

Toward this goal, we have recently collected human specimens of right atrial myocytes from patients with various heart disorders, and obtained the expression profiles of >12,000 genes in the samples by using high-density oligonucleotide microarrays (R.O. et al., submitted). Since the patients in the analysis could be classified into two major groups, i.e., individuals with either normal sinus rhythm or an arrhythmia, chronic atrial fibrillation (Af), we first tried to identify gene sets, expression of which were associated with the presence/absence of chronic Af in vivo. A total of 33 genes were shown to be induced (>1.5-fold) in Af samples compared to those with normal sinus rhythm, while 63 genes were to be suppressed (<0.5-fold) in the Af-ones.

However, such analyses did not fully address a fundamental question as to whether atrial myocytes with Af have a distinct gene expression profile, or “molecular signature” [3], to those with normal sinus rhythm. In other words, with regard to gene expression profiles, are the myocytes with Af distinct from those with normal rhythm?

In this paper, by applying sophisticated statistical methods, we have tried to address these issues. Furthermore, we here tested whether it was possible to identify gene sets, expression level of which was precisely correlated with detailed clinical parameter values of cardiac function. The results were highly successful, and we could even construct “prediction formulae for the values of left ventricular ejection fraction (EF)” based on the expression level of selected genes. To our best knowledge, this is the first report to prove that pumping ability of heart can be predicted by any measures of atrium.

Materials and methods

Microarray analysis. Detailed information on the patients registered for this study and on the microarray experiments will be reported elsewhere (R.O. et al., submitted). Left ventricular EF values in all patients was calculated by dividing the stroke volume (end-diastolic volume minus end-systolic volume) by the end-diastolic volume (both obtained angiographically). From the patients who underwent cardiac surgery in Jichi Medical School, right atrial appendages were obtained with written informed consent. Total RNA was extracted from the specimens with the use of RNazol B (Tel-Test, Friendswood, TX), and a portion (20 µg) of the RNA was converted to double-stranded cDNA by the SuperScript Choice System (Life Technologies, Gaithersburg, MD). Biotin-labeled cRNA was prepared from the resulting cDNA with the use of ENZO BioArray RNA labeling kit (ENZO Diagnostics, Farmingdale, NY), and hybridized with the GeneChip Human U95Av2 array (Affymetrix, Santa Clara, CA) harboring the oligonucleotides corresponding to >12,000 human genes. Detection of the hybridized cRNAs was performed with the GeneChip instrument system according to the manufacturer’s protocol. The fluorescence intensity of each gene was normalized relative to the median fluorescence value for all genes in each array hybridization.

Statistical analysis. In the comparison of normal sinus rhythm- vs Af-specimens, *t* statistic and the effect size (difference in the mean of expression levels between the two classes) [4] were calculated for each gene. When the gene showed $|t| > 4.073$ (corresponding to a significance level of 0.001 in *t* test with 15 degrees of freedom) and $|\text{effect size}| > 0.5$

arbitrary units (U), the difference in expression level between the two classes was regarded as statistically significant. Correspondence analysis [5] was carried out for all genes showing the significant difference by using the ViSta computer software (<http://www.visualstats.org/>). Each sample was plotted in three dimensions based on the coordinates of the three major dimensions from correspondence analysis.

To examine whether these informative genes could predict the class of the present samples, we have here developed a novel class prediction means, “weighted-distance method,” with the points of dimensions obtained from correspondence analysis. There were a total of 17 samples: 10 specimens with sinus rhythm and 7 with Af arrhythmia. A correspondence analysis was conducted once for all 17 samples, and the class prediction was performed for each sample (say sample *X*) under the condition that the classes of only remaining 16 samples were known. The weighted distance from sample *X* to sample *Y* ($Y \neq X$) is defined as $D = \sqrt{\sum_{i=1}^k [v_i(d_i^X - d_i^Y)^2]}$, where *k* is the number of dimensions to be considered, *v_i* indicates the contribution of the *i*th dimension, and *d_i^X* and *d_i^Y* represent points of the *i*th dimension for sample *X* and sample *Y*, respectively. Because *v₁* exceeded 70% in our analysis (i.e., the cumulative contribution to the 1st dimension was very large), *k* was set to be 1 in this study (i.e., $D = \sqrt{v_1(d_1^X - d_1^Y)^2}$). In general, *k* should be determined by the cumulative contribution to the *k*th dimension. Let *D_S* and *D_A* be the averages of weighted distance (*D*) from sample *X* to sinus rhythm samples and from sample *X* to the Af samples, respectively. When $D_S/(D_S + D_A)$ was below a threshold value, *T*, the sample *X* was assigned a “sinus rhythm” class, and when $D_A/(D_S + D_A)$ was below *T*, the sample *X* was assigned an “Af” one. In this study, *T* was set to be 0.4.

Correlation to the clinical grade of tricuspid valve regurgitation (TR) or mitral valve regurgitation (MR) was calculated for the expression level of each gene by a paired Spearman’s rank test, and was considered as statistically significant when $P < 0.001$. Similarly, Pearson’s correlation coefficient (*r*) for EF (in percents) or left atrial diameter (LAD) (in millimeters) was examined for the expression level of each gene.

For each of the EF-linked genes identified above, we conducted the simple regression analysis to generate an EF-calculation formula “ $y = Ax + B$,” where *y* is EF (%) and *x* is the expression level (U) of each gene.

All raw microarray data as well as the details of the genes shown in the figures are available as supplementary information at the web site of *Biochem. Biophys. Res. Commun.*

Real-time reverse transcription-polymerase chain reaction (RT-PCR). Portions of nonamplified cDNA were subjected to PCR with a QuantiTect SYBR Green PCR Kit (Qiagen, Valencia, CA). The amplification protocol comprised incubations at 94 °C for 15 s, 60 °C for 30 s, and 72 °C for 60 s. Incorporation of the SYBR Green dye into PCR products was monitored in real time with an ABI PRISM 7700 sequence detection system (PE Applied Biosystems, Foster City, CA), thereby allowing determination of the threshold cycle (*C_T*) at which exponential amplification of PCR products begins. The *C_T* values for cDNAs corresponding to the glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) and *Calpactin I* genes were used to calculate the abundance of *Calpactin I* mRNA relative to that of *GAPDH* mRNA. The oligonucleotide primers for PCR were 5′-GTCAGTGGTG GACCTGACCT-3′ and 5′-TGAGCTTGACAAAGTGG TCG-3′ for *GAPDH* cDNA and 5′-TCTGGCTGTGGACAAAATAATG-3′ and 5′-TTCCCTTCTGCTTCATGTGTA-3′ for *Calpactin I* cDNA.

Results

Isolation of genes linked to arrhythmia

Among the 17 samples analyzed, 7 were obtained from the patients with chronic, persistent Af and the rest

Table 1
Characteristics of the study subjects

Patient ID	Age	Sex	Disease	MR grade	TR grade	LAD (mm)	Rhythm	EF (%)
1	44	M	AR	0	1	39.7	Sinus	49
2	70	F	MR	3	1	50.1	Sinus	48
3	75	M	IHD	1	1	39	Sinus	61
4	65	M	AS	1	0	45.1	Sinus	71
5	60	M	AS	2	0	39.7	Sinus	33
6	51	F	MS	0	3	71	Af	78
7	55	M	MR	4	2	69.4	Af	55
9	64	M	MR	4	2	77	Af	68
10	74	F	MSR, ASR	3	2	61.1	Af	66
11	75	M	ASR, MR	3	2	59	Af	37
12	64	F	MR	3	3.5	48	Sinus	65
13	64	F	MR, AR	4	3.5	42	Sinus	80
14	14	M	ASD	0	2	32.1	Sinus	67
15	59	F	MS, AR	2	4	76.7	Af	70
16	69	F	MSR, AR	3	4	54	Af	57.5
17	63	M	AR, MR	2	3	52	Sinus	50
18	37	F	ASD	2	0	35	Sinus	60

M, male; F, female; AR, aortic regurgitation; IHD, ischemic heart disease; AS, aortic stenosis; MS, mitral stenosis; MSR, mitral stenosis/regurgitation; ASR, aortic stenosis/regurgitation; ASD, atrial septal defect.

10 were from those with normal sinus rhythm (Table 1). Identification of any genes constantly activated or inactivated in Af samples would shed new light on the pathophysiology of this most prevalent arrhythmia [6]. First, identified were the genes whose expression levels were statistically different (Student's *t* test, $P < 0.001$) between the two classes, i.e., normal sinus rhythm and Af. However, expression levels of many such genes were very low throughout the samples, making the reliability of "arrhythmia-dependence" obscure. Therefore, we further applied another "selection window" that the effect size should be $> 0.5U$ between the two classes, leading to the identification of 11 arrhythmia-dependent genes, expression profile of which should most effectively contrast Af status from normal sinus rhythm.

A dendrogram or "gene tree" is demonstrated in Fig. 1A for these genes including those encoding for sarcoglycan ϵ (SGCE; GenBank Accession No. NM_003919), zinc finger protein 103 (ZFP103; NM_005667), and hepatic leukemia factor (HLF; NM_002126). Here in the tree, genes with similar expression pattern across the samples were placed near each other. HLF is a helix-loop-helix type transcriptional factor that functions to protect cells from apoptosis [7]. Decreased expression of *HLF* in the myocytes with Af arrhythmia may reflect the apoptotic change found in atrial remodeling.

