The gene expression profile represents the molecular nature of liver metastasis in colorectal cancer

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Abstract. The major cause of death in colorectal cancer is related to liver metastasis. Although the metastatic process has been well studied, many aspects of the molecular genetic basis of metastasis remain unclear. Elucidation of the molecular nature of liver metastasis is urgent to improve the outcome of colorectal cancer. We analyzed the chronological gene expression profiles of 104 colorectal samples corresponding to oncogenic development including normal mucosa, localized and metastasized primary tumors, and liver metastatic lesions as fundamental samples using a custom cDNA microarray. The gene expression patterns in 104 samples were classified into four groups closely associated with their metastatic status, and the genes of each group appropriately reflected the metastatic process. To investigate the existence of metastatic potential in primary tumors using metastasis-related genes detected by chronological analysis, we performed a hierarchical cluster and supervised classification analysis of 28 independent primary tumors. Hierarchical cluster analysis segregated the tumors according to their final metastatic status, rather than their clinical stages, and the profile of metastasized primary tumors resembled one of a metastatic lesion apart from a primary lesion rather than one of a non-metastasized primary tumor. Using the supervised classification approach, the expression profile of these genes allowed the classification of tumors diagnosed as localized cancer into two classes, the localized and the metastasized class, according to their final metastatic status. The disease-free survival and overall survival were significantly longer in the localized class than the metastasized class. Chronological analysis of the gene expression profile provides a better understanding of the metastatic process. Our results suggest that the metastatic potential is already encoded in the primary tumor and is detectable by a gene expression profile, which allows the prediction of liver metastasis in patients diagnosed with localized tumors and also the design of new strategies for the treatment and diagnosis of colorectal cancer.

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Abbreviations: cDNA, complementary DNA; CEA, carcinoembryonic antigen; CRC, colorectal cancer; CT, computer tomography; *DCC*, deleted-in-colon carcinoma; ERK, extracellular-signal-regulated kinase; *GDI2*, *GDP dissociation inhibitor 2*; GO, gene ontology; HCA, hierarchical cluster analysis; MAPK, mitogen-activated protein kinase; RT-PCR, reverse transcription polymerase chain reaction; SAGE, serial analysis of a gene expression; TNM, tumor node metastasis; UPGMA, unweighted pair group method using arithmetic averages; VEGF, vascular endothelial growth factor

Key words: colorectal cancer, liver metastasis, gene expression profile, molecular analysis

Introduction

Colorectal cancer (CRC) is one of the most common cancers worldwide and considerable progress has been made in identifying the mechanisms of tumorigenesis based on molecular and biological research (1). The number of completely cured patients has increased because of improvements in screening technology and localized treatment; however, this has not resulted in major improvements in the prognosis of patients with advanced cancers. The major cause of death in patients with CRC is metastasis, particularly liver metastasis (2). Despite the development of various treatment modalities, once a metastatic lesion is discovered, the outcome for the patient is unfavorable. Therefore, elucidation of the global nature of liver metastasis in CRC is clinically important (3).

The phenomenon of cancer metastasis has been extensively studied morphologically and has been characterized as a complex, multistep process, and each step of this process is regulated by various changes on a genetic level (4-6). Thus, to understand cancer metastasis, it is important to comprehensively analyze the alterations of the genes involved in this process (7,8). DNA microarray technology is an efficient approach to a wide range of applications in cancer research (9). Gene expression profiling can identify biologically and clinically important subgroups of malignant tumors such as CRC (10-12). Indeed, it is possible to mark the histopathological differentiation at a molecular level, and the analysis could help to explain the complexity of the disease

process and can more accurately assess prognosis and distinct behavior.

Conventional diagnosis and surveillance have been performed by histopathological and clinical parameters such as the TNM stage and serum tumor markers such as the carcinoembryonic antigen (CEA). An elevated serum CEA level is regarded as a good indicator of metastatic disease and post-operative testing is recommended for the survey of recurrence, whereas ~30% of all CRC recurrences do not produce CEA (13). Currently, the prediction of metastasis or recurrence is also achieved by molecular parameters that focus on individual candidate genes such as the vascular endothelial growth factor (VEGF) and deleted-in-colon carcinoma (*DCC*) genes. However, these molecular diagnoses are not always accurate in predicting metastasis in the individual patient, and have not yet been validated for use as a diagnostic tool applicable to clinical practice (14). Thus, there has been a tremendous amount of effort to diagnose recurrent CRC in clinical practice.

Several investigators have reported that the gene expression profile makes it possible to predict the outcome including metastasis (15-17). These reports suggest that the gene expression profile has the potential to be applied clinically for the diagnosis of metastasis, and that a more precise diagnosis of metastasis than the current one can be achieved based on a comprehensive analysis of each distinct step of metastasis at a molecular level.

The present study was designed to analyze the chronological changes in the gene expression profiles of 104 patients as the fundamental set using cDNA microarray (Colonochip), which was developed for the analysis of CRC (18). We identified the gene expression profiles that reflected each step of cancer progression, including carcinogenesis, metastatic potential and metastatic colonization. To validate the predictability of metastasis by the gene expression profile in the bulk of primary tumors, we focused on the genes that correlated with the metastatic potential in the fundamental set. We then profiled the gene expression of 28 independent primary tumors that were diagnosed as localized or regional diseases at the time of surgery and investigated whether the expression profile in the primary tumors could determine their metastatic potential.

Materials and methods

Tissue samples. Tissues from 12 normal colonic tissues, 12 stage I and 20 stage II primary tumors without metastasis (stage I-LOC and stage II-LOC), 7 stage III and 19 stage IV primary tumors with liver metastasis (stage III-MET and stage IV-MET), and 34 liver metastatic specimens (LIV) were obtained from February 1989 to August 2000 and analyzed as the fundamental sample set. The clinicopathological backgrounds of the patients are summarized in Table I. All samples were immediately frozen in liquid nitrogen after surgical resection and stored at -80°C until further use. Each sample was examined histopathologically and all normal tissues were confirmed to be free of cancer. Samples were collected from patients who had given informed consent and the study was approved by the Ethics Committee of Osaka University.

cDNA microarray, tissue preparation, hybridization and data processing. We used the cDNA microarray 'Colonochip' specifically designed for analyzing CRC. The reliability of Colonochip had been confirmed previously by comparison with the data obtained from two distinct assays: Reverse transcription-polymerase chain reaction (RT-PCR) and serial analysis of the gene expression (SAGE) database (18,19). Tissue preparation, hybridization, washing, scanning and image analysis were performed as described previously (18). In each sample, the values of the Cy3/Cy5 ratio of each spot were log-transformed and normalized so that the median Cy3/Cy5 ratio of whole genes was 1.0. Genes with <85% valid data points in the sample sets were excluded from further analysis, and hence, 1,953 genes were selected at this stage.

Statistical analysis. We calculated the signal-to-noise (S2N) statistics to identify differentially expressed genes with regard to each class distinction [(for example, normal mucosa vs primary cancer and normal mucosa vs metastatic cancer) $(\grave{I}_0-\grave{I}_1)/(\hat{U}_0+\hat{U}_1)$]. The symbol $\grave{I}$ represents the mean and $\hat{U}$ represents the standard deviation of expression for each class of each gene in the dataset. To compare these correlations to what would be expected by chance, permutation of the sample labels was performed and the S2N statistics in each permutation were calculated. One thousand global random permutations were used to build histograms. The assumption was made that these histograms were normally distributed. Based on these histograms, the z-score and significance levels were determined and then compared with the values obtained for the real dataset (20). We defined genes with a 99 percentile set as significantly different.

Gene ontology analysis. GoMiner (http://discover.nci.nih.gov/gominer/) was used to investigate the biological significance of a set of genes represented by the specific expression pattern during the progression of cancer metastasis (21). We calculated whether the gene ontology (GO) category was enriched or depleted for each group of genes represented by the specific expression pattern with respect to what would have been expected by chance alone, using the two-sided Fisher's exact test. We focused our analysis on a GO term that had >10 associated genes in order to evaluate the significance of a GO term.

Independent samples. An additional 28 CRC tumors were profiled as an independent sample set; 10 stage II and 8 stage III primary tumors without metastasis (stage II-LOC and stage III-LOC), and 4 stage II and 6 stage III with metachronous liver metastasis (stage II-MET and stage III-MET). Table I shows the clinicopathological backgrounds of these patients.

Hierarchical cluster analysis. To investigate whether the expression profile in the primary tumor reflected metastatic status, we analyzed the expression profiles of 92 tumors in the fundamental set, using 119 genes that were regarded as relevant to the metastatic potential by chronological analysis. Furthermore, the expression profiles of 120 tumors (adding the 92 tumors to the 28 independent tumors) were analyzed

Table I. Clinicopathological characteristics of the profiled cancer samples.

