use of such reproducible methods generate the results in a reproducible way, considering the degree of differences that we expect between the samples to be compared.

4. Conclusions

The use of ProteoMiner in combination with conventional proteomic modalities such as depletion and anion-exchange columns significantly enhanced trace proteins on SDS-PAGE and increased the number of protein spots on 2D-DIGE, suggesting that the use of a solid-phase hexapeptide ligand library has great potential for intact plasma proteomics. Mass spectrometric protein identification revealed that high- and middle-abundance proteins were enriched by ProteoMiner, and the characteristics of proteins with unique affinity to a solid-phase hexapeptide ligand library remain to be clarified by more extensive mass spectrometric protein identification. Although use of ProteoMiner for biomarker studies is quite feasible and attractive, more extensive characterization of binding proteins and optimized protocols are required for large-scale biomarker studies.

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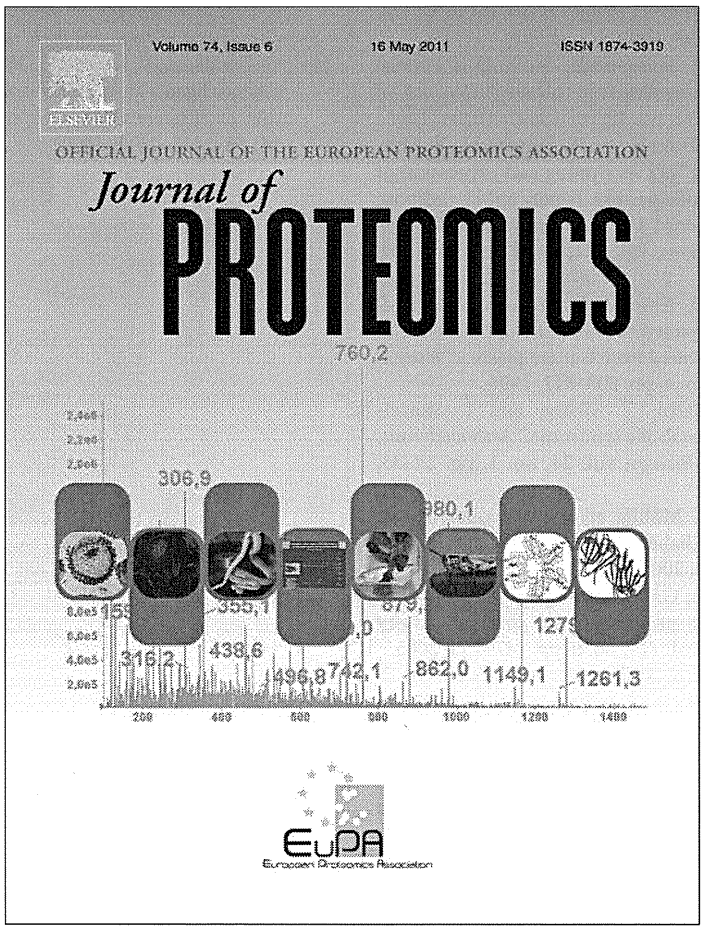

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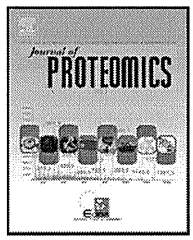

Global expression study in colorectal cancer on proteins with alkaline isoelectric point by two-dimensional difference gel electrophoresis

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ABSTRACT

Colorectal cancer is one of the leading causes of cancer death worldwide. To identify candidates for biomarkers and therapeutic targets, we investigated the proteome of colorectal cancer tissues. Using 2D-DIGE in combination with our original large format electrophoresis apparatus, we compared surgically resected normal and tumor tissues from 53 patients with colorectal cancer. We focused on proteins with an alkaline pI using IPG gels for the alkaline range. We observed 1687 protein spots, and found 100 spots with statistical ($p<0.01$) and significant (>2-fold) differences between the normal and the tumor tissue groups. Among these 100 protein spots, five showed a different intensity between tumor tissues from the stage-II and the stage-III patients. MS experiments revealed that these 100 protein spots corresponded to 58 unique proteins. These included six proteins which had not been previously reported to be associated with colorectal cancer. Among these proteins, five were not reported in any type of malignancy. IEF/western blotting confirmed the differences in protein expression between the normal and the tumor tissues. These results may provide an insight for biomarker development and drug target discovery in colorectal cancer.

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1. Introduction

Colorectal cancer is the third most common type of cancer and the fourth most frequent cause of cancer death worldwide [1]. Annually, more than one million people are diagnosed with colorectal cancer and approximately half of them die from malignancy [1]. Although intensive treatments including surgery, chemotherapy, and molecular targeting therapy have been developed, outcome remains dismal, particularly for those with distant organ metastasis [2]. Moreover, tumors with similar histological characteristics often show different outcomes and responsiveness to therapy. Therefore, it has long been desired to establish individualized therapy for colorectal cancer [3,4]. The five-year survival for patients with localized disease who had undergone curative surgery can reach 90%, but it is 65% for those with lymph node metastases. This emphasizes the importance of early diagnosis. However, there are no specific symptoms at the early stage of colorectal cancer, and the existing modalities for early diagnosis (e.g., fecal occult blood test and plasma biomarkers) have limited sensitivity and specificity. Characterization of tumor cells with an aim of application of clinical utilities needs to be further challenged for drug target discovery and biomarker development.

With this background, a proteomic approach was applied to colorectal cancer using various modern or refined technologies [5–7]. A proteome is a functional translation of a genome, directly regulating cancer phenotypes. Thus, proteomics may give us insights into the carcinogenesis and progression of colorectal cancer. Various technologies, including gel-based separation methods [8,9], MS [10–12], and array-based methods [13–16] have been applied for global protein expression studies, resulting in the identification of aberrantly regulated proteins. The studies on such protein characteristics may increase our understanding of the molecular basis of colorectal cancer and contribute to better management, and therefore, an improved outcome.

The goal of the present study was to provide the "proteomics community" the profile of proteome expression for colorectal cancer. We reported the proteomic differences between surgically resected normal and tumor tissues from 53 patients with colorectal cancer. For quantitative expression profiling, we employed 2D-DIGE and MS. By focusing on evaluating proteins with alkaline pI, we found six proteins whose aberrant expression had not been reported in colorectal cancer. Although antibody-based validation is critical for protein identification and further clinical examination, discordance between the results of 2D-DIGE and SDS-PAGE/western blotting was often observed. We clarified the backgrounds of such discordance using IEF/western blotting by demonstrating the presence of multiple protein isoforms with different isoelectric points.

2. Materials and methods

2.1. Clinical samples

This study involved 53 patients with colorectal cancer who underwent curative surgery at the National Cancer Center Hospital. The clinicopathological data of the cases is summarized in Table 1, and the data of individual patients are listed in Supplemental Table 1.

Tumor tissues and matched normal mucosal tissues were obtained from 53 cases; 106 samples were examined in this study. The specimens were snap-frozen in liquid nitrogen and stored at −80 °C until use. Clinical staging was determined based on diagnostic imaging criteria: the TMN system. None of the patients received antineoplastic therapy before surgery. This study was approved by the ethics committee of the National Cancer Center.

2.2. Protein extraction

Proteins were extracted from surgically resected tissues as described in a previous study [17]. In brief, the frozen tissues were powdered in liquid nitrogen using Multi-beads Shocker (Yasui-kikai, Osaka, Japan). Tissues were then treated with urea lysis buffer (2 M thiourea, 7 M urea, 3% CHAPS, and 1% Triton X-100). After centrifugation, the supernatant was recovered as a soluble protein fraction and stored at −80 °C until use.