Expression profile-based prediction of Af

In the point of view of gene expression profile, are the myocytes with Af arrhythmia different from those with normal sinus rhythm, and, if so, how different? We tried to address this issue by the correspondence analysis to extract three major dimensions from the expression patterns of the 11 arrhythmia-dependent genes. By the cal-

culated coordinates for each sample in these dimensions, the patient samples were projected into the virtual space with the three dimensions. Surprisingly, as shown in Fig. 1B, all samples with Af were clustered in an area clearly far from that for the samples with sinus rhythm. It is, therefore, likely that all Af samples have a common "gene expression signature" which is distinct from that for sinus rhythm samples.

The clear separation of Af and sinus rhythm specimens in Fig. 1B also indicates a possibility of an expression profile-based prediction for Af. As demonstrated in Fig. 1B, class-separation was most prominent in the 1st dimension. Indeed, the contribution ratio of each dimension calculated by the correspondence analysis was 72.74%, 9.5%, and 6.29% for the 1st, 2nd, and 3rd dimensions, respectively. Therefore, we tried to conduct the class prediction (i.e., Af or sinus rhythm) for each sample by using the coordinates for the 1st dimension. The relative distance of a given sample to the Af or sinus rhythm group (excluding the sample for prediction) was calculated, and the sample was assigned a class when the relative distance to the class was ≤ 0.4 . As shown in Table 2, the class prediction based on the correspondence analysis with the 11 genes in Fig. 1A was successful for all cases.

To accurately measure the prediction power of our weighted distance method, we conducted a cross-validation trial (i.e., "drop-one-out" format) for the diagnosis of normal sinus rhythm or chronic Af class. To predict the class of sample *X*, "arrhythmia-associated genes" were extracted from the comparison of remaining 16 samples according to the criteria used in Fig. 1A ($P < 0.001$ in Student's *t* test, and $|\text{effect size}| > 0.5U$). Correspondence analysis was carried out for the expression profiles of the arrhythmia-associated genes, and

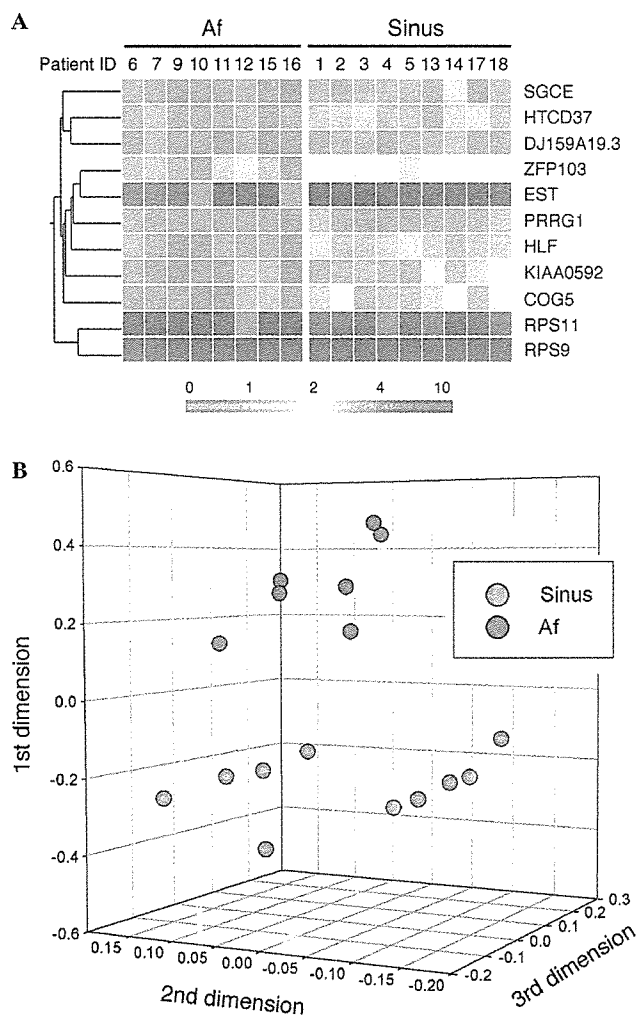


Fig. 1. Correspondence analysis of the data set for the differentiation between Af vs normal sinus rhythm. (A) The expression profiles of 11 arrhythmia-dependent genes are demonstrated as a dendrogram, shown color-coded as indicated by the scale at the bottom. Each column represents a separate patient sample as indicated by the ID number at the top, and each row corresponds to a single gene. The gene symbols are shown at the right. (B) The correspondence analysis of the arrhythmia-dependent genes has identified three major dimensions in their expression profiles. Projecting the samples into a virtual space with these three dimensions demonstrates that specimens of heart with normal sinus rhythm (Sinus) are placed apart from those with Af (Af).

was used to calculate the relative weighted distance of the “dropped” sample X to either normal sinus rhythm or Af class. A clinically matched prediction was obtained for 13 (76.5%) out of 17 cases (not shown). Therefore, even in a cross-validation assay, the weighted distance method could achieve a high accuracy.

Genes linked to the clinical grades of MR or TR

Given the efficient isolation of genes tightly linked to the occurrence of Af, our expression data set could be also used for the characterization of other clinical pa-

rameters of heart. For instance, echocardiographic studies can assess various aspects of cardiac function, such as the severity of TR, MR, and atrium dilation (as LAD), and the contraction ability of heart (as left ventricular EF).

We first tried to identify the genes whose expression level was linked to the stages of MR or TR. In the clinical settings, the severity of MR and TR is represented as widely accepted clinical grades, from normal “grade 0” to the highly damaged “grade 4” [8,9]. The MR or TR grade indicates the severity of volume-overload onto left or right atrium, respectively.

Spearman’s rank test has identified a total of nine genes, expression of which was significantly linked to the clinical grade of MR (Fig. 2A). All genes thus identified had a reverse correlation toward the grade of MR; in other words, expression of these genes became suppressed along with the stage progression of MR. Intriguingly, some protein products in the gene list had been shown to be directly involved in the regulation of apoptosis, such as the nucleoside diphosphate kinase type 6 (NM23-H6; GenBank Accession No. NM_005793), CUG triplet repeat RNA binding protein 2 (CUGBP2; NM_006561), and caspase-8- and FADD-like apoptosis regulator (CFLAR; NM_003879).

Similar statistical analysis has also identified a total of 37 genes, expression of which was significantly linked to the clinical grades of TR (Fig. 2B). Among them, the highest correlation coefficient (forward correlation) was found with the genes for general transcription factor IIIC, polypeptide 1, α (GTF3C1; GenBank Accession No. NM_001520), and thioredoxin 2 (TXN2; NM_012473), and the lowest coefficient (reverse correlation) was with those for general transcription factor IIA2 (GTF2A2; NM_004492) and NF-E2-like basic leucine zipper transcriptional activator (NFE2L2; NM_006164).

Genes linked to the LAD size

Next, among the clinical parameters for cardiac function, we searched for genes whose expression was significantly correlated to continuous variates, such as LAD or EF. Pearson’s correlation coefficient to the size of LAD was examined for the expression level of each gene, and we could identify a total of five genes with statistically significant correlation ($P < 0.001$) to LAD. In Fig. 3 demonstrated are the expression levels of such five genes among the samples as a dendrogram format. Expression of all these genes became suppressed as the size of LAD increased. Interestingly, one of such genes encodes for SGCE that links cytoskeleton proteins to extracellular matrix. SGCE is a member of dystrophin–glycoprotein complex which is essential in the stability of muscle fiber membrane [10]. Mutations in the SGCE gene are responsible for the familial myoclonus–dystonia syndrome [11]. Loss of expression in SGCE may thus be involved in the

Table 2
Prediction of arrhythmia by the weighted-distance method

Patient ID	Clinical diagnosis	Distance to normal sinus rhythm	Distance to Af	Prediction
1	Sinus	0.144	0.856	Sinus
2	Sinus	0.128	0.872	Sinus
3	Sinus	0.125	0.875	Sinus
4	Sinus	0.139	0.861	Sinus
5	Sinus	0.205	0.795	Sinus
6	Af	0.731	0.269	Af
7	Af	0.834	0.166	Af
9	Af	0.840	0.160	Af
10	Af	0.786	0.214	Af
11	Af	0.839	0.161	Af
12	Sinus	0.132	0.868	Sinus
13	Sinus	0.153	0.847	Sinus
14	Sinus	0.289	0.711	Sinus
15	Af	0.668	0.332	Af
16	Af	0.802	0.198	Af
17	Sinus	0.127	0.873	Sinus
18	Sinus	0.250	0.750	Sinus

The relative weighted-distance to the normal sinus rhythm group or to the Af group was calculated as $D_S/(D_S + D_A)$ or $D_A/(D_S + D_A)$, respectively (see Materials and methods).

injured muscle integrity in dilated left atrium. It should be noted that expression of *SGCE* was also linked to the presence/absence of Af (Fig. 1A). Therefore, activation of *SGCE* gene may reflect the pathological changes associated with atrial remodeling.

Calculation of EF values by gene expression profiles

One of our goals in this study was to test the possibility of profile-based prediction of cardiac pump function or patients' prognosis. There have been no reports for such investigation, and it is yet unclear to what extent atrial myocytes reflect the overall function of heart.