	Fundamental samples				Independent samples			
Sample group	Stage I-LOC	Stage II-LOC	Stage III-MET	Stage IV-MET	Stage II-LOC	Stage II-MET	Stage III-LOC	Stage III-MET
Number	12	20	7	19	10	4	8	6
Liver metastatic status	Negative	Negative	Negative	Positive	Negative	Positive	Negative	Positive
Sex								
Male	6	11	4	12	6	2	6	5
Female	6	9	3	7	4	2	2	1
Age (years)								
(mean ±SD)	59.3±8.7	59.3±10.2	63.3±8.9	59.4±10.2	68.3±10.2	64.0±2.7	58.3±8	60.8±6.7
Location								
Right (A,C,T)	2	6	3	4	3	2	0	1
Left (D,S)	2	8	2	10	2	1	2	2
Rectum	8	6	2	5	5	1	6	3
Depth								
Sm, mp	12	0	2	1	0	0	2	0
Ss, a1	0	13	2	9	7	2	3	3
Se, a2	0	7	3	8	3	2	3	3
si, ai	0	0	0	1	0	0	0	0
Lymph node metastatic status								
(-)	12	20	0	10	10	4	0	0
(+)	0	0	7	9	0	0	8	6
Follow-up (month)								
Median	84.5	70.8	51.2	34	77.9	27.2	82.6	46.6
(Range)	(24.8-102)	(25.1-101)	(13.4-76.0)	(4.4-80.5)	(63-115)	(12.7-80.1)	(47.1-102)	(22-56.2)
Month to metastasis								
Median	-	-	(6.2-39.8)	0	-	(6.7-20.1)	-	(6.8-18.5)
(Range)	-	-	17.2	0	-	15.4	-	17

LOC, localized primary tumor; MET, metastasized primary tumor.

using the same genes. Hierarchical cluster analysis (HCA) was performed with Pearson's correlation coefficient as a similarity coefficient and the unweighted pair group method using arithmetic averages (UPGMA) as the clustering algorithm.

Classification analysis with independent samples. We applied the weighted vote method as the class predictor (20). The prediction of a new sample is based on the 'weighted votes' of 119 informative genes. Each such gene g_i votes for either LOC or MET, depending on whether its expression level x_i in the sample is closer to $\grave{I}_{LOC}$ or $\grave{I}_{MET}$ (which denote, respectively, the mean expression levels of LOC and MET in the fundamental set). The magnitude of the vote is $w_i v_i$, where w_i is the S2N statistics between LOC and MET $[|(\grave{I}_{LOC}-\grave{I}_{MET})/(\hat{U}_{LOC}+\hat{U}_{MET})|]$ and $v_i=|x_i-(\grave{I}_{LOC}+\grave{I}_{MET})/2|$. The votes for each class are summed to obtain the total number of votes V_{LOC} and V_{MET}. The sample is assigned to the class (localized signature or metastasized signature) with the higher vote total.

Results

The 1,953 genes were classified into four distinct groups according to the following expression patterns. Group A (A1 and A2) consisted of 369 genes that were differentially expressed during all tumorgenic stages; group B (B1 and B2) consisted of 119 genes that were differentially expressed in synchronously or metachronously metastasized tumors and liver metastasis; group C (C1 and C2) consisted of 430 genes that were differentially expressed in liver metastasis; group D consisted of 1,035 genes that were not characterized by the expression pattern at all steps of cancer development (Fig. 1). The expression patterns of the genes of group A, B and C correlated with the phenomena of cancer progression in CRC; carcinogenesis, metastatic potential and metastatic

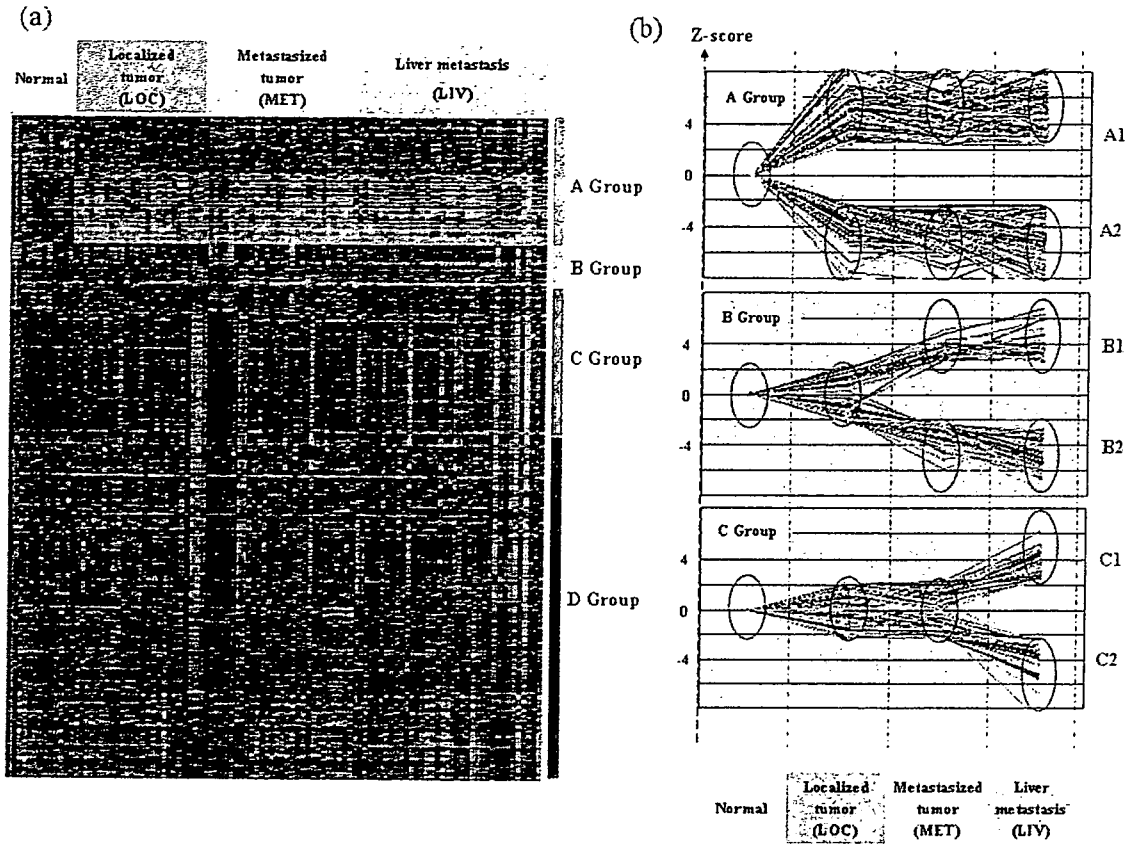

Figure 1. Gene expression patterns associated with the metastatic process. (a) The columns represent 12 normal colon samples and 92 colorectal tumor samples [32 localized tumors (LOC), 26 metastasized tumors (MET) and 34 liver metastatic tumors (LIV)]; the rows represent 1,953 genes. Differentially expressed genes during cancer development were identified by comparison of each sample group with 12 normal colon samples by permutation testing. (b) Line graphs represent the z-score calculated by permutation testing in each sample group at the stage of development. Group A (A1 and A2) consisted of 369 genes that were differentially expressed during the development of the carcinogenic process (A1, up-regulated genes; A2, down-regulated genes); group B (B1 and B2) consisted of 119 genes that were differentially expressed in localized tumors and metastasized tumors; group C (C1 and C2) consisted of 430 genes that were characterized by a differential expression pattern in liver metastasis.

colonization, respectively. The list of genes of group A, B or C are shown in Supplementary Table I, which is available on our website (http://www.dna-chip.co.jp/other/ other/ download_20060822.html).

Functional analysis based on GO was performed to translate the lists of differentially regulated genes in order to gain a better understanding of the underlying biological phenomenon. Table II shows the representative GO functional classes as upper-hierarchical terms in the final branch under the biological-process ontology with a significance of $p<0.05$ in each group, and all of the terms are shown in Supplementary Fig. 1, which is available on our website (http://www.dna-chip.co.jp/other/other/download_20060822.html), based on the directed acyclic graph structure of the GO and their hierarchy.

Group A1 included genes related to DNA metabolism, cell cycle, and response to endogenous stimuli such as response to DNA damage. Response to external stimuli such as defense and immune responses were represented in group A2. Genes related to apoptosis, cell motility and response to external stimuli were included in group B. Group C included genes involved in signal transduction such as the intracellular signaling cascade and cell-cell signaling, defense response and response to stress.

To investigate whether the expression profile in the bulk of primary tumors reflected metastatic status, we analyzed the gene expression profiles of 92 tumors in the fundamental set. HCA of 92 CRCs using the 119 genes in group B, which were detected by chronological analysis as genes closely associated with metastatic potential, was performed, and the tumors were segregated into two major categories, each consisting of 44 and 48 tumors, respectively (Fig. 2A). The left cluster (non-metastatic cluster) was comprised of 28 LOC, 10 MET and 6 LIV, whereas the right cluster (metastatic cluster) was comprised of 4 LOC, 16MET and 28 LIV. These two clusters correlated significantly with the metastatic status of the tumors.

Next, we performed HCA of 120 tumors (92 fundamental tumors and 18 independent ones) (Fig. 2B). The clustering pattern was robust against sample addition. For instance, the partitioning of the clusters and 92 fundamental tumors in the two sub-branches remained similar with little change.

As for the independent samples, 17 of the 18 stage II and III samples without metastasis belonged to the non-metastatic cluster despite of the clinical staging. Unexpectedly, all of the 10 stage II or III samples that metachronously developed liver metastasis although they had been diagnosed as localized or regional disease at the time of initial diagnosis belonged to the metastatic cluster. The expression profile of the independent samples was closely associated with the metastatic potential in the primary tumor rather than the histopathological staging.

Table II. Functional gene classes demonstrating significant differential expression in each group.