2.3. 2D-DIGE

A protein expression profile was created as described in a previous study [16]. In brief, an internal control sample was created by mixing an equal amount of a small portion of individual samples. Fifteen micrograms of the individual and the internal control samples was labeled with Cy3 and Cy5 fluorescent dyes (CyDye DIGE Fluor saturation dye, GE Healthcare, Uppsala, Sweden), respectively, according to manufacturer's instruction. The differently labeled protein samples were mixed together, divided into three portions, and separated using 2D gel electrophoresis. First-dimension separation was achieved by the IPG dry strip gel, with a pI range of 6–9, and Multiphor II (GE Healthcare). Protein samples were applied to the IPG gels by a cup-loading method at the acidic end, and 50,250 Vh was applied to the IPG gels for IEF. The second-dimension separation was done by SDS-PAGE overnight using the original large format gel apparatus [16], with a

Table 1 – Summary of clinicopathological data of the patients.

Age	
Median	61.4
Gender	
Male	37
Female	16
Site	
Colon	29
Rectum	24
Histological grade	
Well differentiated	40
Moderately	10
Poorly	3
TNM stage	
I	7
II	27
III	17
IV	2

separation distance of 33 cm and a circulating water cooling system.

Following gel electrophoresis, gels sandwiched by low-fluorescence glass plates were scanned using a laser scanner (Typhoon Trio, GE Healthcare), and Cy3 and Cy5 images were obtained by single scans. Cy5 spot intensity was normalized with Cy3 (one for all protein spots) using image analysis software (Progenesis SameSpot, Nonlinear Dynamics, Newcastle, UK). The protein expression profile was exported in the format of an XML file, and imported to data-mining software (Expressionist, GeneData, Basel, Switzerland) for statistical studies. For preparative purposes, 100 μg of protein sample was labeled by Cy3 fluorescent dye, and separated as described above. Protein spots of interest were matched between the images of analytical and preparative gels, and recovered into 96-well plates from the preparative gels using our original spot-recovery machine (Molecular Hunter, As One Corporation, Osaka, Japan) [16]. The recovered protein spots were stored at 4 °C until use.

2.4. *Statistical analysis*

Statistical analyses involved scatter plots, hierarchical clustering, principal component analyses, correlation studies and volcano plots. The Wilcoxon test was carried out by Expressionist software. The Wilcoxon test was used to identify the

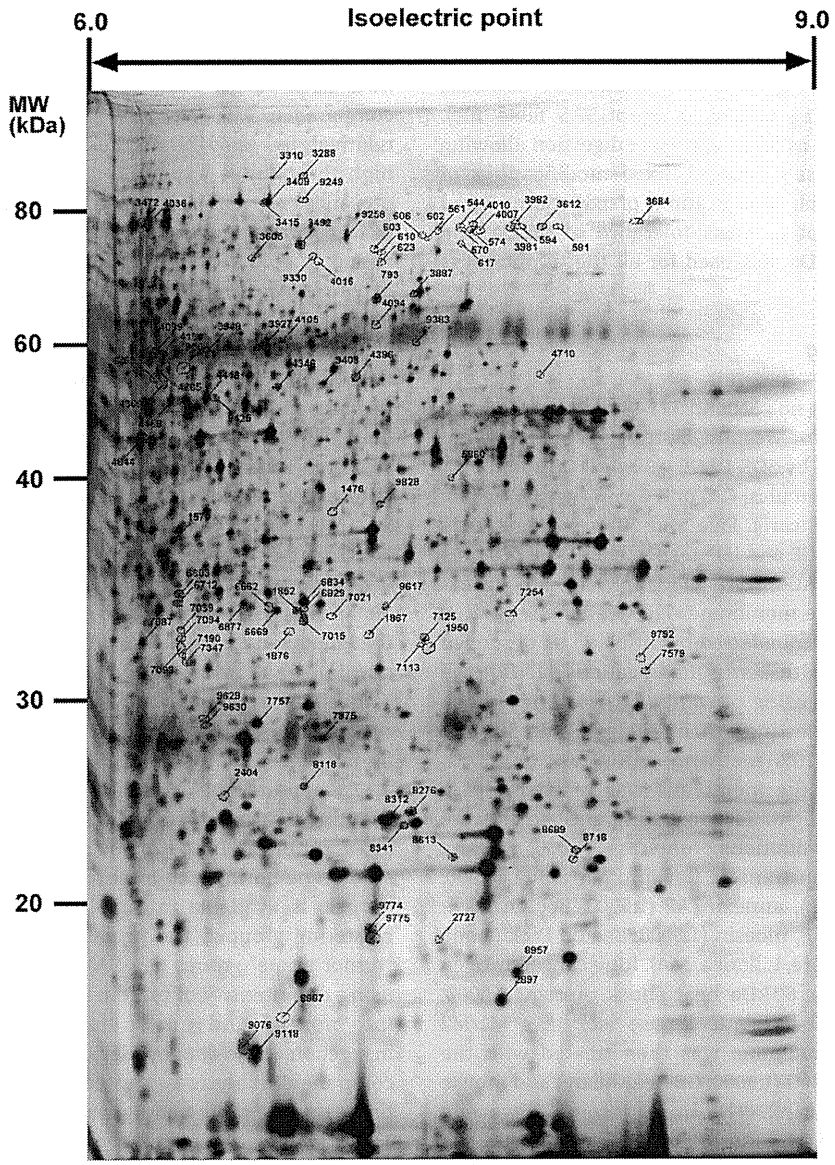


Fig. 1 – 2D image of the Cy3-labled internal control sample was shown. The fluorescently labeled protein sample was separated according to the pI (separation distance of 24 cm) and molecular weight (separation distance of 33 cm). The circled protein spots were later identified differential intensities between normal and tumor tissues. The spot numbers corresponded to those in other figures and tables.

spot intensity which was statistically different between the sample groups.

2.5. *Protein identification using MS*

Proteins were extracted from the protein spots by in-gel digestion as previously reported [16]. In brief, the recovered protein spots were washed extensively with acetonitrile and ammonium bicarbonate minimum solution, and treated with trypsin (Promega, Madison, WI) at 37 °C overnight. Tryptic digests were recovered from the gel pieces, concentrated by a vacuum and re-solubilized with 0.1% trifluoroacetic acid. The final tryptic digests were subjected to LC composed of Paradigm MS4 dual solvent delivery system (Michrom BioResources, Auburn, CA) and an LTQ linear ion trap MS (Thermo Electron, San Jose, CA) equipped with a nano-electrospray ion source (AMR, Tokyo, Japan). Mascot software (version 2.3.0, Matrix Science, London, UK) was used to search for the mass of the peptide ion peaks against the SWISS-PROT database (*Homo sapiens*, 471,472 sequences in Sprot_57.5 fasta file). Search parameters were as follows: trypsin digestion allowing up to three tryptic-mass cleavages, fixed modifications of carbamidomethyl, variable modifications of oxidation, +2 and +3 peptide charge, peptide mass tolerance of 0.8 Da and MS/MS tolerance of 0.8 Da was used for all the tryptic-mass searches.