To address these issues, here we have tried to calculate the exact digits of left ventricular EF (in percents) from the gene expression profiles in right atrium myocytes. First, Pearson's correlation coefficient to EF was calculated for each gene, and we could isolate 15 genes whose expression was correlated to EF ($P < 0.001$) (Fig. 4A). Among them, only the expression of fragile histidine triad gene (FHIT; GenBank Accession No. NM_002012) was induced along with the increase of EF, while the expression of the rest genes had a reverse correlation to the EF level.

A simple regression analysis was applied to these 15 EF-linked genes, constructing for each gene an EF-calculation formula, " $y = Ax + B$," where " y " is EF (%) and " x " is the expression level (U) of each gene. In Table 3 shown are the resultant calculation formulae that gave the lowest P values for the coefficient "A." The EF-calculation ability of the expression levels in these four genes was highly potent, indicating that the "gene expression signature" of right atrial muscle cells reflects the character of left ventricular myocytes, at least, with

regard to the pumping function. To demonstrate the accuracy of the calculated EF by the formulae, clinically observed EF and the calculated one by each formula were compared in a graph (Fig. 4B). It was to us surprising that such first-degree formulae with a single variate based on the expression intensities of the genes could predict precisely the exact digits of EF. Therefore, these four genes may not only be the molecular markers for cardiac pump function, but also be directly involved in the molecular pathology of heart failure.

We have also tried the multiple regression analysis to calculate a multivariate formula with a better prediction power than that by the simple regression analysis. However, the P values for any multivariate formulae were larger than the P values listed in Table 3. Therefore, transcription of the four genes in Table 3 may be under the regulation of common mechanisms.

To confirm the reliability of such EF-calculation approach, we set aside, from the calculation, three "test" samples, ID#5 (with the lowest EF value), ID#16 (with the 7th lowest EF value), and ID#9 (with the 13th lowest EF value), and obtained a set of genes whose expression level correlated with the EF values for the remaining 14 "training" samples (data not shown). Regression analysis was applied to such genes including one for S100A10 (GenBank Accession No. AI201310), generating an EF-calculation formula ($y = -10.017x + 80.327$, $P = 0.0127$) for the S100A10 mRNA level. With this formula, the EF values were then predicted for the test samples. The EF value (33%) for the ID#5 was predicted to be 39.7%, 57.5% for ID#16 was predicted to be 60.6%, and 68% for ID#9 was to be 66.0%. Similarly, regression analysis was conducted on another EF-related gene in the training samples, that for OSF-4 (GenBank

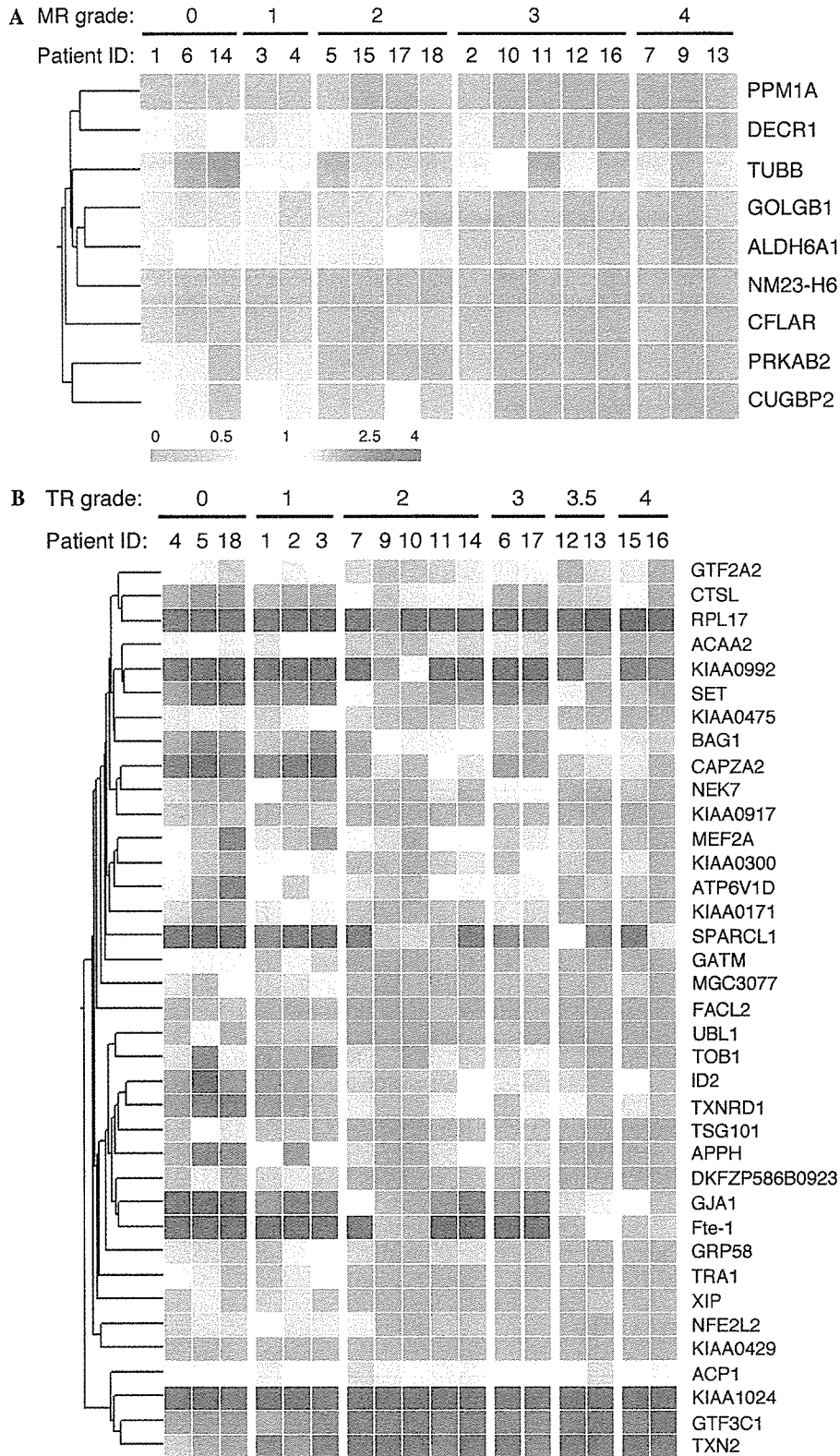


Fig. 2. Genes related to the clinical grades of MR and TR. (A) A dendrogram indicates the expression profiles of nine genes, expression of which was significantly linked to the clinical grade of MR. Each column represents a separate patient sample as indicated by the ID number at the top, and each row corresponds to a single gene. Expression level of each gene in given sample is shown color-coded as indicated by the scale at the bottom. (B) Expression profiles of 37 TR-dependent genes are demonstrated as in (A).

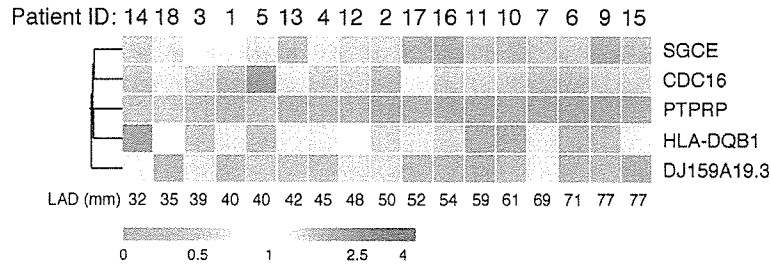


Fig. 3. Genes linked to the LAD size. Expression levels of five genes with statistically significant correlation ($P < 0.001$) to the LAD size are indicated as a dendrogram as in Fig. 2A. The patient ID and its corresponding LAD size (in millimeters) are indicated at the top and the bottom, respectively.

