metabolism, cell proliferation, cell survival, and gene activation. Links were also found to mitotic cell cycle division. Recently, various mechanisms associated with abnormal proliferation or block differentiation by disruption of cell cycle and production of inhibitory oncogenic fusion proteins, which make normal differentiation regulatory proteins inactive, have already been reported in cancers.³⁴ We infer from these findings that our differentially expressed proteins may be deregulated under the disturbance of these signalling pathways or during the cell cycle arrest in disease conditions and may predict the underlying picture. Pathway analysis also created links to the genetic mutation behind ALL (Fig. S8†). According to these findings, our differentially expressed proteins have some type of very important link to leukemic and preleukemic diseases.

HPT and fibrinogen (α , β , and γ chain) were not quantified through ELISA because the depletion column has immunoaffinity towards them. The proteins that showed satisfactory validation results are SAA1 and plasminogen. The SAA1 protein is found in plasma in response to malignancy and can be used as an indicator biomarker for late-stage diseases.³⁵⁻³⁷ Its links with a number of malignancies have already been reported *via* involvement with tumour pathogenesis and gene polymorphism of SAA1.^{37,38} Some say that SAA1 affects the tumour microenvironment and adds to metastasis.³⁹ In our study, SAA1 was found to be up-regulated in ALL, MDS, and APA compared to healthy samples. Results show significant concordance with 2D-GE. These promising results may help in progression studies of APA and MDS to ALL (Fig. 4). Plasminogen deficiency leads to the progression of pseudo membranes, with consequent end-organ damage of the affected tissue.⁴⁰ Components of the plasminogen-plasmin system are found in most malignancies and their expression conveys a prognostic worth.⁴¹ Plasminogen levels were found down-regulated in ALL and MDS in comparison with healthy group (in accordance with 2D-GE results), but results did not follow the same trend for ALL and APA.

ApoE, CFH, and complement factor C7 showed no significant results in accordance with the 2D-GE results, and the reason behind their difference could be the presence of several subunits of a single protein. In 2D-GE not all subunits of a protein were found to be deregulated, and possibly a specific unit was deregulated in the disease condition while ELISA technique is able to quantify a single protein which nullifies the effect of that subunit. The second reason could be that in the disease condition, some of the subunits of that specific subunit of protein might have changed because of PTMs and changed the position in the 2D-GE maps, resulting in a low intensity of those spots because of the changed pI and molecular mass. Therefore, in the light of these points, we recommend that



further protein profiling of this type should be done on a large number of samples for a better statistical correlation.

Conclusion

Plasma proteomic analysis is an intricate task because of factors that range from the large number of protein analytes to the marked variation in the physical properties of the proteins in the human proteome. This study shows that employing a multi-fractionation strategy like immunodepletion, ZOOM IEF, 2D-GE and MALDI-MS is a powerful approach for detecting low abundance proteins in plasma. This strategy has been successfully applied for the protein profiling of ALL, AA, MDS and the healthy control group. Differentially expressed proteins in our study have shown links to some signalling pathways, particularly p53, which are important in carcinogenesis, and the results of this study show that SAA1 and plasminogen proteins can be used as characteristic molecules, which may be used as additional predictive molecules when there is a case report of progression of preleukemic diseases towards the ALL. We further recommend validation on a large number of individual samples, particularly on those patients who have a history of preleukemic disease before ALL.

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Conflict of interest

Authors of the study declare no conflict of interest.

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