Function name	Total	P (X2)	P (X1)	P (X)
A group				
Regulation of transcription	189	0.998	0.008	0.581
Regulation of transcription, DNA-dependent	184	0.997	0.011	0.582
Response to external stimuli	135	0.008	0.932	0.14
Mitotic cell cycle	48	0.628	1E-04	0.003
Ion transport	46	0.057	0.214	0.026
Regulation of cell cycle	46	0.901	0.001	0.055
Lipid metabolism	36	0.013	0.844	0.082
Protein folding	22	0.926	0.038	0.261
Alcohol metabolism	20	1	0.026	0.365
DNA replication and chromosome cycle	20	0.668	0.001	0.009
Response to endogenous stimulus	20	1	0.026	0.365
DNA replication	18	0.609	0.003	0.015
Nuclear organization and biogenesis	18	1	0.016	0.278
DNA repair	17	1	0.013	0.236
Main pathways of carbohydrate metabolism	14	0.808	0.029	0.126
Nucleocytoplasmic transport	14	1	0.029	0.297
DNA packaging	13	1	0.004	0.096
Carbohydrate catabolism	11	1	0.012	0.157
B group				
Transport	170	0.041	0.617	0.07
Response to external stimuli	135	0.019	0.219	0.01
Electron transport	56	0.026	0.65	0.045
Apoptosis	44	0.109	0.187	0.043
Energy pathways	37	0.003	0.497	0.005
Cell motility	36	0.455	0.024	0.06
Induction of programmed cell death	18	0.037	0.04	0.003
C group				
Protein metabolism	340	0.002	0.895	0.009
Biosynthesis	190	0.041	0.99	0.181
Response to stress	96	0.045	0.076	0.01
Defense response	85	0.642	0.047	0.296
Intracellular signaling cascade	82	0.022	0.04	0.003
Cell-cell signaling	36	0.081	0.319	0.05
Vehicle-mediated transport	36	0.424	0.024	0.101
Ribosome biogenesis and assembly	33	0.046	1	0.114
Protein kinase cascade	24	0.335	0.038	0.077

[a]Total number of genes represented in each group corresponding to a specific gene ontology term, [b]p-value in the X group (X=A, B or C).

We assessed the utility of these 119 genes to identify patients who would develop liver recurrence after surgery. The expression of these 119 genes was used to build a weighted vote-based classifier that could predict liver metastasis at the time of surgery. We applied this classifier to the 28 independent samples. Eighteen and 10 patients were assigned to the localized signature and metastasized signature, respectively. Seventeen of the 18 (94.4%) patients assigned to the localized signature did not relapse at least 47 months after surgery, and 9 of the 10 (90%) patients assigned to the

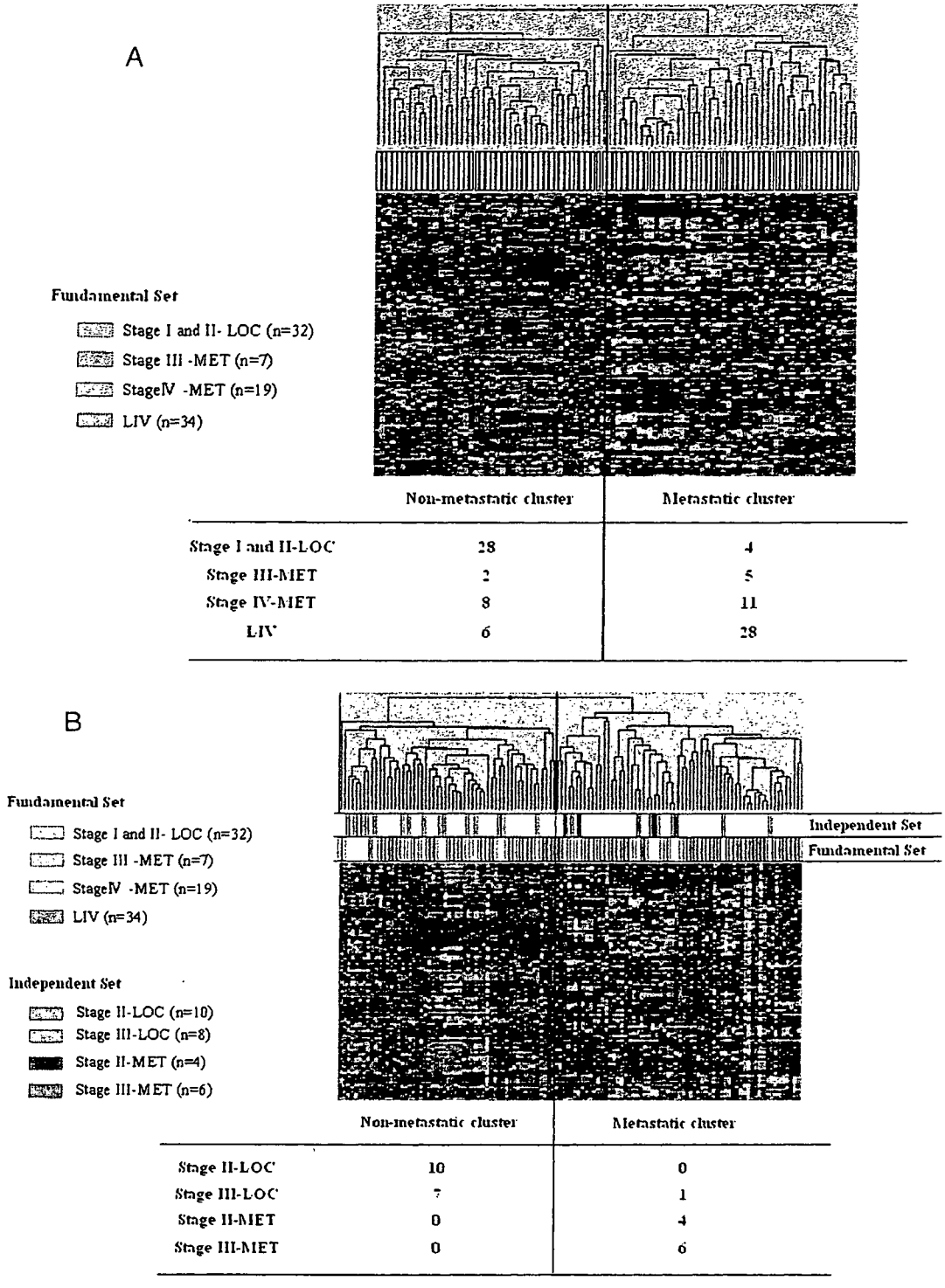

Figure 2. Hierarchical cluster analysis of metastasized and non-metastasized tumor signatures. The genes in group B are hierarchically clustered with respect to the 92 tumors in the fundamental set (A) and the 120 tumors adding these 92 to the 18 tumors in the independent set (B). Each row represents a gene and each column represents a sample. For the samples, the color bars below the dendrogram represent sample annotation in clinicohistopathology. The aqua bars represent localized primary tumors (LOC), the orange and pink bars represent stage III- and stage IV- ones (stage III -MET and stage IV -MET) and the red bars represent liver metastatic lesions (LIV) in the fundamental set. The blue and green bars represent LOC with stage II and III (stage II-LOC and stage III-LOC), and the brown and red bars represent MET with stage II and III (stage II-MET and stage III-MET), respectively, in the independent set. (A) Two major branches of the hierarchical tree are observed. The left and right branches are mainly comprised of non-metastasized (non-metastatic cluster) and metastasized tumors (metastatic cluster), respectively. These two clusters significantly correlated with the metastatic status of the tumors. (B) The clustering pattern was so robust against sample addition that the partitioning of the 92 fundamental tumors remained the same and showed little change. Out of the 28 independent tumors, all of the 10 metastasized tumors are in the metastatic cluster, and 17 of the 18 non-metastasized tumors are in the non-metastatic cluster.

metastasized signature recurred to liver metastasis after surgery (Table III). The successful prediction of liver metastasis could be shown in the independent set of tumors.

To assess the association between class assigned by gene expression profile and survival, we plotted Kaplan-Meier survival curves of 28 patients in the independent set (Fig. 3A

Table III. The predictive diagnosis of liver metastasis in the independent samples.

		Clinical diagnosis	
		Non-relapse	Relapse
Profiling diagnosis	LOC	17	1
	MET	1	9

and B). A significant difference was observed in the disease-free survival ($p<0.0001$) and overall survival ($p=0.0065$) of patients between the localized and metastasized signature.

Discussion

The gene expression profile using DNA microarray is a promising approach to investigate the molecular complexity of cancer. Several studies have reported the usefulness of this technique such as the gene identification related to metastasis and possible prediction of metastasis in various cancers (16,17). However, these studies simply compared the gene expression profile of tumors between partial stages and did not directly address the metastatic process. To elucidate the phenomenon of metastasis more accurately, it is critical to analyze comprehensively the process of gradual change in cancer progression. Thus, we analyzed the gene expression profiles of 104 samples at four time points in cancer development; normal colon, localized and metastasized primary