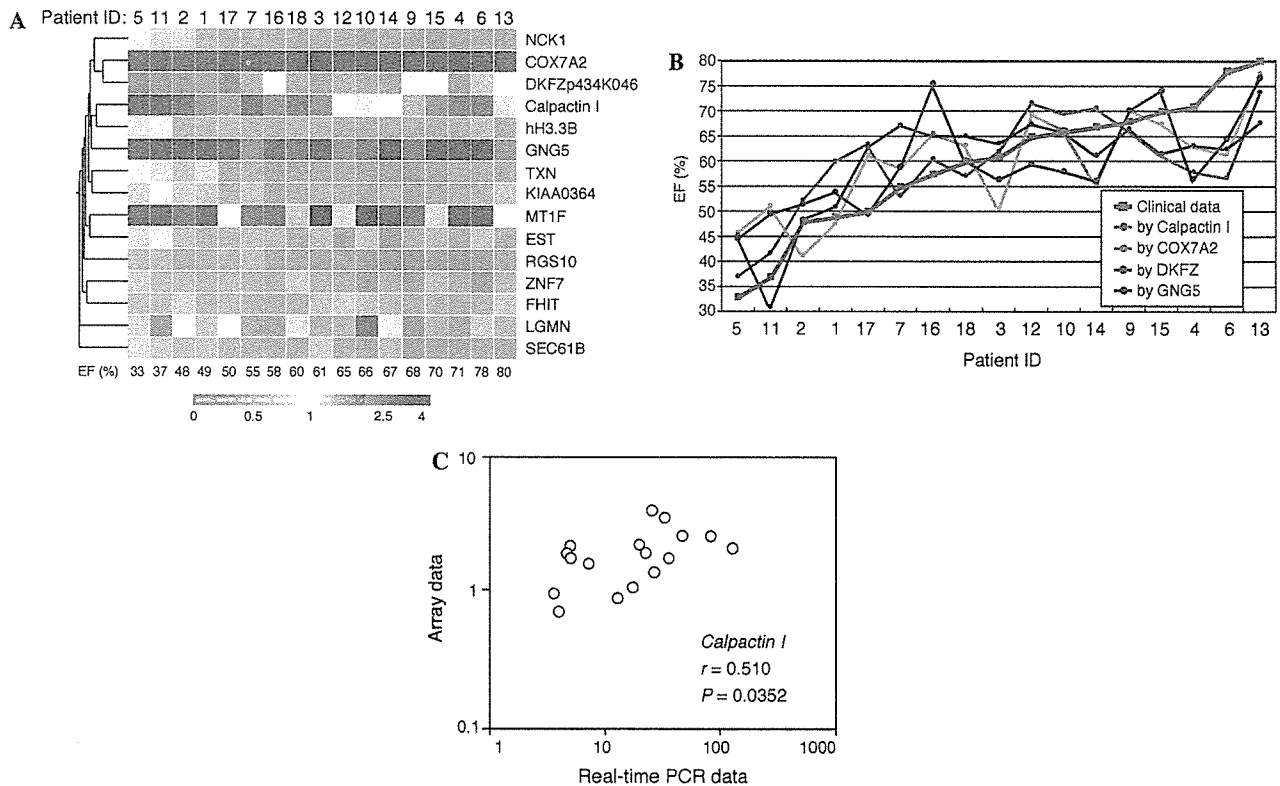


Fig. 4. Prediction of EF values by gene expression intensities. (A) Expression levels of 15 genes with statistically significant correlation ($P < 0.001$) to the EF values are indicated as a dendrogram as in Fig. 2A. The patient ID and its corresponding EF value (in percents) are indicated at the top and the bottom, respectively. (B) The clinically observed EF values are compared with the predicted ones by the expression levels of four genes including that for DKFZp434K046 (DKFZ). Samples are sorted according to the clinically observed EF values. (C) Expression levels of Calpactin I mRNA are compared between the normalized microarray data and the normalized real-time RT-PCR data. Pearson's correlation coefficient (r) between the two data sets was 0.510, and this correlation was statistically significant ($P = 0.0352$).

Table 3
Prediction of EF on the basis of gene expression levels

Gene	GenBank Accession No.	Prediction formula	P value for prediction
Calpactin I	A1201310	$y = -11.18x + 82.03$	0.0005
COX7A2	AA978033	$y = -1.75x + 91.12$	0.0006
DKFZP434K046	AC004382	$y = -27.58x + 99.94$	0.001
GNG5	A1541042	$y = -4.03x + 74.99$	0.0004

y represents EF (%) and x represents gene expression level (U).

Accession No. D21254). The prediction of the EF values by the OSF-4 expression level was again significantly accurate; 29.8%, 66.0%, and 71.9% for ID#5, ID#16, and

ID#9, respectively. These data imply that left ventricular function can be predicted at a substantial accuracy by measures of right atrium.

Reliability of our gene expression data was confirmed by another mRNA quantitation method, real-time RT-PCR. The relative expression levels of *Calpactin I* to that of *GAPDH* were, for instance, calculated by real-time RT-PCR analysis, and were compared with the normalized expression intensities of *Calpactin I* in the microarray data (Fig. 4C). The correlation coefficient between the two data sets was 0.510, and this correlation was statistically significant ($P=0.0352$). Similar quantitation was also conducted on other genes including those for ribosomal protein L17 (*RPL17* in Fig. 2B; GenBank Accession No. X53777) ($r=0.68$, $P=0.003$), 90kDa heat-shock protein (*HSPCA*; X15183) ($r=0.613$, $P=0.009$), and high mobility group protein 14 (*HMGNI*; J02621) ($r=0.444$, $P=0.074$).

Discussion

In this paper, with human atrial myocytes as a test case, we have tried to address whether large scale expression profiling can identify genes whose expression level is closely associated with various clinical parameters of disorders. As demonstrated in the paper, the results with an extensive statistical analysis were surprisingly informative.

We could isolate, for instance, a total of 11 genes that were regulated in a dependent manner to the presence of chronic Af arrhythmia (Fig. 1A), and that were highly potent to differentiate heart specimens with normal sinus rhythm from those with Af (Fig. 1B and Table 2). The clear separation of these two classes in a virtual space argues that protein products of these Af-dependent genes may function in the pathogenesis and/or maintenance of Af. Many genes in this list are yet only known to encode hypothetical proteins, such as HTCD37 (GenBank Accession No. AI829890), DJ159A19.3 (NM_015699), KIAA0592 (AB011164), and an EST (W28612).

A number of genes have been reported to be involved in the maintenance of Af and heart remodeling [12], including those encoding L-type Ca^{2+} channels, potassium channels, Connexins, and proteolytic enzymes (such as Calpain I). In our data set, however, we could not detect dependent changes in the expression levels of the genes for a voltage-gated potassium channel Kv11 or calcium channel proteins. The genes for other potassium channels and Calpain I were not included on the Affymetrix HGU95Av2 array.

Severe MR often induces volume-overload onto left atrium. It is still unknown to what extent such stress on left atrium affects the gene expression in right atrial myocytes. It was therefore interesting to find a number of apoptosis-related genes in the “MR-dependent” gene list (Fig. 2A). CFLAR, for instance, binds to and inhibits the activity of, caspase-8, or FLICE, and thereby protects cells from apoptotic changes [13]. CUGBP2 or

NAPOR, a binding protein to CUG repeats, is known to regulate splicing mechanism of RNAs, and the *CUGBP2* message is induced during apoptosis [14]. Intriguingly, *CUGBP2* is a candidate gene whose product is responsible for heart developmental defects observed in the patients with monosomy 10p [15]. NM23-H6 functions as a nucleoside diphosphate kinase and is involved in a wide range of cell signaling. It is localized in mitochondria, and overexpression of this kinase results in growth suppression and cell cycle arrest [16]. Loss of expression of these genes may, therefore, play a role in the apoptotic changes found in the enlarged atrium associated with MR.

Apoptosis-related genes were again found in the TR-related gene list (Fig. 2B). Bcl2-associated athanogene 1 (*BAG1*) binds to and enhances the anti-apoptotic activity of BCL-2 [17]. Thioredoxin reductase 1 (*TXNRD1*; GenBank Accession No. NM_003330) functions in detoxification within cells by its reducing activities and also helps to prevent cells from apoptosis.

Finally, we have tried to construct “EF-calculation formulae” based on the expression level of EF-linked genes. In the analysis of the whole samples, a total of four such genes were used, including those for Calpactin I or S100A10, cytochrome *c* oxidase subunit VIIa polypeptide 2 (*COX7A2*; AA978033), guanine nucleotide binding protein $\gamma 5$ (*GNG5*; AI541042), and a hypothetical protein (DKFZp434K046; AC004382). Given the very high prediction ability of these genes (Table 3), expression levels of them (and their products) may be important determinants of cardiac pump function.

Calpactin I is an intracellular protein that binds to and regulates the activity of Annexin II [18], a well-known substrate of Src protein-tyrosine kinase. Although the in vivo function of Calpactin I is still obscure, a recent report indicates the Calpactin I regulation of a sodium ion channel, NaV1.8 [19]. *GNG5* is a γ subunit of heterotrimeric G proteins and should function to transduce upstream signals from cell surface receptor proteins [20]. Heterotrimeric G proteins play pivotal roles in the signal transduction mechanism of soluble reagents that regulate cardiac functions, such as catecholamines, endothelins, and angiotensins. Given the fact that overexpression of certain types of heterotrimeric G proteins induces cardiac hypertrophy in vivo [21], *GNG5*-driven intracellular signals may also directly participate in the regulation of myocyte contraction. It would be an intriguing question as to which cell surface receptors work in concert with *GNG5*.

Parts of atrial appendages are routinely removed in a wide array of heart surgery. Therefore, it would be intriguing if these removed samples can “tell” pathophysiological status of not only atrium but of whole heart. Our data analysis has proved that the transcriptome of right atrium provides a wealth of information in this aspect, probably more so than people had expected.

Further validation of the in vivo functions for the genes thus identified would shed a new light on the molecular pathology of heart failure. In addition, our statistical approach should be applicable not only to the investigation of heart functions, but to that of a wide variety of human disorders. Gene expression profiling is likely a very potent means to assess the detailed clinical parameters.

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Transcriptional profile of genes induced in human atrial myocardium with pressure overload

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Abstract

Background: The molecular response of human myocardium to mechanical stimuli, particularly the difference between pressure or volume overload cardiac hypertrophy, remains incompletely defined. **Methods:** We investigated the transcriptional profile of genes induced in human pressure- or volume-overloaded myocardium with DNA microarray technology. We used right atrial tissue from patients who underwent cardiac surgery. On the basis of pressure data and echocardiographic findings, the patients were divided into three groups: control group ($n=3$), pressure overload group (mean right atrial pressure of >7 mm Hg, $n=3$), and volume overload group (moderate or severe tricuspid regurgitation, $n=3$). Expression profiles of 2139 human genes were investigated with mRNA obtained from the samples. **Results:** In the pressure overload group, expression of genes of cyclin-dependent kinase inhibitor 1A (CDKI1A, 11.7 ± 3.1 -fold vs. control), and mitogen-activated protein kinase phosphatase-1 (MKP-1, 26.2 ± 2.1 -fold) was significantly increased compared with those in control or volume overload group ($P < 0.05$). The specificity of these gene expressions was confirmed by a quantitative “real-time” polymerase chain reaction (PCR) analysis. In addition, mechanical strain induced CDKI1A and MKP-1 protein expressions in neonatal rat cardiac myocytes in an amplitude-dependent manner. In contrast, transcripts of growth factors did not significantly increase. **Conclusions:** This study demonstrated that gene expressions of CDKI1A and MKP-1, but not growth factors, are induced in chronic pressure-overloaded myocardium. These findings suggest that suppressors of the cell cycle or cell proliferation may play a critical role in the pathophysiology of pressure overload.