2.6. *Western blotting*

Protein samples (sample no.; 3N and 3T) extracted using urea lysis buffer were used for western blotting. In brief, protein samples were separated by SDS-PAGE gels with Criterion TGX Precast Gels (Bio-Rad, Hercules, CA) or IPG gels (length, 24 cm; pI range 3–10; GE Healthcare). Five and 50 μg proteins were separated using SDS-PAGE and IEF, respectively. The proteins separated using SDS-PAGE were electrophoretically transferred to a nitrocellulose membrane. The proteins separated using the IPG gels were transferred by diffusion as described in a previous report, with some modifications [17,18]; the transfer was performed using conventional western blotting with a buffer system consisting of 20 mM Tris (pH 7.5), 500 mM sodium chloride, and 20% methanol. After blocking with skimmed milk for 1 h, the membrane was reacted with a primary antibody overnight. The following antibodies were used at the following dilutions; fumarase (1:200; Abcam, Cambridge, UK), electron transfer flavoprotein alpha (1:500; ProteinTech, Chicago, IL), annexin A2 (1:5000; Becton Dickinson, Franklin Lakes, NJ), moesin (1:5000; Becton Dickinson), lamin A/C (1:150; Millipore, Billerica, MA), lung cancer antigen NY-LU-1 (1:100; Abcam), 60 kDa heat shock protein (1:5000; Becton Dickinson), and pyruvate kinase isozymes M1/M2 (1:100; Abcam). The membrane was then treated with the second antibody: rabbit IgG (1:1000; GE Healthcare) and mouse IgG (1:1000; GE Healthcare). The immunocomplexes were detected by enhanced chemiluminescence (ECL Plus; GE Healthcare) and LAS-3000 (FujiFilm, Tokyo, Japan). The intensity of protein bands was measured by ImageQuant software (GE Healthcare). The intensity of individual protein bands in the SDS-PAGE/western blotting was normalized with the intensity of the actin band in identical membranes. Normalization was done using the same amount of loaded proteins in the IPG/western blotting.

3. Results and discussion

Proteomic studies on colorectal cancer using surgically resected tissues have been achieved for biomarker development and drug target discovery. The proteomics of colorectal cancer in this report were characterized by two factors. First, the present study included a large sample size (106 samples) of surgically resected colorectal cancer tissues. We ran triplicate gels amounting to a total of 318 large format gels being examined. Use of 2D-DIGE helped to avoid a labor intensive experiment. In 2D-DIGE, simple laser scanning generates the gel images in less than 1 h for Cy3- and Cy5-labeled protein samples, omitting the rate-limiting step of gel-based proteomics such as gel staining with silver or CBB. In addition, compared to MS, the cost of electrophoresis equipment is relatively low, also the parallel use of multiple devices enabled high-throughput experiments. The second factor in the present study was that we focused on proteins with alkaline pI. By concentrating specifically on the proteomic analyses, we aimed to obtain a unique data that was available from the experiments using IPG gels with a wider range of pI.

A typical 2D-DIGE image of the Cy3-labeled internal control sample is shown in Fig. 1. We observed 1687 protein spots in the alkaline area. System reproducibility was examined by running an identical sample thrice. The scattergram in Fig. 2 demonstrates that the intensity of ≥96% protein spots is scattered within 2-fold differences, and >90.5% within 1.5-fold differences. Similar system reproducibility was observed in our previous proteomic studies, in which a large-format electrophoresis apparatus and internal control sample were used for protein expression profiling [19–22]. A long separation distance of a large-format gel could result in clear focusing of the spots and the internal control sample, which could normalize all protein spots in the present study. This compensated for gel-to-gel variation and resulted in high reproducibility of 2D images. A wide dynamic range of fluorescent signal also contributed to the high reproducibility.

To capture the overall feature of proteome data, we examined unsupervised classification on the basis of the intensity of all 1687 protein spots observed in the present study. The normalized intensity of 1687 protein spots across all gels is available in Supplemental Table 2. Hierarchical clustering grouped the protein samples into "normal" and "tumor tissue" groups (Fig. 3A). Principal component analysis using the intensity of protein spots also divided the samples into normal and tumor tissue groups (Fig. 3B). Visual inspection of the data by hierarchical clustering and principal component analysis suggested that the proteome of normal tissue may be more homogeneous than that of tumor tissues. This may reflect the similar genomic contents of these tissues. These speculations were supported by the data from the correlation matrix, in which the correlation coefficient of spot intensity was calculated for all paired samples and demonstrated by colors (Fig. 3C). Compared with the tumor samples, the proteome contents of normal tissues were more similar to