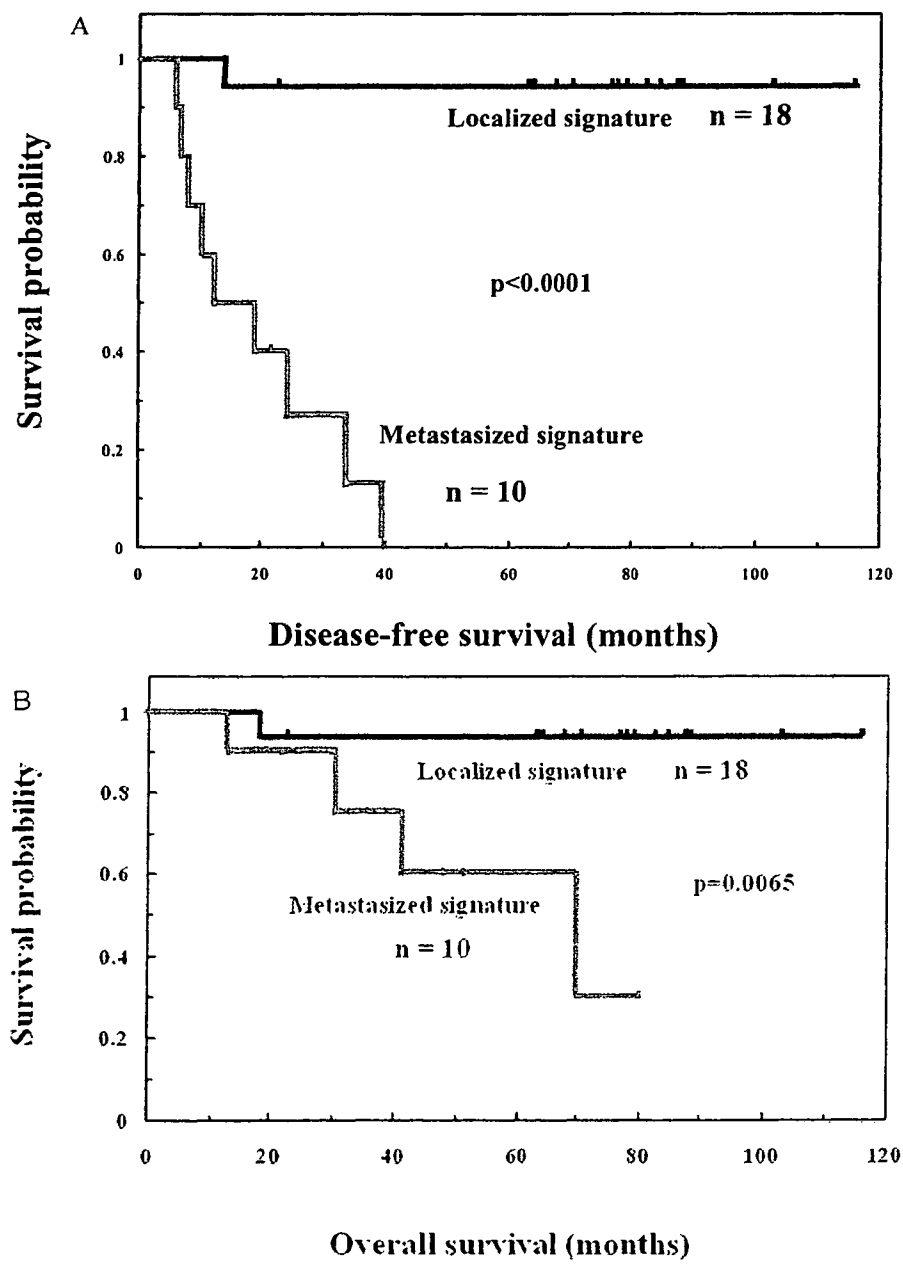

Figure 3. Kaplan-Meier plot of disease-free (A) and overall (B) survival of patients with the localized and metastasized signature. (A) Disease-free survival curves of patients with the localized signature were also higher than those of patients with the metastasized signature (log-rank test, $p<0.0001$). (B) Overall survival curves of patients with the localized signature were higher than those of patients with the metastasized signature (log-rank test, $p=0.0065$).

tumor and liver metastasis. These analyses indicate that each step of cancer progression can be characterized by a gene expression profile.

The expression pattern of group A is considered to be associated with the promotion of carcinogenesis in CRC. This group contained a significantly high proportion of genes with functions relevant to carcinogenesis such as cell proliferation and response to external and endogenous stimuli, and any imbalance in these functions initiates colorectal carcinogenesis. If these genes were expressed on the cell surface or secreted, this could be detected by easier methods such as immunohistochemical analysis and be applicable clinically as candidate diagnostic markers for the early detection of CRC (cellular-component, data not shown).

The expression of the genes represented in group B is significantly different in the primary tumor with or without metastasis, which directly reflects the event of metastasis itself. The loss or acquisition of this function in this group was closely relevant to the liver metastatic potential in colorectal cancer. This group contained a significantly high proportion of genes with functions relevant to the process of metastasis such as cell motility and apoptosis. The acquisition of cell motility is essential for the invasion of interstitial tissue and lymphatic or vascular vessel walls and the survival of cancer cells against immune and non-immune defenses while escape from apoptosis allows cancer cells to arrest a secondary organ apart from the primary lesion. Genes such as *DCC* and *GDP dissociation inhibitor 2* (*GDI2*), which are referred as relevant to metastasis, are included in group B. For example, *DCC* is a putative tumor suppressor gene, which has considerable homology to neural cell adhesion molecules and may be involved in the regulation of cell-to-cell or cell-to-substrate interactions with a potential functional role in the control of cell growth and the development of metastasis (22-24). Various studies reported that *DCC* is a predictor of distant metastasis and prognosis in colorectal cancer (24-26). Furthermore, *DCC* expression has been shown recently to predict clinical outcome to fluorouracil-based chemotherapy (27). Other studies have reported that the *DCC* gene product induced apoptosis through a caspase-dependent mechanism (28,29). In another study, *GDI2* was identified as a metastasis-suppressor gene (30). *GDI2* is an inhibitor of guanine nucleotide dissociation from RHO and RAC proteins, strongly inhibiting *GDP*/GTP exchange reaction. *GDI2*, RHO and RAC also modulate signal transduction such as the ERK, JNK and p38 MAPK pathways, three arms of which are involved in invasion, growth-factor-receptor signaling, the mitogen-activated protein kinase pathway, cell-cell communication and transcription, which are the main factors involved in the induction of liver metastasis (31,32).

The expression pattern of group C is closely associated with the colonization and maintenance of metastasis, which is the outgrowth of cancer cells after arrival at a secondary organ. Functional analysis indicated that metastatic colonization occurs as a result of the cancer cells' modification following interaction with the surrounding environment in the liver. Other investigators also reported similar results (16,33,34). Nishizuka *et al* (34) reported that cytokines produced by glial cells *in vivo* may contribute in a paracrine manner to the development of brain metastases from breast cancer cells. Metastatic colonization differs from growth in the primary lesion by its requirement for angiogenesis, and changes in the local microenvironment in metastatic lesions and stressful conditions. The requirement for various growth factors and chemokines, the cell-cell or cell-extracellular matrix interaction and the activity of intracellular signaling pathways regulated by various stimuli and interactions could have considerable influence upon not only the initiation but also the maintenance of metastatic colonization (35,36). For example, *MAP3K4* and *ERK1*, which are differentially expressed in the metastatic tumor, stimulate the p38 and JNK MAPK pathway, and the MAPK-ERK pathway, respectively. Reduced JNK and p38 signals facilitate metastatic colonization by preventing apoptosis induced by the stress of a foreign environment (37). Numerous reports have linked the activation of *ERK1* with metastasis, motility and invasion, and angiogenesis (38,39). This result suggests that the cross-talk between signaling pathways, which were represented in the MAPK pathway, such as the ERK, p38 and JNK pathways, are linked closely within the cancer cells and interstitial tissue to adhesion, motility, proliferation, angiogenesis and apoptosis in metastatic lesions, which represents the final step in cancer development. These genes might be candidate markers of metastasis and could be suitable targets for the treatment of metastatic disease.

Chronological analysis allowed us to clarify each step of cancer progression, carcinogenesis to metastasis, at the molecular level. In particular, we were successful in separating metastasis into the acquisition of metastatic potential (group B) and the initiation and maintenance of metastatic colonization (group C).

Does the gene expression pattern correlate with the metastatic potential (such as that represented in group B) already present in the bulk of the primary tumor and detectable at the time of initial diagnosis? The conventional hypothesis about metastasis is that acquisition of the metastatic phenotype may occur late in tumor progression. Primary CRC cells arise from the normal colorectal epithelium through oncogenic mutations. The occasional cancer cells possessing metastatic ability in the primary tumor population can accumulate additional genetic changes that mediate metastasis to the liver. Thus, it has been hypothesized that primary tumors have gene expression profiles in which only a fraction of the metastatic potential exists. However, some groups have challenged this hypothesis (16,17). Ramaswamy *et al* (16) reported that the expression profile of primary tumors that had metastasized resembled that of metastatic tumors, and that a predictive diagnosis for metastasis was possible based on the analysis of the primary tumor profile. Van't Veer *et al* (17) also reported that patients with early-stage breast cancer could be classified according to their prognosis based on the gene expression signature obtained from the primary tumors, and specific gene expression profiles were predictive for distant metastases. Thus, the new hypothesis indicates that the acquisition of metastatic ability does not begin in just a few cells in the primary tumor but instead most cells in such tumors are inherently capable of metastasis.

Our hierarchical clustering with the expression profile of the genes closely relevant to the metastatic potential shows

that the profile of the metastasized primary tumor resembled one of a metastatic lesion apart from a primary lesion rather than one of a non-metastasized primary tumor. This means that the tumors are segregated according to their final metastatic status rather than their clinical stages. This suggests that the metastatic potential of CRC is not acquired in proportion to cancer progression but has already been encoded in the primary tumor. Thus, our findings support the above new hypothesis rather than the conventional one.

We also succeeded in the verification of this hypothesis using independent primary tumors. Clustering analysis with these genes on CRC samples diagnosed as localized or regional disease allowed the robust classification of metastasized tumors vs non-metastasized tumors. Supervised classification analysis enabled us to predict the postoperative relapse risk of the patients who were diagnosed as localized or regional disease at the time of surgery. The classification appropriately reflected the outcome of CRC patients. Our microarray data provide important information on the metastatic potential in CRC and indicate that the expression profiles in the bulk of primary tumors reflect the character of individual tumors and are possible and valid enough to predict metastasis.

The clinical outcome of patients with CRC is governed to some extent, if not fully, by the inherent character of tumor cells. The programmed expression pattern is detectable in the bulk of primary tumors. The characterization of cancer based on gene expression profile promises to shift the paradigm of cancer diagnosis from general taxonomy by clinicohistopathological parameters to individualized risk assessment.