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1. Introduction

Cardiac hypertrophy is an independent risk factor of cardiac morbidity and mortality [1]. There are two distinct forms of cardiac hypertrophy. Pressure overload conditions such as aortic stenosis and hypertension result in concentric hypertrophy, which is characterized by an increase in ventricular wall thickness, little or no chamber dilation, and the parallel addition of sarcomeres [2,3]. Conversely, volume overload conditions such as mitral regurgitation promote an eccentric (dilated) form of hypertrophy, which is characterized by relatively little increase in wall thickness, a disproportionately large increase in chamber vol-

ume, and the serial addition of sarcomeres [4,5]. Recently, we have demonstrated that there are differences in molecular signal transduction between pressure and volume overload in vitro [6]. However, the molecular response in human pressure- or volume-overloaded myocardium remains incompletely defined.

In contrast to differential display, DNA microarray technology allows expression monitoring of hundreds or thousands of genes simultaneously and provides a format for parallel gene expression studies [7,8]. In addition to identifying large clusters of genes that respond to a given stimulus, DNA microarray technology may be used to identify a few genes that comprise highly specific molecular responses [9,10].

In the present study, we investigated the transcriptional profile of genes induced in human pressure- or volume-overloaded atrial myocardium with DNA microarray

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technology. We found that gene expressions of cyclin-dependent kinase inhibitor 1A (CDK1A) and mitogen-activated protein kinase phosphatase-1 (MKP-1), but not growth factors, are induced in chronic pressure-overloaded atrial myocardium. These results suggest that suppressors of the cell cycle or cell proliferation may play a critical role in the pathophysiology of pressure overload.

2. Methods

2.1. Materials

Fibronectin, fetal calf serum, and Hanks' balanced salt solution were purchased from Life Technologies (Rockville, MD). All other chemicals were purchased from Sigma (St. Louis, MO).

2.2. Subjects

This study group consisted of five men and four women (mean age 59 ± 19 years) who underwent cardiac surgery. Hemodynamic studies were performed the morning after an overnight fast. Vasodilators were withheld for at least 24 h before evaluation. Chronic, stable doses of digoxin and diuretics were continued but were administered on an evening schedule. Right and left heart studies, including measurement of pressure, biplane left ventriculography and coronary angiography, were performed using a percutaneous catheter. The severity of tricuspid regurgitation was estimated by color Doppler echocardiography with a 2.5-MHz transducer (SONOS 2500 system, Hewlett Packard, Palo Alto, CA). The severity of tricuspid regurgitation was graded on a four-point scale, based on the distance reached by the abnormal signals from the tricuspid orifice toward the posterior wall in the parasternal four-chamber view [11]. Tricuspid regurgitation was classified as trivial, mild, moderate, or severe. This study was approved by our institutional human investigations committee, and written informed consent was obtained from all patients before participation.

2.3. Atrial myocardium samples

Right atrial appendages were obtained from the patients during cardiac surgery. Pieces of right atrial appendage weighing 200–1400 mg were frozen immediately in liquid nitrogen and stored at -80°C .

2.4. Transcriptional profiling

Total RNA was isolated by the guanidinium thiocyanate and phenol chloroform method [12]. Preparation of biotin-labeled cRNA probes were performed with the

following steps; conversion of RNA to single strand cDNA by reverse transcriptase reactions and synthesis of double strand cDNA template using SuperScript II kit (Life Technologies), purification of double-strand cDNA template using QIAquick PCR purification kit (QIAGEN, Valencia, CA), and transcription of biotin-labeled cRNA (AmpliScribe kit, Epicentre Technologies, Madison, WI) according to the manufacturer's instructions. The DNA microarray hybridization of biotin-labeled cRNA was performed using ExpressChip HO1 and HO2 arrays (Mergen, San Leandro, CA) according to the manufacturer's instructions. The ExpressChip HO1 and HO2 arrays have 2139 well-characterized genes with putative functions. A complete listing of genes contained within ExpressChip HO1 and HO2 can be found at http://www.mergen-ltd.com/HO1/HO1abc_genelist.htm and http://www.mergen-ltd.com/HO2/HO2abc_genelist.htm. The chips were subjected to the laser scanning and signal detection by the GMS418 Array Scanner (Takara Biomedicals, Shiga, Japan). The intensity of emission signals in each oligonucleotide hybridization was normalized to that of the glyceraldehyde-3 phosphate dehydrogenase (GAPDH) signal and analyzed using the GeneSpring software package (Silicon Genetics, Redwood City, CA).

2.5. Real-time reverse transcription–polymerase chain reaction (PCR) analysis

For reverse transcription, RNA was reverse transcribed using T7-dT primer (5' -TCT AGT CGA CGG CCA GTG AAT TGT AAT ACG ACT CAC TAT AGG GCG TTT TTT TTT TTT TTT TTT-3') and Superscript II reverse transcriptase (Life Technologies). Real-time quantitative PCR was performed in optical tubes in a 96-well microtiter plate (Perkin-Elmer/Applied Biosystems, Foster City, CA) with an ABI PRISM 7700 Sequence Detector Systems (Perkin-Elmer/Applied Biosystems) according to the manufacturer's instructions. By using the SYBR Green PCR Core Reagents Kit (Perkin-Elmer/Applied Biosystems, P/N 4304886), fluorescence signals were generated during each PCR cycle via the 5' - to 3' - endonuclease activity of Taq Gold [13] to provide real-time quantitative PCR information. The oligonucleotide primers used for real-time PCR analysis were shown in Table 1. No template controls as well as the samples were added in a total volume of 50 μl /reaction. Potential PCR product contamination was digested by uracil-*N*-glycosylase, because dTTP is substituted by dUTP [13]. All PCR experiments were performed with the hot start method. In the reaction system, uracil-*N*-glycosylase and Taq Gold (Perkin-Elmer/Applied Biosystems) were applied according to the manufacturer's instructions [13,14]. Denaturing and annealing reactions were performed 40 times at 95°C for 15 s, and at 60°C for CDK1A, 54°C for MKP-1, 56°C for glutathione S-transferase theta 1 and 62°C

Table 1
Design of primers for real-time PCR

Gene		Primer sequences	PCR product (bp)
CDKI1A	Sense	5' -GACCTGTCACTGTCTTGTACCCTT-3'	120
	Antisense	5' -GTAGAAATCTGTCATGCTGGTCTG-3'	
MKP-1	Sense	5' -TTTTGAGGGTCACTACCAGTACAA-3'	191
	Antisense	5' -TAGTCCTCATAAGGTAAGCAAGGC-3'	
GSTT1	Sense	5' -GTAGCCATCACGGAGCTGAT-3'	146
	Antisense	5' -CTTGGCCTTCAGAATGACCT-3'	
SCYA5	Sense	5' -AAGGAGTATTCTACACCAGTGGC-3'	132
	Antisense	5' -GCTCATCTCCAAGAGTTGATGTA-3'	

CDKI1A, cyclin-dependent kinase inhibitor 1A; GSTT1, glutathione S-transferase theta 1; MKP-1, mitogen-activated protein kinase phosphatase-1; SCYA5, small inducible cytokine A5.

for small inducible cytokine A5 for 1 min, respectively. The increase in the fluorescence signal is proportional to the amount of specific product [15]. The intensity of emission signals in each sample was normalized to that of β -actin as an internal control.

2.6. Culture of neonatal rat ventricular myocytes (NRVM)

NRVM from 1-day-old Sprague–Dawley rats were isolated by previously described methods [16]. The ventricles were excised from the rat, cut into several pieces, and incubated overnight at 4 °C in 1 mg/ml of 1:300 trypsin in Hanks' balanced salt solution. The ventricular tissue was then digested with 1 mg/ml of collagenase type II (239 U/mg, Worthington Biochemicals, Freehold, NJ) in Hanks' balanced salt solution, centrifuged twice at 50 × g to remove less dense cells such fibroblasts, and then plated. The cells were cultured at 37 °C, 5% CO₂ in Dulbecco's modified Eagle's medium (BioWhittaker, Walkersville, MD) containing 7% fetal calf serum, 50 U/ml penicillin and 50 µg/ml streptomycin. We routinely obtained primary cultures with >95% myocytes, as assessed by microscopic observation of spontaneous contraction and by immunofluorescence staining with a monoclonal human ventricular myosin heavy chain antibody (Biogenesis, Poole, UK) [16].

This investigation was performed according to the *Guide for the Care and Use of Laboratory Animals* published by US National Institutes of Health (NIH publication No. 85-23, revised 1996).

2.7. Mechanical strain device and preparation of cells

Mechanical deformation was applied to a thin and transparent membrane on which cells were cultured, an approach which produces controlled cellular strain as well as visualization of cells [17].