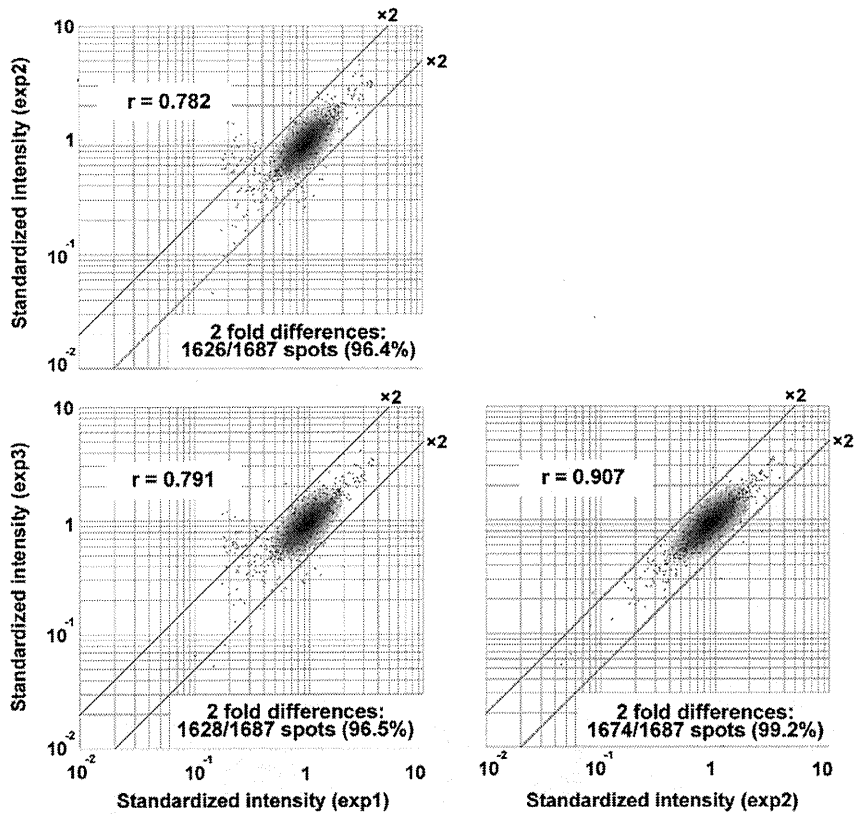


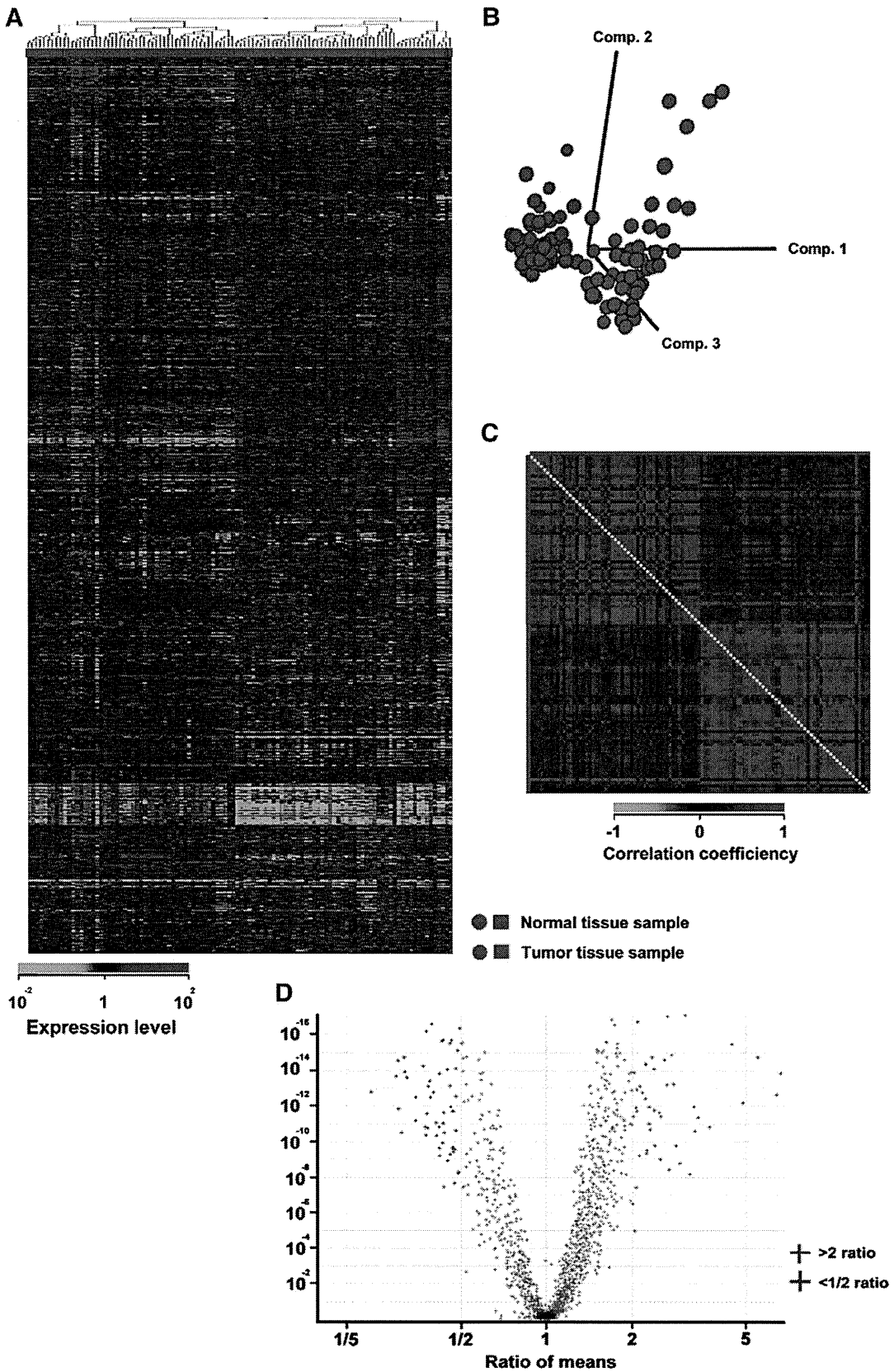
Fig. 2 – System reproducibility was measured by scatter plot. The identical protein sample was independently examined three times, and the spot intensity was compared among the experiments. The correlation coefficient values for the independent experiments were at least 0.78, and at least 96.4% of protein spots intensity was scattered within 2-fold differences.

each other. These observations suggest that the overall proteome features possibly undergoes a drastic change during carcinogenesis.

To identify the protein spots whose intensity was responsible for the results of unsupervised classification (Fig. 3), we compared the normal and the tumor tissue groups. Among 1687 protein spots observed, we detected 100 with statistically ($p<0.01$) and significantly (>2-fold average intensity) different intensities between the normal and the tumor tissue groups (Fig. 4A). We observed 45 and 55 protein spots with higher (Group A in Fig. 4A) and lower intensities (Group B in Fig. 4A) in tumor tissues compared with their normal counterparts, respectively. Except for spots 3981 and 610, the intensity of the 100 protein spots was scattered within 2-fold differences when the identical samples were examined three times (Fig. 2). These 100 protein spots were subjected to protein identification using MS. The row data are available as Supplemental Data. Consequently, 58 unique proteins were identified (right side in Fig. 4A; Table 2 and Supplemental Table 3). These 100 protein spots included five spots with statistically ($p<0.01$) and significantly (>2-fold average intensity) different intensities among stage-II and stage-III patients. The identified proteins were classified according to their association with different types of malignancies. Five proteins had not been previously reported in malignancies, including colorectal cancer (Group D), and one protein was previously reported in another malignancy excluding colorectal cancer (Group C) (Table 2). The observed *pI* was close to the theoretical ones (Table 2), and the use of IPG gels with an alkaline range allowed identification of aberrant regulation of the proteins involved in colorectal cancer.

The results of functional classification of the identified 58 proteins are summarized in Table 2. Limited portions of the proteome were observed by 2D-DIGE and their functional classifications were affected by the characteristics of 2D-DIGE. Hence, we did not make any conclusions on the basis of the

Fig. 3 – Overall features of colorectal cancer proteome visualized by 2D-DIGE were examined by hierarchical clustering (A) and principal component analyses (B). The samples were grouped based on differential intensities of 1687 protein spots. These two analyses demonstrated that the samples were grouped according to the histological classification. C. The correlation matrix demonstrated the similarity of samples along histological classification. D. The volcano plot demonstrated the protein spots with p value and ratio of means between normal and tumor tissues. We selected protein spots with >2-fold intensity difference between the normal and the tumor tissue for further examination.



functional classifications regarding the likelihood of certain proteins being involved in colorectal cancer. Proteins with low abundance such as transcription factors, receptors, and the proteins in signal transduction pathways are known to contribute to carcinogenesis and cancer development. However, in our study we did not detect these proteins; this may indicate the limitation of 2D-DIGE. 2D-DIGE permits quantitative observation of multiple protein species and this advantage is unique to 2D-PAGE-based methods. We observed that 19 proteins appeared in multiple protein spots. These multiple proteins may correspond to post-translational modifications that are associated with the molecular mechanisms of malignant phenotypes. Thus, 2D-DIGE remains indispensable for cancer proteomics. The combined use of 2D-DIGE and other methods that counterbalance the limitations of 2D-DIGE should be considered for analyses of cancer proteomics. For instance, we may consider using antibody-based proteomics [23] and multiple reaction monitoring systems [24] to measure the expression level of faint proteins.

To validate the aberrant expression level of identified proteins in tumor tissues, we examined their expression by western blotting. Certain proteins may present as multiple forms with unexpected pI, and the intensity of single protein spots may not represent its total expression level. For such proteins, the data of SDS-PAGE/western blotting did not match those of 2D-DIGE (data not shown). This can be avoided by using western blotting and 2D-PAGE gel; however, carrying out western blotting using a large-format 2D gel is challenging because of the fragility of the gel. To compensate for these problems, we employed IPG/western blotting. We separated the proteins according to their pI using IPG gels, then transferred those to a membrane and allowed to react with specific antibodies (Fig. 5). Comparison of the intensity in 2D-DIGE and IPG/western blotting demonstrated that among 12 protein spots examined, 11 showed a consistent increase or decrease in intensity between the normal and the tumor tissues. These observations suggest that IPG/western blotting can be used for validation of 2D-DIGE results using antibodies. Only 1 spot, 9383, showed inconsistency between IPG/western blotting and 2D-DIGE results. The experimental factors of western blotting (e.g., transfer efficiency and antibody reactivity) may be the reason for such inconsistencies. To establish the clinical utilities of proteins identified by 2D-DIGE, more number of clinical cases should be used for the purpose of validation. In this report, we examined one protein sample for 12 protein spots to demonstrate the novel application of IPG, and the IPG/western blotting may be useful for such studies. IPG/western blotting can be used for the studies on multiple samples, because the parallel electrophoresis for the IPG can be achieved by a conventional device for isoelectric focusing electrophoresis, such as Multiphor II and Ettan IPGphor III (GE).