Currently, because it is clinically difficult to accurately predict metachronous liver metastasis at the time of initial diagnosis, a lot of time and effort is directed toward the detection of asymptomatic recurrences using postoperative monitoring such as CT and the CEA test. Therefore, a more accurate prediction of liver metastasis and clinical outcome should benefit the optimization of cancer treatment, including adjuvant therapy and postoperative surveillance, for individual patients, and at the same time avoid over- or unnecessary treatment and reduce overall cost. Chronological analysis of the gene expression profile should enable a better understanding of the metastatic process. The identified 'interesting' genes and profiles could help design new strategies for the treatment and diagnosis of metastasis.

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遺伝子発現プロファイルによる消化器癌転移推測の可能性を探る

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KEY WORDS

遺伝子発現プロファイル，消化器癌，転移予測，DNA マイクロアレイ

SUMMARY

進行消化器癌治療における主たる目的は癌の再発・転移の制御にあり，精度の高い診断技術とそれに対応した治療方針が重要である．従来の確率論的な医療から脱却を図り，癌治療成績を改善するためには，分子生物学的な手法を積極的に臨床応用し，癌腫，宿主の生物学的な特性を反映した個別化診断・治療戦略の確立が急務である．ヒト全遺伝子の発現情報が1枚のDNA マイクロアレイで解析可能な時代となり，遺伝子発現プロファイル解析は，癌の発育・進展の分子生物学的な解明において大きな役割を果たすようになった．今後，癌転移・再発のメカニズムの解明を進め，悪性度診断や治療方針の個別化に役立てることが期待されている．

はじめに

癌の死亡者数は年約2%ずつ増加し，2005年には32万5885人となり，消化器癌はその54%を占めている．消化器癌の致死率に最も影響を与える因子は転移であり，その制圧を目的とした新しい診断・治療体系の確立が急務である．癌細胞は無秩序に多数の臓器に転移するのではなく，ある一定の臓器選択性をもって転移する特徴がある．その機構は，原発巣から遊離した癌細胞が血液動態に伴い転移巣を形成するという血液動態説と，癌細胞と転移標的臓器との密接な相互作用による“seed and soil”説によって説明されてきた．その後，腫瘍には組織不均一性があり，癌の発育・進展過程において比較的後期に，ごくわずかな細胞が遺伝子レベルで変異を起こすことで転移能を有し，それらの細胞が原発巣から離脱することで遠隔転移のステップが開始されるとする多段階発癌説が提唱され，一般的な癌転移モデルとして解釈されている．しかし，実際には同一病期内でも症例により再発の有無，予後にはばらつきがある．このような症例による違いを従来の多段階発癌モデルだけで説明することは困

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難であるため，癌は臓器による違いだけでなく，同種の癌でもそれぞれのケースにおける宿主，癌腫両面の遺伝的表現型の違いにより種々の個性をもち，さまざまな臨床経過をたどると考えられるようになった[1]．

2003年，ヒトゲノムの解読完了が宣言され，癌医療はこれまでの生命科学研究の集大成を土台に大きな革新を迎えている．なかでも網羅的な遺伝子発現解析は，癌の発育・進展の分子生物学的な解明において大きな役割を果たすようになった．最近の遺伝子発現プロファイルの研究で，癌の転移能力は発育段階の早期にすでに確立されており，転移に関与する特有の遺伝子発現プロファイルが原発性腫瘍に存在するとした報告があいつぎ，癌の転移メカニズムに関する新たな知見と，それらを応用した転移・再発予測診断の可能性がさかんに議論されるようになった[2]．

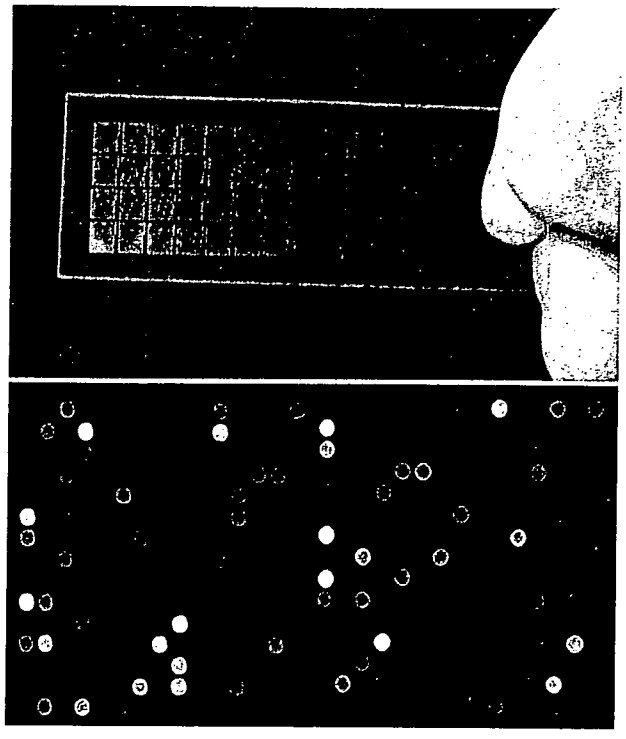
本稿では，われわれの教室の取り組みを含め，消化器癌の転移予測診断における遺伝子発現プロファイルの研究の現状を概要する．

癌の遠隔転移について

正常の細胞が増殖異常を起こして悪性化した後，転移巣を形成するまでには，細胞間接着能の低下による癌細胞の主病巣からの離脱にはじまり，基底膜への接着と浸潤，組織内移動，血管内への侵入と移動，遠隔臓器の血管内皮細胞への接着，血管外への脱出，遠隔臓器での浸潤，血管新生を伴う増殖といった数多くの複雑なステップが存在する[3]．また癌細胞は癌周囲の間質細胞と互いに影響を及ぼしあい直接的，間接的に転移を促進させるとともに，それぞれの段階で異なる遺伝子群が特有の変化を起こし，転移過程が推移すると考えられている．よって，局所的に単一分子を解析するよりも包括的に腫瘍の遺伝子変化を解析することことで，はじめて転移過程の分子生物学的な全体像をとらえることが可能となると考えられる[4]．

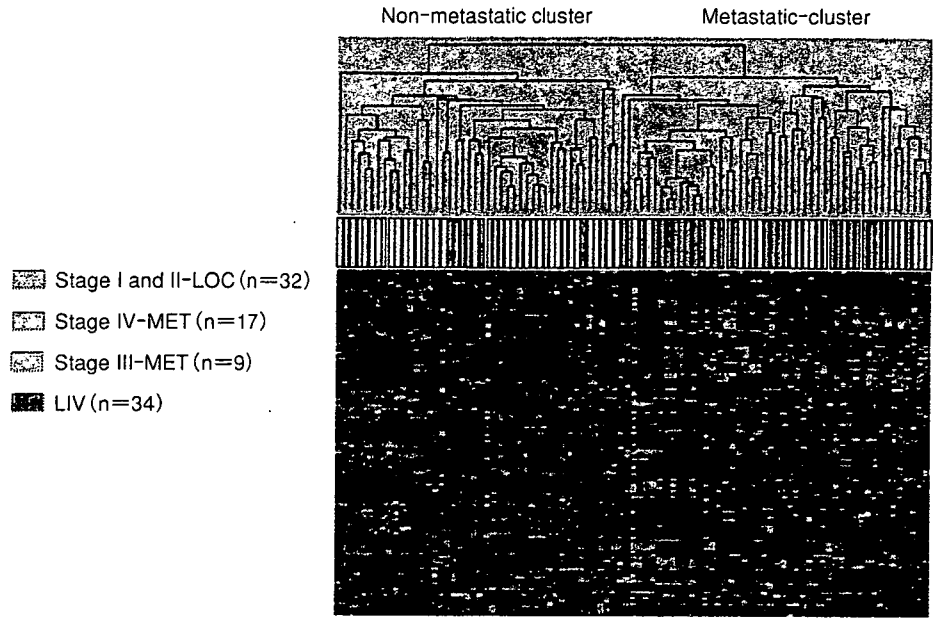
癌の遺伝子発現プロファイル解析研究の現状とは？

遺伝子発現プロファイル解析とは，網羅的な遺伝子発現情報と生物学的な特徴の関係を比較検討し，有意義な情報を検索することである[5]．現在では，ヒト全遺伝子の発現情報が1枚のDNAマイクロアレイで解析可能となり，遺伝子発現プロファイル研究に拍車がかかってきている(図❶)．癌研究でも遺伝子発現プロファイル解析がさかんに用いられ，すべての癌腫で報告がみられるようになった．当初は癌細胞と対照細胞を比較する単純なものが中心であったが，技術が進むにつれ，多数の癌の生物学的特徴と発現プロファイルによる分類の対応をつけようという総合的な試みがされるようになり，癌の個性化診断・治療への応用に関する報告も多数みられるようになった．なかでも2002年頃より癌の遠隔転移・再発に関係する重要な論文があいついで報告されるようになった．



図❶ ヒト全遺伝子型DNAマイクロアレイ（AceGene：DNAチップ研究所）とハイブリダイゼーションイメージ
50 merのオリゴヌクレオチド30000種あまりが搭載されたDNAマイクロアレイ．

van't Veerら[6]は117例の若年性乳癌を対象として遠隔転移を特有の遺伝子発現の刻印により予測できると報告した．引き続きvan de Vijverら[7]はstage IまたはIIの若年性乳癌295例を70種の遺伝子発現パターンによって，腋窩リンパ節転移など従来の臨床病理予後指標



図❷ 大腸癌原発巣と肝転移巣の遺伝子発現プロファイル解析
119種類の大腸癌の発育進展に関与する遺伝子群の発現パターンでは，肝転移のある原発巣（MET）は肝転移のない原発巣（LOC）よりもむしろ肝転移巣（LIV）の発現プロファイルに近い．（Yamasaki M *et al*, 2007[19]より引用）