For the preparation of NRVM to be subjected to mechanical strain, autoclaved membrane dishes were coated with 2 µg/ml of fibronectin in 13 ml of Hanks' balanced salt solution for 6–12 h at 4 °C and then

washed twice with 10 ml of phosphate-buffered saline. NRVM were plated on the coated membrane dish at a density of 2,000,000 cells/dish in 13 ml of Dulbecco's modified Eagle's medium containing 7% fetal calf serum and incubated 48 h. NRVM were then made quiescent by washing with 10 ml of Hanks' balanced salt solution twice and incubating with 10 ml of Dulbecco's modified Eagle's medium containing 1% insulin, transferrin, selenium media supplement (ITS; Sigma), 50 U/ml penicillin, and 50 µg/ml streptomycin. All experiments were performed on NRVM that had been serum-starved for 24 h.

2.8. Western analysis

NRVM were lysed directly in each dish by application of a buffer containing 50 mM Tris–HCl (pH 7.5), 1 mM EDTA, 1 µM leupeptin, 1 µM pepstatin A, 0.1 mM phenylmethylsulfonyl fluoride, and 1 mM dithiothreitol, and sonicated. The homogenates were then centrifuged at 100,000 × g for 20 min. Total protein concentration was measured by the Bradford method (Bio-Rad Laboratories, Hercules, CA) and equal quantities of total protein were loaded on a 13% SDS–polyacrylamide gel and transferred to a nitrocellulose membrane in 25 mM Tris base (pH 8.5), 0.2 M glycine, and 20% methanol. The nitrocellulose membrane was blocked by 5% non fat dried milk in Tris-buffered saline washing buffer containing 20 mM Tris base (pH 7.6), 137 mM NaCl, and 0.1% Tween 20 for 2 h. For the detection of CDKI1A and MKP-1, the membrane was incubated with 1:1000 diluted mouse monoclonal anti-CDKI1A antibody (sc-6246, Santa Cruz Biotechnology, Santa Cruz, CA) or rabbit polyclonal anti-MKP-1 antibody (sc-1199, Santa Cruz Biotechnology) for 1 h at 37 °C and washed with Tris-buffered saline washing buffer for 30 min. After application of sheep anti-mouse IgG (Amersham Life Science, Arlington Heights, IL) or goat anti-rabbit IgG (Santa Cruz Biotechnology) coupled to peroxidase, the membrane was developed with the enhanced chemiluminescent method (Amersham Life Science).

Table 2
Patient characteristics

Patient (no.)	Age (years)	Sex	Diagnosis	mRAP (mm Hg)	Systolic PAP (mm Hg)	TR grade
Control						
1	44	M	AR	3	19	trivial
2	70	F	MR	4	28	trivial
3	60	M	AS	6	34	trivial
Pressure overload						
1	64	M	MR	10	52	mild
2	74	F	MR, AS	15	65	mild
3	75	M	MR, AR	8	53	mild
Volume overload						
1	64	F	MR	4	32	moderate
2	64	F	AR, MR	5	32	severe
3	15	M	ASD	5	23	moderate

AR, aortic regurgitation; AS, aortic stenosis; ASD, atrial septal defect; F, female; M, male; MR, mitral regurgitation; mRAP, mean right atrial pressure; PAP, pulmonary artery pressure; TR, tricuspid regurgitation.

2.9. Statistical analysis

Data are expressed as mean \pm S.D. The data were analyzed by nonparametric Kruskal–Wallis methods for the group comparisons to avoid assumptions about the distribution of the measured variables. Subsequent pairwise comparisons were made with the Mann–Whitney *U* test. A *P* value <0.05 was considered significant.

3. Results

3.1. Clinical characteristics of participating subjects

On the basis of pressure data of Swan–Ganz catheters and echocardiographic findings, the patients were divided into the following three groups: control group ($n=3$), pressure overload group (mean right atrial pressure of >7 mm Hg, $n=3$), and volume overload group (moderate or severe tricuspid regurgitation, $n=3$) (Table 2).

3.2. DNA microarray analysis

Among the 2139 well-characterized genes with putative functions, expression of genes of CDKI1A (11.7 ± 3.1 -fold vs. control), MKP-1 (26.2 ± 2.1 -fold), glutathione S-transferase theta 1 (65.1 ± 29.7 -fold) and small inducible cytokine A5 (8.3 ± 1.8 -fold) in the pressure overload group significantly increased compared with those in control ($P<0.05$) or volume overload group (CDKI1A, 3.0 ± 2.0 -fold vs. control; MKP-1, 8.1 ± 6.5 -fold; glutathione S-transferase theta 1, 19.2 ± 10.1 -fold; small inducible cytokine A5, 2.1 ± 0.7 -fold, $P<0.05$), as shown in Fig. 1. In contrast, transcripts of growth factors such as fibroblast growth factor, hepatocyte growth factor, insulin-like growth factor, platelet-derived growth factor and vascular endothelial growth factor, and cytokines including interleukin 1,

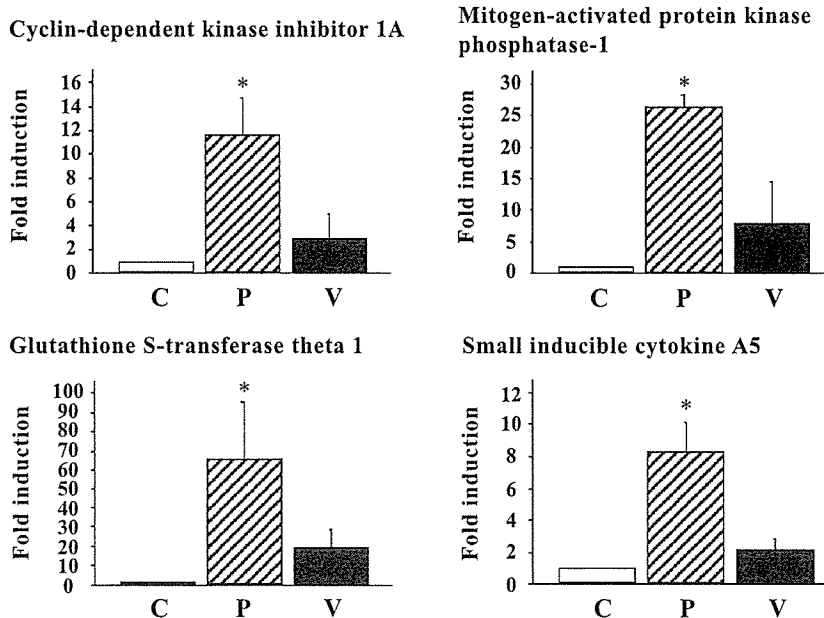


Fig. 1. Oligonucleotide microarray analysis of pressure- or volume-overloaded human myocardium. Total RNA was obtained from the right atrial appendages of the patients: control group (C, open bar), pressure overload group (P, hatched bar), and volume overload group (V, closed bar). Preparation of biotin-labeled cRNA probes was performed as described in the Methods. The DNA microarray hybridization of biotin-labeled cRNA was performed using ExpressChip HO1 and HO2 arrays (Mergen). The chips were subjected to the laser scanning and signal detection by the GMS418 Array Scanner (Takara Biomedicals). The intensity of emission signals in each oligonucleotide hybridization was normalized to that of the glyceraldehyde-3 phosphate dehydrogenase signal, and analyzed using the GeneSpring software package (Silicon Genetics). The mRNA expression was expressed as relative change standardized to control group. Bar graphs with error bars represent the mean \pm S.D. ($n=3$). * $P<0.05$ vs. control or volume overload group.

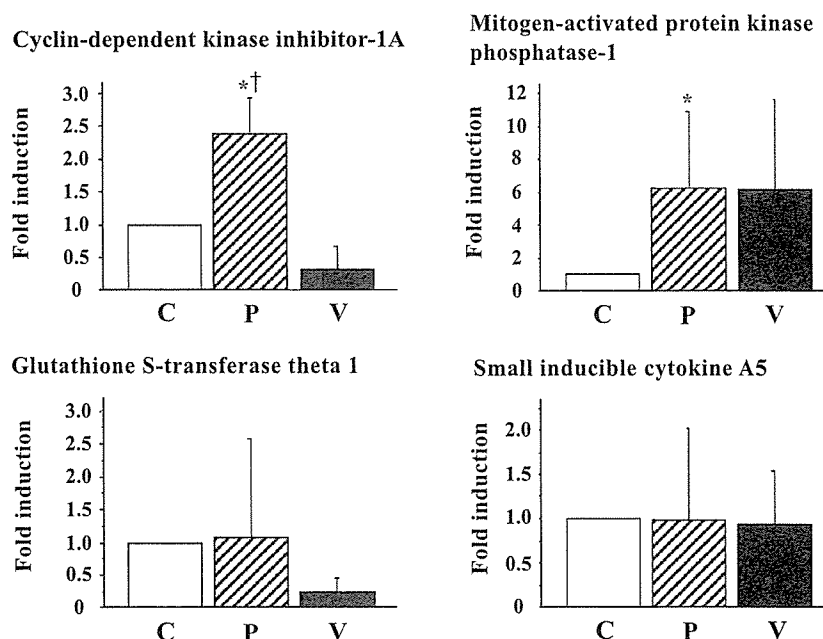


Fig. 2. Quantitative real-time reverse transcription–PCR analysis. The cDNA was prepared from the right atrial appendages of the patients: control group (C, open bar), pressure overload group (P, hatched bar), and volume overload group (V, closed bar), and then subjected to real-time PCR with primers specific for cyclin-dependent kinase inhibitor 1A, mitogen-activated protein kinase phosphatase-1, glutathione S-transferase theta 1, small inducible cytokine A5 or β -actin. The ratio of the abundance of each transcript to that of the β -actin transcript was calculated, and the amount of mRNA expression was expressed as relative change standardized to control group. Bar graphs with error bars represent the mean \pm S.D. ($n=3$). * $P<0.05$ vs. control. † $P<0.05$ vs. volume overload group.

interleukin 6, interleukin 8, and tumor necrosis factor α were not significantly different among the three groups.