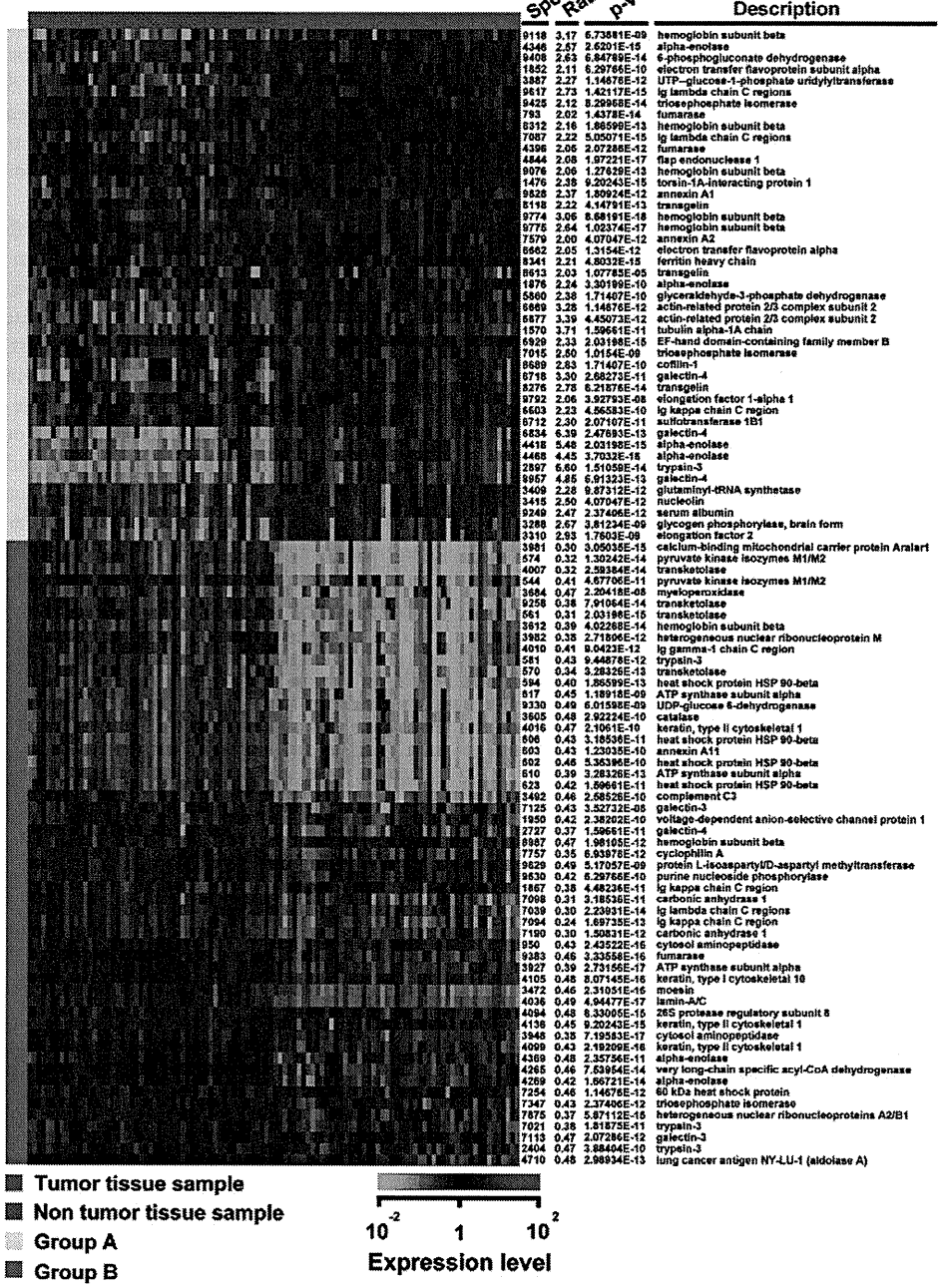
For the proteins with pI range of 6–9, in addition to the protein bands corresponding to the identified protein spots, we observed bands that were different between normal and tumor tissues (e.g., protein band in Fig. 5, panel e). 2D-DIGE uncovered the proteins with a molecular weight approximately between 10 kDa and 200 kDa (Fig. 1), and the proteins with excess molecular weight may not be uncovered by 2D-DIGE. For the proteins within less than 6 pI range, we observed protein bands with different intensities between the normal and the tumor tissues in four proteins (Fig. 5, panels c, d, e, and g). We had not expected to obtain these results from 2D-DIGE experiments. Thus, IPG/western blotting provided additional data on the identified proteins which were not obtained by conventional 2D-DIGE experiments.

We found that among the 58 identified proteins, aberrant expression of six proteins had not been reported in colorectal cancer tissues until now. These proteins were: torsin-1A-interacting protein 1, moesin, calcium-binding mitochondrial carrier protein Aralar1, sulfotransferase 1B1, EF-hand domain-containing family member B, and protein L-isoasparatyl/D-asparatyl methyltransferase. Among these six proteins, only moesin has been reported in malignancies other than colorectal cancer. Moesin is a cell adhesion protein, and upregulation of its expression has been associated with metastatic risk in node-negative breast cancer [25], pancreatic cancer [26], and oral squamous cell carcinoma [27]. Further investigation on moesin may provide novel insights into common mechanisms underlying carcinogenesis and cancer development.

Colorectal cancer has been extensively studied by the proteomic approach [28]. However, the results reported by various studies have not always been in accordance. For instance, Xuezhi et al. reported the aberrant expression of 11 proteins in tumor tissues using 2D-DIGE with a ReadyStrip, pH 7–10 (BioRad) in seven patients with colorectal cancer [29]. From among these 11 proteins, we identified four proteins (enolase 1, fructose-bisphosphate aldolase A, GAPDH, and transgelin) as the colorectal cancer-associated proteins in the present study. Considering that these proteins have been reported in other proteomic studies, the association of these proteins with colorectal cancer could be reliable. Even if the results seem to be discordant, it does not suggest that the experiments were carried out inappropriately. The different number of samples and statistical criteria for different proteins can affect the results of comparison; the clinical status of donors is another factor. In addition, the method followed in the experiments can also affect the results of comparative studies. Further validation studies using standard methods and larger sample size should be undertaken to obtain conclusive results. IPG/western blotting could be a powerful tool for validation because, as opposed to immunohistochemistry and conventional SDS-PAGE/western blotting,

Fig. 4 – Results of spot comparison and protein identification were demonstrated as a format of heat-map. (A) The protein spots whose intensity showed >2-fold differences with statistical significance ($p < 0.01$) were selected, and the level of spot intensity was shown as a heat-map, and the protein names were also shown in the right side of the color panel. Groups A and B indicated the protein spots with higher and lower intensities in the tumor samples, respectively. Total 100 protein spots were then examined using mass spectrometry, resulted in identification of 58 unique proteins. (B) Among the 100 protein spots, five protein spots had the different intensities between the patients with different clinical stages; stage-II and stage-III. Note that when multiple proteins were identified from single protein spots, the proteins with highest Mascot score are appeared in the figure. The proteins with different Mascot score are summarized in Supplemental Table 3.

A



B

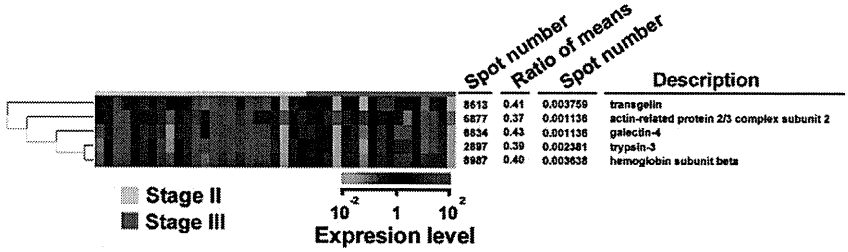


Table 2 – List of proteins from human CRC tissue resolved on pH 6–9 2D-DIGE gels and identified by LTQ linear ion trap mass spectrometer.