の有無とは独立して予後良好群と不良群に判別することができ，さらに予後不良群を示す発現パターンは遠隔転移に深く関連していていることを示した．これらの結果より，遠隔転移能は比較的早期よりすでに獲得されており，腫瘍内に本質的に備わっているという仮説がたてられるようになった．

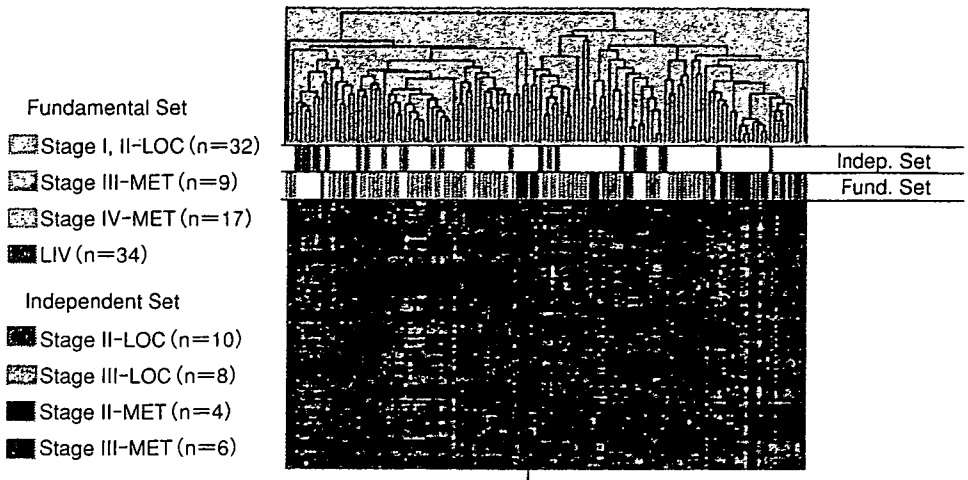
Ramaswamy ら[8]は，数種類の腺癌原発巣64例と転移巣12例の遺伝子発現プロファイルを比較し，原発巣，転移巣それぞれで転移に関与深い64種ずつの遺伝子群による刻印を同定することによって，この刻印を有する原発巣はさまざまな癌腫において有意に予後不良であることを示した．これは，原発巣内にはすでに転移能をもった細胞が十分量存在し，その個体の予後を規定する因子となっていることを示している．また Ye ら[9]は，肝細胞癌の原発巣と転移巣では遺伝子発現プロファイルは類似するが，転移の有無によってプロファイルは大きく異なることより，原発性肝細胞癌の段階で転移する可能性はすでに決まっているとし，90%の確率で転移予測できることを示した．

Kang ら[10]は種々の乳癌の cell line を用いて，骨，肺，肝に転移する遺伝子発現プロファイルを比較し，原発腫瘍内には予後不良な遺伝子発現の刻印が存在するだけでなく，遠隔転移巣別に組織特有の遺伝子発現パターンが内在するとことを示した．

これらの報告は遺伝子発現プロファイル解析が，遠隔転移・再発のメカニズムの解明の一助となり，転移予測に大きく貢献することを証明したものであるとともに，従来の癌転移モデルとは異なる解釈の可能性を示したものである．

大腸癌の転移予測診断の可能性を探る

大腸癌でも遺伝子プロファイルによるリンパ節転移，遠隔転移，再発の予測診断の可能性について多数報告されている．Kwon ら[11]はリンパ節転移に関与する遺伝子群を同定し，その発現プロファイルによる転移予測の可能性を報告した．Croner ら[12]はリンパ節転移の予測判断には従来の臨床病理因子より遺伝子発現プロファイルが優れているとした．Wang ら[13]は23種の遺伝子発現パターンによって，Dukes'B 大腸癌の術後3年以内の再発が13倍もの高危険度となる群を予測できるとし．Eschrich ら[14]は43種の遺伝子の発現プロファイルによる分子 staging が Dukes' 病期より予後予測に優れている



	Non-metastatic cluster	Metastatic-cluster
Stage II-LOC	10	0
Stage III-LOC	7	1
Stage II-MET	0	4
Stage III-MET	0	6

図❸ 肝転移の有無による大腸癌の遺伝子発現プロファイル解析
64種類の転移関連遺伝子群の発現パターンは転移のある症例(MET)と肝転移のない症例(LOC)ではまったく異なっている. (Yamasaki M *et al*, 2007[19]より引用)

と報告した. Barrier ら[15][16]は, stage II大腸癌の異時性転移の予測診断の可能性について, さらには切除された癌周囲の大腸粘膜からも同様に再発予後予測が可能であることを示した. Stage II結腸癌は一般的に予後良好で, 術後補助療法の有用性は検証されていないが, 個々の症例の分子生物学的特性を反映した予後予測診断が可能となれば, 一部の高リスク症例群に対して効率的な補助化学療法など個別化医療の実践が期待できる点で臨床的意義が大きいと考えられる. また Arango ら[17]は Dukes'C 大腸癌の予後予測に従来の分子マーカーである TP-53 や K-RAS の遺伝子変異, 18 q 染色体のゲノム不安定性よりも遺伝子プロファイルが優れていたと報告した.

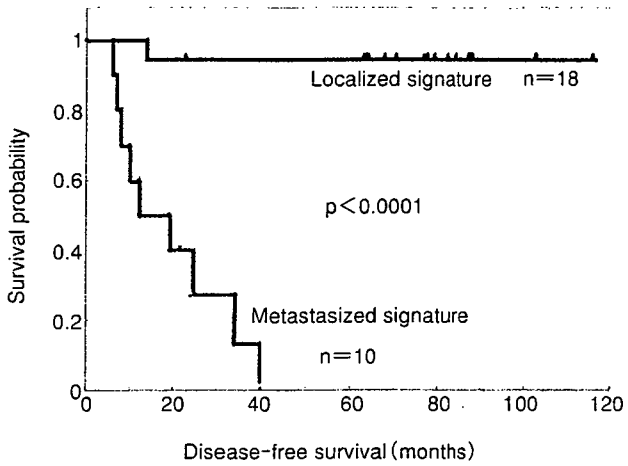
われわれ[18]の教室では大腸癌解析用の cDNA マクロアレイを用いて大腸癌の肝転移予測診断に取り組んでいる. 肝転移を起こした原発巣は肝転移を伴わない原発巣よりも肝転移巣の発現プロファイルに近いこと(図❷), また Dukes 病期によらず, 原発巣の解析により肝転移の有無によりその発現パターンはまったく異なることがわかってきた(図❸). これら結果は大腸癌の肝転移に関しても, 原発巣に転移刻印が内在することを示唆しており, 刻印の違いによって disease free survival, overall survival ともに有意差があることを示した(図❹, ❺)[19].

遺伝子発現プロファイル研究の今後の展望とは?

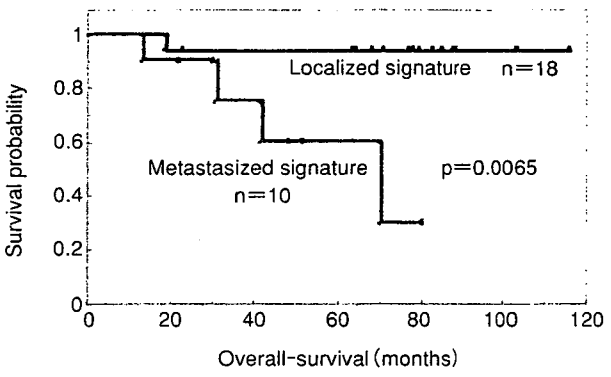
今後の消化器癌の転移研究は DNA マイクロアレイ技術による遺伝子発現プロファイルをはじめ, 各種の解析手段を組み合わせることで DNA, RNA, 蛋白質での相互作用を包括的に解析する方向へ発展すると思われる. しかし基礎的研究で得られた成果を実際の臨床に応用するためにはまだ多くの課題と改善点が残されている.

転移という現象をより明確にとらえるためには, 解析サンプルの対象を, laser captured microdissection (LCM)法によって純粋な癌細胞だけとするのか, 周囲細胞との interaction も考慮にいれて whole tissue とするのか議論が続けられている[20]. また全身麻酔下手術も遺伝子発現に影響があり研究デザインには十分な注意が必要である[21].

解析デザインに関しては, 解析遺伝子数に対する症例数が少ないことや, 同一データを対象としても用いる解



図❹ 刻印による disease-free survival
(Yamasaki M *et al*, 2007[19]より引用)



図❺ 刻印による overall-survival
(Yamasaki M *et al*, 2007[19]より引用)

析手法により結果が異なるといった問題点があげられる．実際に研究単位により報告されている転移関連遺伝子の相関性が少ないことや，判別信頼性が不足していることが指摘されている[22]．その他DNAマイクロアレイのplatformの種類，対照サンプルの設定でも予測精度が変動することが知られるようになり注意深い検討が必要である．

今後はより多数症例の解析によるvalidationと再現性を確保し，さらにプロスペクティブな臨床試験によって，予後予測の臨床応用のエビデンスを証明することが必要である[23]．

おわりに

遺伝子発現プロファイル解析による癌の転移研究と新たな知見について概説した．今後，網羅的な分子生物学的研究により，どのような癌細胞集団が，どのような転移様式をとって転移巣を形成するのか，そのメカニズムの解明がさらに進むと考えられる．近い将来，従来困難であった個々の患者の転移・再発状況に即した予後を予測することが可能になり，消化器癌の個性化医療の実践が期待される．

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研究テーマは, 消化器癌における OMICS 解析の臨床応用.