3.3. Quantitation of the selected genes by real-time PCR

To confirm the preferential expression of the selected genes in pressure overload group, we prepared cDNAs from the same RNA as that used in microarray analysis, and then subjected these cDNAs to “real-time” PCR analysis with primers specific for CDKI1A, MKP-1, glutathione S-transferase theta 1, small inducible cytokine A5 and β -actin (Fig. 2). The abundance of CDKI1A (2.4 ± 0.5 -fold vs. control) mRNA relative to that of β -actin mRNA in pressure overload group was markedly greater than that in control ($P<0.05$) or volume overload group (0.3 ± 0.4 -fold, $P<0.05$). The abundance of MKP-1 (6.2 ± 4.7 -fold) mRNA relative to that of β -actin mRNA in pressure overload group was significantly greater than that in control ($P<0.05$), but not in volume overload group (6.2 ± 5.5 -fold). However, the abundance of glutathione S-transferase theta 1 and small inducible cytokine A5 mRNA was not significant different among three groups (glutathione S-transferase theta 1: pressure overload group, 1.1 ± 1.5 -fold vs. control; volume overload group, 0.3 ± 0.2 -fold and small inducible cytokine A5: pressure overload group, 1.0 ± 1.0 -fold vs. control; volume overload group, 0.9 ± 0.6 -fold). Thus, these findings demonstrated that gene expressions of CDKI1A and MKP-1 are increased in the human atrial myocardium with pressure overload.

3.4. Effects of mechanical strain on CDKI1A and MKP-1 protein accumulation

Next, we investigated whether CDKI1A and MKP-1 proteins were induced by mechanical strain in cardiac myocytes. The expressions of CDKI1A and MKP-1 proteins were analyzed by immunoblotting with anti-CDKI1A and MKP-1 antibodies, respectively. As shown in Fig. 3, mechanical strain at a frequency of 1 Hz induced CDKI1A and MKP-1 protein expressions in an amplitude-dependent manner.

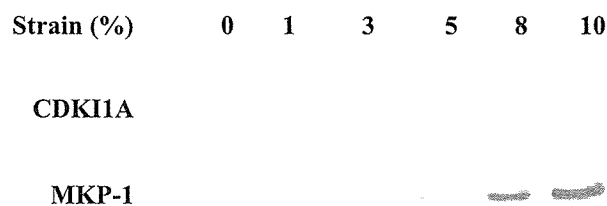


Fig. 3. Effects of mechanical strain on cyclin-dependent kinase inhibitor 1A (CDKI1A) and mitogen-activated protein kinase phosphatase-1 (MKP-1) protein expressions in cardiac myocytes. Cardiac myocytes were plated on 2 μ g/ml of fibronectin in Dulbecco’s modified Eagle’s medium containing 7% fetal calf serum for 24 h. After serum deprivation for 24 h, myocytes were exposed to 0%, 1%, 3%, 5%, 8%, or 10% cyclic mechanical strain (1 Hz) for 2 h. Cell extracts were subjected to SDS–PAGE followed by immunoblot analysis using the anti-CDKI1A or MKP-1 antibody. Data are representative of two independent experiments with nearly identical results.

4. Discussion

Most previous studies have focused on the activation of pathways of signal transduction in the cardiac hypertrophy or remodeling. In the present study, gene expressions of CDK11A and MKP-1, but not growth factors, were induced in chronic pressure-overloaded myocardium. In addition, mechanical strain induced CDK11A and MKP-1 at a protein level in cultured rat cardiac myocytes in an amplitude-dependent manner. These findings suggest that negative regulators of cell cycle or cell proliferation also may play an important role in the pathophysiology of pressure overload.

Relatively little is known about the molecular changes associated with volume-overload hypertrophy. Lattion et al. [18] reported that aortocaval fistula in rat caused a highly significant increase in atrial natriuretic factor gene expression in the left ventricle. In addition, Calderone et al. [19] reported that pressure overload, but not volume overload, increased mRNA levels for β -myosin heavy chain and skeletal α -actin in rats, while both pressure overload and volume overload caused comparable increases in left ventricular weight. Our results also demonstrated that there are molecular differences between pressure- and volume-overloaded myocardium.

Many intracellular signaling pathways are thought to play important roles in mechanotransduction. Recent studies of myocardial hypertrophy have focused on activation of protein kinases including protein kinase C, Raf-1 kinase, S6 peptide kinase and mitogen-activated protein (MAP) kinases, which precede an increase in specific gene expression and protein synthesis [20–22]. The MAP kinase signaling pathways consist of three major phosphorylation cascades: the extracellular signaling-regulated protein kinases, the c-Jun NH₂-terminal kinases, and the p38-MAP kinases [23]. MKP-1 has dual catalytic activity toward phosphotyrosine- and phosphothreonine-containing proteins and is known to inactivate extracellular signaling-regulated protein kinases, possibly c-Jun NH₂-terminal kinases and p38-MAP kinases [24–27]. MKP-1 is an important member of the dual specificity phosphatase family that is expressed in the heart. Transient transfection of an MKP-1-encoding expression vector into cardiac myocytes was shown to downregulate multiple hypertrophy-induced promoter constructs *in vitro* [28,29]. Recently, Bueno et al. [30] reported that transgenic mice constitutively expressing MKP-1 in the heart showed attenuation in normal developmental hypertrophy and concomitant ventricular dilation, and demonstrated that adult MKP-1 transgenic mice failed to mount a significant hypertrophic response when stressed by pressure overload or isoproterenol infusion. Interestingly, in the present study, MKP-1 mRNA and protein expressions were induced in chronic human pressure-overloaded myocardium and mechanically stimulated cardiac myocytes, respectively. Taken together, these findings suggest that MKP-1 as well as MAP kinase pathway may be a critical regulator of cardiac hypertrophy or remodeling.

Cyclin/cyclin-dependent kinase complexes facilitate progression through the cell cycle and are activated at specific

points during the cell cycle [31]. CDK11A (also named WAF1, and CIP1), p21, is involved in regulating cell cycle progression. CDK11A, which functions by binding to and inactivating a number of the cyclin/cyclin-dependent kinase complexes including cyclin-dependent kinase 2, is a regulator of the G₁-S cell cycle checkpoint. Poolman and Brooks [32] reported that CDK11A is induced during the 2–5-day developmental period in rat cardiac myocytes. The induction and sustained expression of CDK11A is considered to be a contributory mechanism by which myocytes irreversibly exit the cell cycle upon terminal differentiation [33]. However, cell cycle in adult cardiac myocytes, particularly when stimulated by hypertrophic stimuli, remains fully undefined. Recently, Liao et al. [34] demonstrated that cardiac overexpression of cyclin-dependent kinase 2 resulted in increased numbers of smaller, less-differentiated mononuclear cardiac myocytes in adult hearts, and that surgically induced pressure overload caused an exaggerated maladaptive hypertrophic response in transgenic mice. Beltrami et al. [35] reported that a subpopulation of human adult myocytes evidently reentered the cell cycle and underwent nuclear mitotic division early after myocardial infarction. The present study demonstrated that CDK11A mRNA expression was induced in chronic human pressure-overloaded myocardium and that CDK11A protein expression was induced by mechanical strain in cardiac myocytes in an amplitude-dependent manner. Therefore, it is likely that the mechanism of cell cycle withdrawal is not irreversible in cardiac myocytes.

4.1. Study limitations

The number of patients in this study was small and might not be representative for conditions investigated. In addition, we used the atrial samples, because it is very difficult to obtain human left ventricles.

A greater understanding of the cell cycle or cell proliferation that is related to cardiac hypertrophy or remodeling will be critical for implementing novel and more effective therapeutic strategies in the future. However, the mechanism of cell cycle or cell proliferation in cardiac myocytes, particularly adult cardiac myocytes, is complicated and poorly understood. The present study demonstrates that gene expressions of CDK11A and MKP-1, but not growth factors, are induced in chronic pressure-overloaded myocardium and suggests that suppressors of cell cycle or cell proliferation may modulate the pathophysiology of pressure overload. Furthermore, additional studies are needed to clarify the mechanism of cell cycle or cell proliferation in the heart.