Spot no.[a]	Accession no.[b]	Protein description[b]	Protein score[c]	No. of matched peptides	Sequence coverage (%)[d]	MW (Da)[e]	Reference pI[e]	Actual pI[f]	Molecular function[g]	Reports by 2D-PAGE[h]	Reports in CRC[i]
544	P14618	Pyruvate kinase isozymes M1/M2	933	21	32.2	58,470	7.96	7.54	Enzyme	[9,30,32]	A [9,30,32–35]
561	P29401	Transketolase	616	11	24.4	68,519	7.58	7.46	Enzyme	[36,38]	A [34,36–38]
570	P29401	Transketolase	907	18	30.8	68,519	7.58	7.54	Enzyme	[36,38]	A [34,36–38]
574	P14618	Pyruvate kinase isozymes M1/M2	99	2	3.4	58,470	7.96	7.60	Enzyme	[9,30,32]	A [9,30,32–35]
581	P35030	Trypsin-3	119	2	6.6	33,306	7.46	7.95	Metal binding	Not reported	B [39,40]
594	P08238	Heat shock protein HSP 90-beta	1322	23	34.5	83,554	4.97	7.80	ATP binding	[36]	A [34,36]
602	P07900	Heat shock protein HSP 90-alpha	223	3	5.2	83,554	4.97	7.41	ATP binding	[36]	A [34,36,41]
603	P50995	Annexin A11	590	12	19.2	54,697	7.53	7.20	Metal binding	[38,42]	A [38,42,43]
606	P08238	Heat shock protein HSP 90-beta	883	17	24.6	83,554	4.97	7.39	ATP binding	[36]	A [34,36]
610	P25705	ATP synthase subunit alpha	1115	25	40.9	59,828	9.16	7.22	ATP binding	[36,38,44]	A [36,38,44]
617	P25705	ATP synthase subunit alpha	1022	18	36.2	59,828	9.16	7.56	ATP binding	[36,38,44]	A [36,38,44]
623	P08238	Heat shock protein HSP 90-beta	1322	23	34.5	83,554	4.97	7.22	ATP binding	[36]	A [34,36]
793	P07954	Fumarase	316	5	14.3	54,773	8.85	7.20	Enzyme	[36,38]	A [34,36,38, 45–47]
950	P28838	Cytosol aminopeptidase	504	12	20.4	56,530	8.03	6.41	Metal binding	[36]	A [34,36]
1476	Q5JTV8	Torsin-1A-interacting protein 1	106	3	3.9	66,379	8.22	7.01	Other	Not reported	D
1570	Q71U36	Tubulin alpha-1A chain	410	14	24.2	50,788	4.94	6.36	Nucleic acid binding	Not reported	B [34,48–50]
1852	P13804	Electron transfer flavoprotein subunit alpha	256	4	15.6	35,400	8.62	6.86	Electron carrier activity	[38]	A [34,38,51]
1867	P01834	Ig kappa chain C region	122	2	32.1	11,773	5.58	7.16	Antigen binding	[52]	A [30,34,52–54]
1876	P06733	Alpha-enolase	811	21	38.5	47,481	7.01	6.82	Enzyme	[8,29,30,36]	A [8,29,30,36]
1950	P21796	Voltage-dependent anion-selective channel protein 1	637	8	40.6	30,868	8.62	7.41	Other	[11,29,38]	A [11,29,38]
2404	P35030	Trypsin-3	113	2	6.9	33,306	7.46	6.56	Metal binding	Not reported	B [39,40]
2727	P56470	Galectin-4	159	2	11.8	36,032	9.21	7.45	Sugar binding	[38]	A [34,38]
2897	P35030	Trypsin-3	113	2	6.9	33,306	7.46	7.73	Metal binding	Not reported	B [39,40]
3288	P11216	Glycogen phosphorylase, brain form	1297	26	33.8	97,319	6.40	6.90	Enzyme	[38]	A [34,38,55]
3310	P13639	Elongation factor 2	3671	27	25.5	96,246	6.41	6.77	Nucleic acid binding	[8,30,38]	A [8,30,38]
3409	P47897	Glutaminyl-tRNA synthetase	179	4	5.9	88,655	6.71	6.75	ATP binding	[38]	A [38]
3415	P19338	nucleolin	446	9	14.2	76,625	4.60	6.73	Nucleic acid binding	Not reported	B [34]
3472	P26038	Moesin	685	13	24.1	67,892	6.08	6.23	Antigen binding	Not reported	C [56–59]
3492	P01024	Complement C3	211	4	2.6	188,569	6.02	6.88	Antigen binding	[29]	A [29,34,53,60,61]
3605	P04040	Catalase	485	9	18.0	59,947	6.90	6.68	Enzyme	[36,38]	A [30,36,38,46,62]
3612	P68871	Hemoglobin subunit beta	215	4	28.6	16,102	6.75	7.88	Metal binding	[30,36,52]	A [30,36,52]
3684	P05164	Myeloperoxidase	213	4	5.8	84,784	9.19	8.27	Enzyme	Not reported	B [63]
3887	Q16851	UTP–glucose-1-phosphate uridylyltransferase	343	6	13.8	57,076	8.16	7.35	Enzyme	[38]	A [38]
3927	P25705	ATP synthase subunit alpha	428	6	12.8	59,828	9.16	6.73	ATP binding	[36,38,44]	A [36,38,44]
3948	P28838	Cytosol aminopeptidase	448	8	21.0	56,530	8.03	6.51	Metal binding	[36]	A [34,36]

3981	O75746	Calcium-binding mitochondrial carrier protein Aralar1	276	5	8.0	75,144	8.58	7.76	Metal binding	Not reported	D
3982	P52272	Heterogeneous nuclear ribonucleoprotein M	82	2	4.1	77,749	8.84	7.78	Nucleic acid binding	Not reported	B [34]
4007	P29401	Transketolase	317	5	12.4	68,519	7.58	7.63	Enzyme	[36,38]	A [34,36–38]
4010	P01857	Ig gamma-1 chain C region	182	5	17.6	36,596	8.46	7.59	Antigen binding	Not reported	B [34,49,53]
4016	P04264	Keratin, type II cytoskeletal 1	220	4	6.2	66,170	8.15	6.96	Sugar binding	[52]	A [34,52]
4036	P02545	Lamin A/C	375	8	17.5	74,380	6.57	6.24	other	[38]	A [34,38,64]
4094	P62195	26S protease regulatory subunit 8	974	19	47.8	45,768	7.11	7.20	ATP binding	[36]	A [36]
4099	P04264	Keratin, type II cytoskeletal 1	92	2	3.4	66,170	8.15	6.28	Sugar binding	[52]	A [34,52]
4105	P13645	Keratin, type I cytoskeletal 10	123	3	3.4	59,046	5.09	6.81	Sugar binding	[52]	A [34,52]
4136	P04264	Keratin, type II cytoskeletal 1	120	2	4.0	66,170	8.15	6.32	Sugar binding	[52]	A [34,52]
4265	P49748	Very long-chain specific acyl-CoA dehydrogenase	810	15	25.6	70,745	8.92	6.30	Enzyme	[38]	A [38,65]
4269	P06733	Alpha-enolase	530	10	24.2	47,481	7.01	6.28	Enzyme	[8,29,30,36]	A [8,29,30,36]
4346	P06733	Alpha-enolase	525	8	21.2	47,481	7.01	6.79	Enzyme	[8,29,30,36]	A [8,29,30,36]
4369	P06733	Alpha-enolase	850	16	36.9	47,481	7.01	6.30	Enzyme	[8,29,30,36]	A [8,29,30,36]
4396	P07954	Fumarase	290	5	17.8	54,773	8.85	7.11	Enzyme	[36,38]	A [34,36,38, 45–47]
4418	P06733	Alpha-enolase	222	3	10.6	47,481	7.01	6.49	Enzyme	[8,29,30,36]	A [8,29,30,36]
4468	P06733	Alpha-enolase	621	15	26.0	47,481	7.01	6.36	Enzyme	[8,29,30,36]	A [8,29,30,36]
4710	P04075	Lung cancer antigen NY-LU-1 (aldolase A)	229	4	15.4	39,851	8.30	7.88	Enzyme	[29,30,38]	A [29,30,38]
4844	P39748	Flap endonuclease 1	108	2	5.8	42,908	8.80	6.23	Nucleic acid binding	Not reported	B [66,67]
5860	P04406	Glyceraldehyde-3-phosphate dehydrogenase	400	6	31.3	36,201	8.57	7.50	Enzyme	[29,30,52,68]	A [29,30,41,52,68]
6603	P01834	Ig kappa chain C region	122	2	32.1	11,773	5.58	6.38	Antigen binding	[52]	A [30,34,52–54]
6662	P13804	Electron transfer flavoprotein subunit alpha	108	2	7.5	35,400	8.62	6.75	Electron carrier activity	[38]	A [34,38,51]
6669	O15144	Actin-related protein 2/3 complex subunit 2	114	3	10.3	34,426	6.84	6.79	Actin binding	[36]	A [36,69,70]
6712	O43704	Sulfotransferase 1B1	141	3	13.2	35,048	6.57	6.38	Enzyme	Not reported	D
6834	P56470	Galectin-4	171	2	11.8	36,032	9.21	6.90	Sugar binding	[38]	A [34,38]
6877	O15144	Actin-related protein 2/3 complex subunit 2	279	7	20.0	34,426	6.84	6.66	Actin binding	[36]	A [36,69,70]
6929	Q8N7U6	EF-hand domain-containing family member B	66	2	1.8	94,558	7.50	6.90	Metal binding	Not reported	D
7015	P60174	Triosephosphate isomerase	443	9	32.9	26,938	6.45	6.90	Enzyme	[29,30,35,71,72]	A [29,30,34,68, 71–73]
7021	P35030	Trypsin-3	128	2	6.6	33,306	7.46	7.01	Metal binding	Not reported	B [39,40]
7039	P0CG04	Ig lambda chain C regions	142	2	23.8	11,401	6.92	6.40	Antigen binding	Not reported	B [34,53,54]
7087	P0CG04	Ig lambda chain C regions	226	3	41.9	11,401	6.92	6.23	Antigen binding	Not reported	B [34,53,54]
7094	P01834	Ig kappa chain C region	169	3	32.1	11,773	5.58	6.40	Antigen binding	[52]	A [30,34,52–54]
7098	P00915	Carbonic anhydrase 1	272	5	25.7	28,909	6.59	6.40	Enzyme	[32,38,74]	A [32,38,74–77]
7113	P17931	Galectin-3	166	4	16.0	26,193	8.57	7.37	Sugar binding	[29,38,78]	A [29,34,38,78]
7125	P17931	Galectin-3	166	4	14.8	26,193	8.57	7.39	Sugar binding	[29,38,78]	A [29,34,38,78]
7190	P00915	Carbonic anhydrase 1	282	5	26.1	28,909	6.59	6.40	Enzyme	[32,38,74]	A [32,38,74–77]
7254	P10809	60 kDa heat shock protein	493	9	17.8	61,187	5.70	7.74	ATP binding	[29,52,72,79]	A [29,52,72,79, 80]