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RESEARCH ARTICLE

A simple and highly successful C-terminal sequence analysis of proteins by mass spectrometry

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A simple and efficient method for C-terminal sequencing of proteins has long been pursued because it would provide substantial information for identifying the covalent structure, including post-translational modifications. However, there are still significant impediments to both direct sequencing from C termini of proteins and specific isolation of C-terminal peptides from proteins. We describe here a highly successful, *de novo* C-terminal sequencing method of proteins by employing succinimidyloxycarbonylmethyl tris (2,4,6-trimethoxyphenyl) phosphonium bromide and mass spectrometry.

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C-terminal peptide / Isolation / Mass spectrometry / Post-translational modification / Sequencing

1 Introduction

Determining amino acid sequences of proteins, including their PTM, is important in life sciences because the covalent structures themselves are responsible for the functions of individual proteins in living systems. MS has emerged as a key technology for determining the covalent structures of proteins, and two approaches based on MS, categorized as "top-down" and "bottom-up", have been developed [1]. The former approach is more attractive [2, 3] because a particular series of fragment ions from the N and C terminus of an intact protein is obtained with high sensitivity and accuracy, by which its amino acid sequence, including PTM, is directly read out. However, it is still difficult to effectively dissociate large proteins into a series of fragment ions for sequencing, although sophisticated analyzers such as FT-ICR and orbitrap mass spectrometers have been developed. Therefore, the latter approach is generally used to determine the covalent structures of proteins [4]. It involves two steps: (i) determination of the molecular weight of the target protein as accurately as possible, (ii) structural analyses by PMF and/or MS/MS, utilizing information from genome and protein databases. These analyses are very useful, but they often fail to identify post-translationally modified residues, or to detect sequence polymorphisms observed in various protein isoforms. This is because sequence coverage by PMF is usually less than 60% and protein databases are still insufficiently comprehensive to effectively search for any protein from the various creatures on the Earth. Therefore, it is necessary to determine the complete covalent structures of proteins by orthogonal methodologies. The addition of information from N- and C-terminal sequencing of proteins into databases is practically significant and is expected to maximize the chance of identifying sequence variants [5]. In line with this expectation, several methods for N-terminal [6–8] and C-terminal [9, 10] sequence analyses by MS have been reported, and we have proposed that this scientific category be called "terminal proteomics" [11].

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Abbreviations: **DITC**, *p*-phenylenediisothiocyanate; **LysC**, lysyl endopeptidase; **Pfu**, *Pyrococcus furiosus;* **RPA**, replication protein A; **TCEP**, tris (2-carboxyethyl) phosphine hydrochloride; **TMPP-Ac-OSu**, succinimidyloxycarbonylmethyl tris (2,4,6-trimethoxyphenyl) phosphonium bromide

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The development of a simple and highly successful method for C-terminal sequencing by MS has particularly been a growing need for a long time.

This paper describes selective recovery and *de novo* sequencing of C-terminal fragments of proteins of interest. The method is based on highly specific modification of the α-amino group of peptides for attaching a positively charged group in a pool of lysyl endopeptidase (LysC) digest of proteins, and scavenging peptides having a free amino group for isolating the desired C-terminal fragment that does not contain a free amino group.

2 Materials and methods

2.1 Materials

Chicken ovalbumin, chicken lysozyme, bovine α-casein, horse cytochrome *c*, and iodoacetamide were obtained from Sigma (St. Louis, MO). Tris (2-carboxyethyl) phosphine hydrochloride (TCEP) and succinimidyloxycarbonylmethyl tris (2,4,6-trimethoxyphenyl) phosphonium bromide (TMPP-Ac-OSu) were obtained from Fluka (Switzerland). LysC, sodium hydrogen carbonate ($NaHCO_3$), ACN, 2-propanol and TFA were purchased from Wako Pure Chemical Industries, (Osaka, Japan). CHCA (high-purity mass-spectrometric grade) was obtained from Shimadzu GLC (Tokyo, Japan). Four peptides (RKRSAE, AAKIQASFRGMHARKK, TRDIYETDYYRK, and MHRQETVDCLK-NH2) were from AnaSpec (San Jose, CA). A peptide (GFETVPEG-NH_2) was synthesized in house using Shimadzu peptide synthesizer PSSM-8 by the Fmoc strategy. A recombinant of replication protein A (RPA) complex from the hyperthermophilic archaeon, *Pyrococcus furiosus* (Pfu) (PfuRPA; 1.54 mg/mL solution containing 50 mM Tris-HCl, 0.4 M NaCl, 0.5 mM DTT, 0.1 mM EDTA, and 10% glycerol) was provided by Professor Ishino (Kyushu University). *p*-Phenylenediisothiocyanate (DITC) resin used in this study was obtained from Shimadzu Corporation (Kyoto, Japan) as an item packaged in an ORFinder-NB Mass Sequencing Kit. Water used in all experiments was purified using a Milli Q water Purification System. All other chemicals were of analytical reagent grade and were used without further purification.

2.2 Methods

2.2.1 General protocol

One hundred micrograms of sample protein was dissolved in 23 μL of 8 M urea-50 mM $NaHCO_3$. To the solution was added TCEP solution (1 μL; 0.1 μmol/μL) and incubated for 1 h at 37°C, followed by addition of iodoacetamide solution (1 μL; 0.3 μmol/μL, 1-h incubation at room temperature). To this solution was added LysC solution (10 μg in 250 μL of ACN-50 mM $NaHCO_3$; 1:9), and this was left standing for 15 h at 37°C. An aliquot corresponding to 10 pmol of protein was taken from the digest solution and diluted to 10 μL with 50 mM $NaHCO_3$. To this diluted solution was added 3 μL of 1 mM TMPP-Ac-OSu [12] solution (ACN-water; 1:4), followed by sonication in a water bath for 30 min. DITC resin (5 mg) was pre-washed with 20% ACN solution (60 μL; three times) and 50 mM $NaHCO_3$ (60 μL; three times). To the washed resin the TMPP modified solution was added, which was allowed to stand for 2 h in a water bath at 60°C. The extraction was carried out using ACN-50 mM $NaHCO_3$ (1:9, 60 μL; twice) and 2-propanol-acetonitrile-0.1%TFA (1:1:2, 60 μL; three times). The extracts were combined and dried in a vacuum centrifuge.

2.2.2 General protocol for proteins on gel slices

A sample protein (30 pmol) was separated by SDS-PAGE in a 12.5% acrylamide gel. The Coomassie-stained protein band was excised and washed with 50% v/v ACN in 100 mM $NaHCO_3$. The washed gel piece was dehydrated with ACN and dried in a vacuum centrifuge. To the dried gel 100 μL of 10 mM aqueous TCEP solution was added to reduce disulfide bonds. This solution was incubated for 30 min at 37°C. S-alkylation was accomplished by replacing the TCEP solution with 55 mM iodoacetamide in 100 mM $NaHCO_3$. After a 45-min incubation at room temperature in the dark, the gel piece was washed with 100 μL of 50 mM $NaHCO_3$, shrunk by dehydration in ACN, and dried in a vacuum centrifuge. The gel piece was then rehydrated with 2 μL of ACN-50 mM $NaHCO_3$ (1:9) containing 200 ng of LysC. After 5 min, 50 mM of $NaHCO_3$ solution (15 μL) was added to keep the gel piece moist during digestion (37°C, overnight). To extract the resulting peptides, 30 μL of 50% ACN containing 0.05% TFA was added to the digestion mixture, and the gel piece was sonicated in a water bath for 10 min, after which the supernatant was collected. This extraction procedure was repeated three times. The extract was combined and lyophilized. The resulting powder was dissolved with 10 μL of ACN-50 mM $NaHCO_3$ (1:9). To this solution 1 μL of TMPP-Ac-OSu solution (10 mM in ACN-water, 1:4) was added and the mixture was sonicated in a water bath for 30 min. The TMPP-modified solution was added to the pre-washed DITC resin (described above), and this was allowed to stand for 2 h in a water bath at 60°C. The extraction was done using ACN-50 mM $NaHCO_3$ (1:9, 60 μL; twice) and 2-propanol-ACN-0.1%TFA (1:1:2, 60 μL; three times). The extracts were combined and dried in a vacuum centrifuge.

2.2.3 MALDI-TOF MS

MALDI mass spectra were recorded on AXIMA CFR-plus and AXIMA TOF^2 (SHIMADZU/KRATOS, Manchester, UK) reflectron TOF mass spectrometers equipped with a nitrogen laser (337 nm, 3-ns pulse width). All measurements were performed in positive-ion reflectron mode. The ion acceleration voltage was set to 20 kV, and the reflectron detector was operated at 24 kV. The flight path in the reflectron mode is

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about 240 cm for both types of instruments. For MS/MS experiments, CID was carried out using helium at a pressure of *ca.* 5×10^{-6} mbar in the collision cell.

CHCA was used as a matrix, which was dissolved to saturation in 50% aqueous ACN containing 0.05% TFA. A portion (0.5 μL) of sample solution was mixed with an equivalent volume of matrix solution on the MALDI target plate and analyzed after drying. A double layer protocol [12] was used for TMPP-Ac peptides. The *m/z* values in spectra were externally calibrated with angiotensin II (human) and ACTH fragment 18–39 (human) using CHCA as a matrix.

3 Results and discussion

Our project for terminal sequencing of protein has set the goal on both of isolation and *de novo* sequencing of N- [8, 13] and C-terminal peptides [14, 15] by MS. In the course of the study, we found that TMPP-Ac-OSu [12] exhibited selectivity exclusively for the α-amino group, which was more than expected. Furthermore, because side reactions were described but were not actually seen in mass analysis, we thought of using this selective tagging agent for LysC digest of protein, and amino-reactive group immobilized material. Hence, we tried DITC resin as a scavenger of peptides having free amino group(s), which in turn afforded good recovery of peptides devoid of amino group(s).