(continued on next page)

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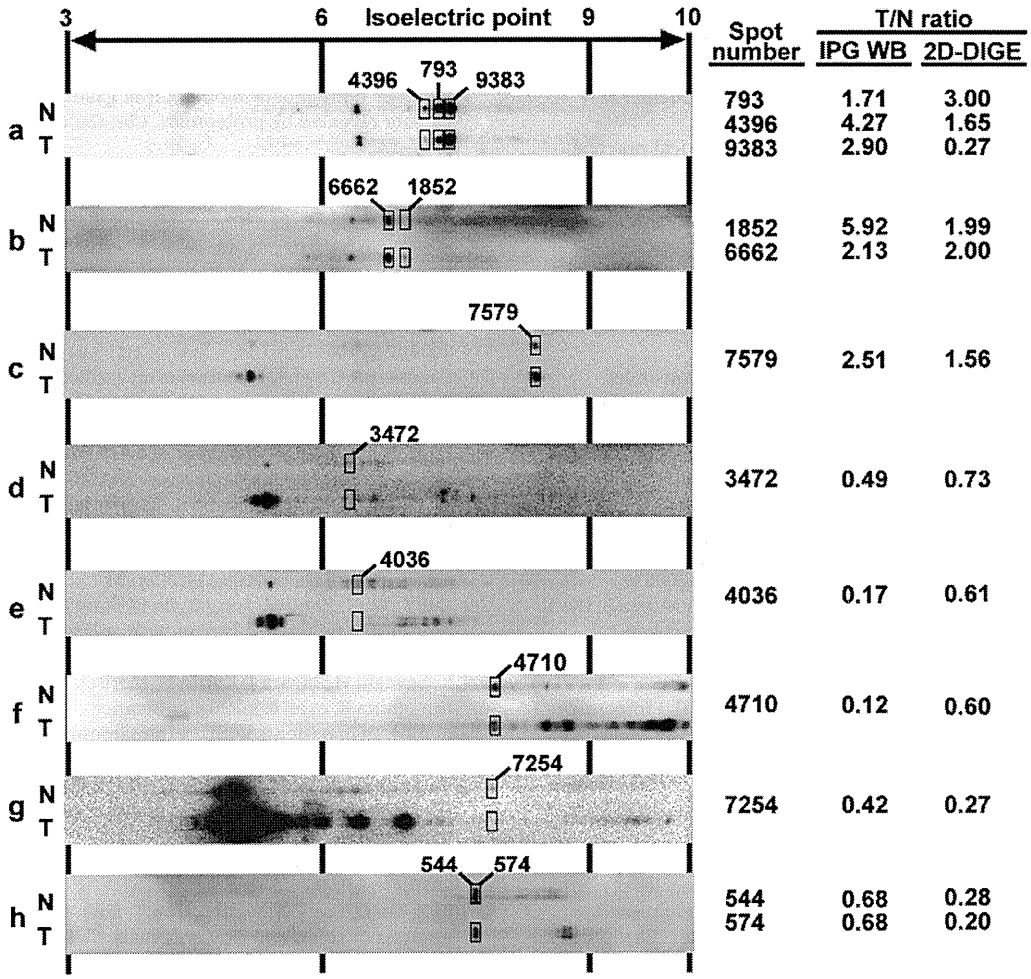
Table 2 (*continued*)

Spot no.[a]	Accession no.[b]	Protein description[b]	Protein score[c]	No. of matched peptides	Sequence coverage (%)[d]	MW (Da)[e]	Reference pI[e]	Actual pI[f]	Molecular function[g]	Reports by 2D-PAGE[h]	Reports in CRC[i]
7347	P60174	Triosephosphate isomerase	200	3	22.5	26,938	6.45	6.41	Enzyme	[29,30,35,71,72]	A [29,30,34,68, 71–73]
7579	P07355	Annexin A2	112	2	6.2	38,808	7.57	8.31	Metal binding	[8,9,29,42,74]	A [8,9,29,42,74]
7757	P62937	Cyclophilin A	215	4	28.5	18,229	7.68	6.70	Enzyme	[34,81]	A [31,34,36,81,82]
7875	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	117	2	8.8	37,464	8.97	6.98	Nucleic acid binding	[29,38]	A [29,38,83–85]
8118	Q01995	Transgelin	94	2	9.5	22,653	8.87	6.90	Actin binding	[29,30,32,86,88]	A [29,30,32,34, 86–88]
8276	Q01995	Transgelin	117	2	9.5	22,653	8.87	7.33	Actin binding	[29,30,32,86,88]	A [29,30,32,34, 86–88]
8312	P68871	Hemoglobin subunit beta	205	4	31.3	16,102	6.75	7.24	Metal binding	[30,36,52]	A [30,36,52]
8341	P02794	Ferritin heavy chain	158	3	21.3	21,883	5.30	7.31	Enzyme	[9,36]	A [9,34,36,38]
8613	Q01995	Transgelin	84	2	8.5	22,653	8.87	7.50	Actin binding	[29,30,32,86,88]	A [29,30,32,34, 86–88]
8689	P23528	Cofilin-1	155	3	25.3	18,719	8.22	8.02	Actin binding	[29,38,52,71]	A [29,34,38,52,71]
8718	P56470	Galectin-4	124	5	19.2	36,032	9.21	8.01	Sugar binding	[38]	A [34,38]
8957	P56470	Galectin-4	110	2	7.4	36,032	9.21	7.78	Sugar binding	[38]	A [34,38]
8987	P68871	Hemoglobin subunit beta	349	6	53.1	16,102	6.75	6.81	Metal binding	[30,36,52]	A [30,36,52]
9076	P68871	Hemoglobin subunit beta	320	5	48.3	16,102	6.75	6.64	Metal binding	[30,36,52]	A [30,36,52]
9118	P68871	Hemoglobin subunit beta	170	3	28.6	16,102	6.75	6.70	Metal binding	[30,36,52]	A [30,36,52]
9249	P02768	Serum albumin	643	13	19.2	71,317	5.92	6.90	Nucleic acid binding	[9]	A [9,51,90]
9258	P29401	Transketolase	341	6	16.4	68,519	7.58	7.07	Enzyme	[36,38]	A [34,36–38]