A technique using the combination of LysC and DITC resin for isolating C-terminal peptide was reported almost two decades ago [16]. In the method, the sequence determination of an isolated C-terminal peptide was carried out by Edman method (not by MS) after cleavage of the peptide from the resin with use of hazardous conc. TFA. Therefore, compared with the present method, some drawbacks in the technique can be pointed out as follows: (i) sequence analysis by Edman reaction remains ambiguous for identifying several amino acids as Ser, Thr etc. and post-translationally modified residues, (ii) low yield of PTH-amino acid adjacent to the C terminus leads to difficulty for complete sequence analysis, (iii) mixture sample can not be analyzed without further fractionation of isolated C-terminal peptide, and (iv) C-terminal determination is not possible if the peptide consists of only one amino acid. With this in mind, we set out to the investigation of selective isolation of C-terminal peptides and their *de novo* sequencing with combinational use of an α-amino group selective modifying reagent (TMPP-Ac-OSu) and MS.

Before describing the results, we will present the outline of our method in Fig. 1. First, the protein of interest is digested with LysC to yield peptides that have amino groups at both ends, but a C-terminal peptide has only the α-amino group in it. If a protein is N-terminally blocked by any PTM, the N-terminal peptide has only the ε-amino group. The next step is TMPP-Ac derivatization with TMPP-Ac-OSu to produce TMPP-Ac peptides. These peptides are selectively modified at the α-amino group (not at the ε-amino group on the lysine residue). Hence, the resultant modified peptides have free amino groups at their lysine residue, but the C-terminal peptide itself has no free amino group left. In the final step, peptides with free amino groups are attached covalently to the DITC resin, and the C-terminal peptide thus recovered in the supernatant solution is subjected to *de novo* sequencing analysis by MALDI-MS.

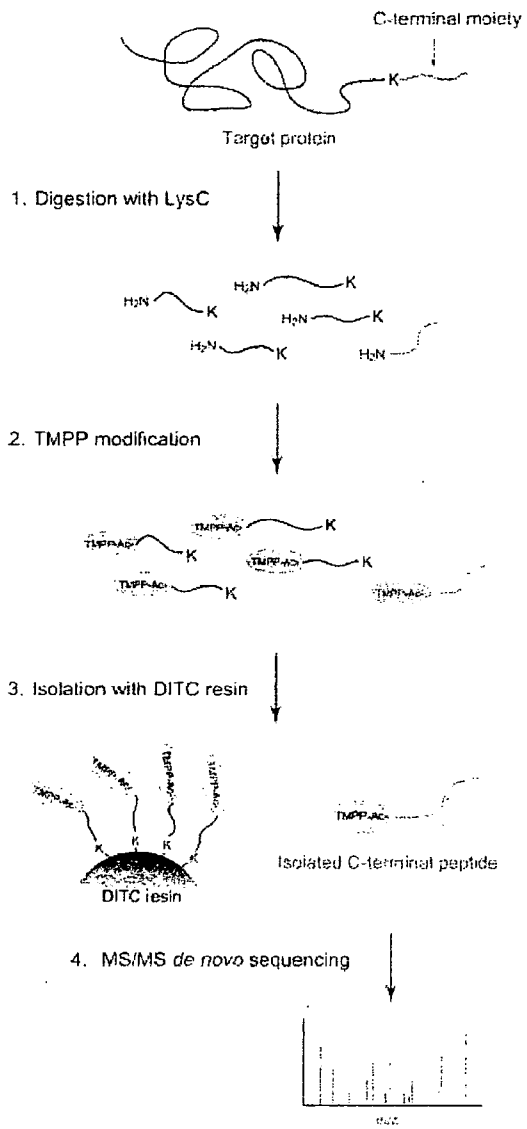

Figure 1. Schematic overview of the method. A protein is first digested with LysC to yield peptides incorporating amino groups at both ends but the C-terminal peptide contains only an α-amino group. This is followed by selective attachment of the TMPP-Ac moiety to α-amino groups, and isolation of the C-terminal peptide using a DITC resin.

The results obtained are described using (i) model peptides, (ii) model proteins, and (iii) a recombinant protein (PfuRPA).

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3.1 Model peptides

To demonstrate the usefulness of the method, we tried this strategy using model peptides. Five peptides were used for a model peptide mixture (1) RKRSRAE (*m/z* 901.5), (2) GFETVPETG-NH_2 (*m/z* 934.4), (3) MHRQETVDCLK-NH_2 (*m/z* 1357.7), (4) TRDIYETDYYRK (*m/z* 1621.8), and (5) AAKIQASFRGHMARKK (*m/z* 1799.0). Peptide (2) is devoid of lysine residue and thus has only one amino group at its N terminus. It was expected that peptide (2) would be isolated after treatment with DITC resin. Fifty microliters of equimolar solution of these five peptides (2 pmol/μL each) was prepared, and to this solution was added TMPP-Ac-OSu solution (5 μL of 1 mM solution in ACN-water, 1:4). The solution was then sonicated in a water bath for 30 min. An aliquot (4 μL) was taken and treated with DITC resin for 2 h at 60°C. Figure 2 presents the MALDI-MS spectra of the equimolar mixture of the five peptides before and after TMPP

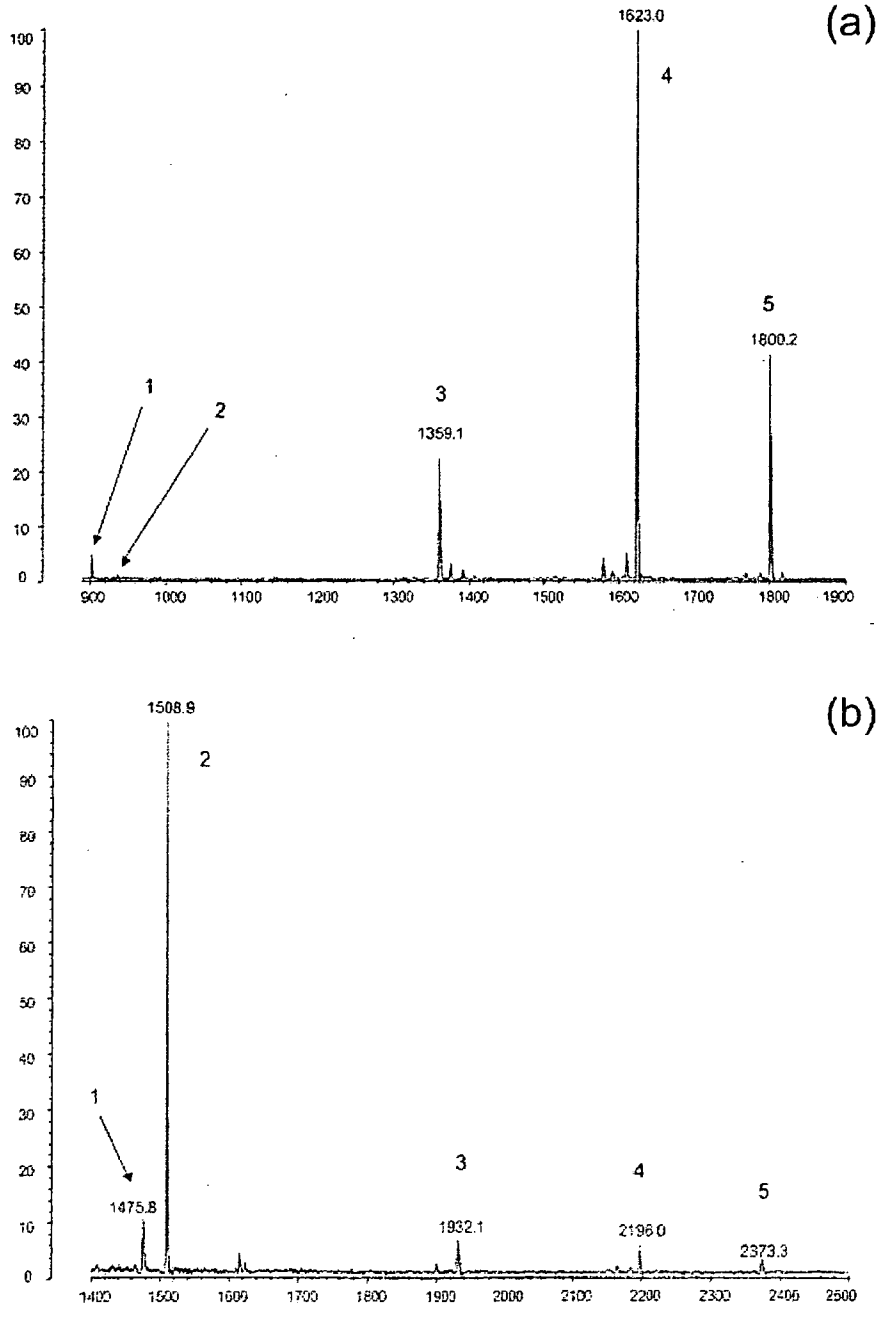

Figure 2. MALDI-TOF mass spectra before and after TMPP-Ac modification of the mixture of five model peptides. The five peptides are as follows: (1) RKRSRAE (*m/z* 901.5); (2) GFETVPETG-NH_2 (*m/z* 934.4); (3) MHRQETVDCLK-NH_2 (*m/z* 1357.7); (4) TRDIYETDYYRK (*m/z* 1621.8); (5) AAKIQASFRG—HMARKK (*m/z* 1799.0). Panel (a) shows the spectrum before TMPP-Ac modification, while (b) shows the signals of TMPP modified peptides after TMPP-Ac modification. The x-axis and y-axis represent *m/z* and % intensity, respectively, for all mass spectra.

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