9330	O60701	UDP-glucose 6-dehydrogenase	515	9	27.7	55,674	6.73	6.94	Enzyme	[29,38]	A [29,34,38,89]
9383	P07954	Fumarase	509	8	24.7	54,773	8.85	7.37	Enzyme	[36,38]	A [34,36,38, 45–47]
9408	P52209	6-Phosphogluconate dehydrogenase	336	4	15.3	53,619	6.80	6.98	Enzyme	Not reported	B [34]
9425	P60174	Triosephosphate isomerase	228	4	15.7	26,938	6.45	6.53	Enzyme	[29,30,35,71,72]	A [29,30,34,68, 71–73]
9617	P0CG04	Ig lambda chain C regions	127	2	23.8	11,401	6.92	7.24	Antigen binding	Not reported	B [34,53,54]
9629	P22061	Protein L-isoaspartyl/D-aspartyl methyltransferase	229	4	22.9	24,806	6.70	6.49	Enzyme	Not reported	D
9630	P00491	Purine nucleoside phosphorylase	485	11	42.9	32,325	6.45	6.49	Nucleic acid binding	[36]	A [36]
9774	P68871	Hemoglobin subunit beta	133	2	19.7	16,102	6.75	7.18	Metal binding	[30,36,52]	A [30,36,52]
9775	P68871	Hemoglobin subunit beta	154	2	17.0	16,102	6.75	7.18	Metal binding	[30,36,52]	A [30,36,52]
9792	P68104	Elongation factor 1-alpha 1	180	3	8.4	50,451	9.10	8.29	Nucleic acid binding	[36,38]	A [31,34,36]
9828	P04083	Annexin A1	304	5	20.2	38,918	6.57	7.22	Metal binding	[36,42,49,78]	A [36,42,49,78]

[a] Spot numbers were referred to those in Figs. 1 and 3.
[b] Accession numbers of proteins and protein name were derived from Swiss-Prot.
[c] Protein score for the identified proteins was based on the peptide ions score ($P<0.05$) (http://www.matrixscience.com).
[d] Reference isoelectric point and molecular weight were obtained from Swiss-Prot.
[e] Sequence coverage was derived from amino acids sequence.
[f] Actual isoelectric point was calculated from 2D-DIGE gel scanning image.
[g] Molecular function was categorized by accessing Gene Ontology database (http://www.geneontology.org/) and literature curation.
[h] Proteins previously reported in 2D-PAGE based proteomics study using CRC tissue.
[i] Proteins previously reported in 2D-PAGE based proteomics study using CRC only (A), those in CRC (B), those in other cancer only (C), and the proteins previously not reported the correlation with cancer (D).



Spot number	T/N ratio IPG WB	T/N ratio 2D-DIGE
793	1.71	3.00
4396	4.27	1.65
9383	2.90	0.27
1852	5.92	1.99
6662	2.13	2.00
7579	2.51	1.56
3472	0.49	0.73
4036	0.17	0.61
4710	0.12	0.60
7254	0.42	0.27
544	0.68	0.28
574	0.68	0.20

Fig. 5 – The validation study was performed using specific antibodies after the proteins separated according to their pI. Ratios of intensity between normal (N) and tumor tissue (T) samples are shown in the left side for all protein bands (IPG/WB) and spots (2D-DIGE) as T/N ratio. Spot number corresponded to those in other figures and tables. Covered pI range of the present study is between 6 and 9, and the corresponding area is indicated in the figure. Protein names are as follows; a. fumarase, b. electron transfer flavoprotein subunit alpha, c. annexin A2, d. moesin, e. lamin A/C, f. lung cancer antigen NY-LU-1, g. 60 kDa heat shock protein, and h. pyruvate kinase isozymes M1/M2. Note that the protein intensity in the IPG/western blotting and the 2D-DIGE was quite concordant except spot, 9383. Sample numbers 3N and 3T are used for these analyses.

it reproduces 2D-PAGE results by separating proteins according to their pI.

4. Conclusions

We reported the proteomic differences of normal and tumor tissues of patients with colorectal cancer. Focusing specifically on proteins with alkaline pI and using 2D-DIGE with a large-format electrophoresis apparatus in a relatively large sample size, we observed novel aberrant regulation of six proteins in colorectal cancer tissues. Further investigation of these proteins may provide more insights in colorectal cancer, and contribute to development of biomarkers and drug target discovery. We also demonstrated the utility of IPG/western blotting for cancer proteomics. IPG/western blotting may be a useful tool to confirm the 2D-DIGE results, since it permits measurement of the amount of individual protein species, and enables study of the proteins which cannot be identified by 2D-DIGE.

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Original contribution

Hepatocyte nuclear factor 4A expression discriminates gastric involvement by metastatic breast carcinomas from primary gastric adenocarcinomas

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Summary Breast carcinomas sometimes metastasize to the stomach, and the histopathologic distinction of such metastases from primary gastric adenocarcinomas is often difficult. We characterized the clinicopathologic features of 21 breast carcinomas that had metastasized to the stomach and examined the use of a panel of antibodies, including hepatocyte nuclear factor 4A, for distinguishing the metastases from primary gastric diffuse-type adenocarcinomas. Histologically, all the metastatic breast carcinomas showed a poorly differentiated and/or signet ring cell morphology. Although most metastatic breast and primary gastric carcinomas contained signet ring cell components, the cases that were predominantly or exclusively composed of univacuolated-type signet ring cells were limited to metastatic breast carcinomas. Immunohistochemically, hepatocyte nuclear factor 4A was expressed in all 33 primary gastric carcinomas that were examined but was never expressed in metastatic breast carcinomas. Previously reported markers for breast and gastric carcinomas also showed a high specificity, but their sensitivities were quite variable. Estrogen receptor α, progesterone receptor, mammaglobin, and gross cystic disease fluid protein 15 were expressed in 76%, 33%, 52%, and 62%, respectively, of the metastatic breast carcinomas, whereas none of the primary gastric carcinomas expressed these antigens. CDX2, MUC5AC, MUC6, and CK20 were expressed in 36%, 85%, 27%, and 55%, respectively, of the primary gastric carcinomas. All the metastatic breast carcinomas were negative for these antibodies except for 1 case that expressed MUC5AC. Overall, the use of immunohistochemistry efficiently discriminated metastatic breast carcinomas from primary gastric carcinomas. In particular, the present study identified hepatocyte nuclear factor 4A as an excellent marker for differentiating the 2 lesions.

1. Introduction

In surgical pathology practice, we sometimes encounter breast cancer metastases to the gastrointestinal tract, especially to the stomach. Interestingly, most previous

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