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Schedule-dependent synergism and antagonism between pemetrexed and paclitaxel in human carcinoma cell lines in vitro

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Abstract Pemetrexed is a novel multitargeted antifolate with significant clinical activity against a variety of tumors. We studied the schedule-dependent cytotoxic effects of pemetrexed in combination with paclitaxel in vitro to improve our understanding of how this combination might be used clinically. Human lung cancer A549 cells, breast cancer MCF7, ovarian cancer PA1, and colon cancer WiDr cells were exposed to both pemetrexed and paclitaxel in vitro. Cell growth inhibition after 5 days was determined and the effects of drug combinations were analyzed by the isobologram method (Steel and Peckham). Simultaneous exposure to pemetrexed and paclitaxel for 24 h produced antagonistic effects in A549 and PA1 cells, additive/antagonistic effects in MCF7 cells, and additive effects in WiDr cells. Pemetrexed for 24 h followed by paclitaxel for 24 h produced synergistic effects in A549 and MCF7 cells and additive effects in PA1 and WiDr cells, while the reverse sequence produced additive effects in all four cell lines. Cell cycle analysis supported these observations. Our findings suggest that the simultaneous administration of pemetrexed and paclitaxel is suboptimal. The optimal schedule of pemetrexed in combination with paclitaxel is the sequential administration of pemetrexed followed by paclitaxel, and this schedule should be assessed in clinical trials for the treatment of solid tumors.

Keywords Pemetrexed · Paclitaxel · Isobologram · Synergism · Antagonism

Introduction

The development of several new antifolates with distinctive chemical features and target enzymes has provided new opportunities to expand the role of antifolates in cancer chemotherapy. Multitargeted antifolate (MTA, pemetrexed) is a pyrrole-pyrimidine analogue of folate [33] currently in broad clinical evaluation. Pemetrexed is transported into cells mainly through the reduced folate carrier system and metabolized to polyglutamated forms [7] which inhibit thymidylate synthase, dihydrofolate reductase, and glycinamide ribonucleotide formyl transferase [30, 31], and has antithymidylate and antipurine effects [5]. Preclinical studies of pemetrexed have demonstrated its antitumor activity against a variety of human cancer cells [2, 29].

Phase I studies have shown that the dose-limiting toxicity includes neutropenia and thrombocytopenia, and other toxicities which are manageable, such as mucositis, skin rashes and transient elevations of transaminases [18, 23–25]. Daily and weekly schedules are associated with severe toxicity and 500 mg/m² of pemetrexed every 3 weeks was selected as the optimal schedule and dose for the further development of pemetrexed. Patients with a folate-deficient state showed severe toxicity. In preclinical models, folate supplementation reduced toxicity while maintaining antitumor activity. Based on these observations, folate and cobalamin administration before pemetrexed has been routine in recent clinical trials of pemetrexed [9, 26]. Pharmacokinetic studies have shown that pemetrexed undergoes biphasic plasma clearance with a terminal half-life of 1.1–3.1 h, depending on the schedule of administration [23]. The findings from the phase II trial results are encouraging: clear responses were observed in colorectal cancer, pancreatic cancer, lung cancer, breast cancer, mesothelioma, etc. [3, 4, 8, 10, 19–21, 26, 37]. A recent

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phase III study has shown that treatment with pemetrexed and cisplatin results in survival times superior to those achieved with cisplatin alone in patients with malignant pleural mesothelioma [39].

Paclitaxel is an established anticancer agent with activity against a variety of solid tumors [1, 6]. Paclitaxel is a mitotic inhibitor that promotes the polymerization and stabilization of tubulin to microtubules [27]. Clinical studies have indicated that neutropenia is the dose-limiting toxicity of paclitaxel [1, 6]. Other toxicities include hypersensitivity reactions, neurotoxicity, mucositis, mild nausea and vomiting, and cardiac injury.

The combination of pemetrexed and paclitaxel may have a major role in the treatment of a variety of solid tumors. The wide range of antitumor activity of pemetrexed and paclitaxel, their different cytotoxic mechanisms and toxic profiles, and the absence of cross-resistance, provide the rationale for using combinations of these agents. Since pemetrexed and paclitaxel are cell cycle-specific agents [17, 38], the disturbances of the cell cycle produced by these agents may influence the cytotoxic effects of each agent, and the drug schedule may play a significant role in the outcome. Therefore, the design of a protocol using them in combination requires careful consideration. As expected, experimental studies for the combination of pemetrexed [22, 30, 36] or paclitaxel [13–15] with other agents have shown schedule-dependent interactions.

The aim of the present study was to elucidate the cytotoxic effects of combinations of pemetrexed and paclitaxel in various schedules on four human carcinoma cell lines. The data obtained were analyzed using the isobologram method of Steel and Peckham [32]. The combination showed schedule-dependent synergism and antagonism.

Materials and methods

Cell lines

Experiments were conducted with the human lung cancer A549, breast cancer MCF7, ovarian cancer PA1, and colon cancer WiDr cell lines. These cells were obtained from the American Type Culture Collection (Rockville, Md.) and maintained in 75-cm² plastic tissue culture flasks containing RPMI-1640 medium (Sigma Chemical Co., St Louis, Mo.) supplemented with 10% heat-inactivated fetal bovine serum (FBS) (Grand Island Biological Co.) and antibiotics. The cells used were devoid of mycoplasma infection. The doubling times of A549, MCF7, PA1, and WiDr cells under our experimental conditions were in the range 20–24 h.

Drugs

Pemetrexed was kindly provided by Eli Lilly and Company (Indianapolis, Ind.). Paclitaxel was purchased from

Bristol-Myers Squibb Japan Co. (Tokyo). The drugs, at a concentration of 1 mM, were stored at –20°C and diluted with RPMI-1640 plus 10% FBS prior to use.

Cell growth inhibition using combined anticancer agents

On day 0, cells growing in the exponential phase were harvested with 0.05% trypsin and 0.02% EDTA and resuspended to a final concentration of 5.0×10^3 cells/ml in fresh medium containing 10% FBS and antibiotics. Cell suspensions (100 μ l) were dispensed into the individual wells of a 96-well tissue culture plate (Falcon, Oxnard, Calif.). Each plate had one eight-well control column containing medium alone and one eight-well control column containing cells without drug. Eight plates were prepared for each drug combination. The cells were preincubated overnight to allow attachment.

Simultaneous exposure to pemetrexed and paclitaxel

After the overnight incubation for cell attachment, solutions of pemetrexed and paclitaxel (50 μ l) at different concentrations were added to the individual wells. The plates were also incubated under the same conditions for 24 h. The cells were then washed twice with culture medium containing 1% FBS, and then fresh medium containing 10% FBS (200 μ l) and antibiotics was added. The cells were incubated again for 4 days.

Sequential exposure to pemetrexed followed by paclitaxel or the reverse sequence

After overnight incubation, medium containing 10% FBS (50 μ l) and solutions (50 μ l) of pemetrexed (or paclitaxel) at different concentrations was added to individual wells. The plates were then incubated under the same conditions for 24 h. The cells were washed twice with culture medium containing 1% FBS; then fresh medium containing 10% FBS (150 μ l) and antibiotics was added, followed by the addition of solutions (50 μ l) of paclitaxel (or pemetrexed) at different concentrations. The plates were incubated again under the same conditions for 24 h. The cells were then washed twice with culture medium, and fresh medium containing 10% FBS (200 μ l) and antibiotics was added. The cells were then incubated again for 3 days.

MTT assay

Viable cell growth was determined by the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay as described previously [12]. For all four cell lines examined, we were able to establish a linear relationship between the MTT assay value and the cell number within the range shown.

Isobologram

The dose-response interactions between pemetrexed and paclitaxel for the MCF7, PA1 and WiDr cells were evaluated at the IC_{80} level by the isobologram method (Fig. 1) [32]. The IC_{80} was defined as the concentration of drug that produced 80% cell growth inhibition, i.e., an 80% reduction of absorbance. Since the A549 cells were resistant to pemetrexed and the IC_{80} level was not obtained, the interactions between pemetrexed and paclitaxel were evaluated at the IC_{50} level. We used the isobologram method of Steel and Peckham because this method can cope with any agents with unclear cytotoxic mechanisms and a variety of dose-response curves of anticancer agents [32]. The concept of the isobologram has been described in detail previously [11, 16].

Three isoeffect curves, mode I and mode II, were constructed, based upon the dose-response curves of pemetrexed and paclitaxel (Fig. 1). Mode I and mode II were generated by the assumption regarding overlap and non-overlap damage in combinations, respectively. Thus, when the data points of the drug combination fell within the area surrounded by mode I and/or mode II lines (i.e., within the envelope of additivity), the combination was described as additive. We used this envelope not only to evaluate the simultaneous exposure combinations of pemetrexed and paclitaxel, but also to evaluate the sequential exposure combinations, since the

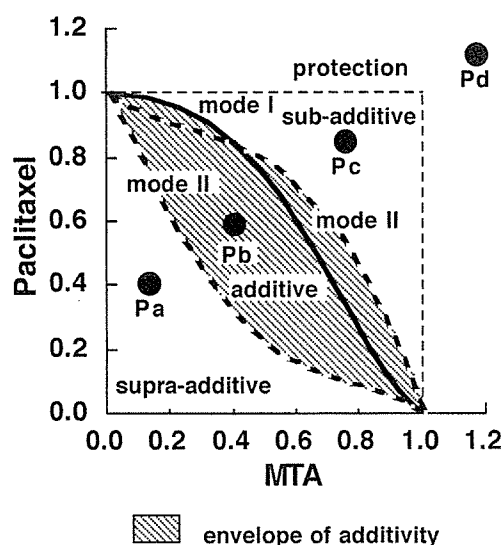


Fig. 1 Schematic representation of an isobologram (Steel and Peckham) [32]. The envelope of additivity, surrounded by mode I (solid line) and mode II (dotted lines) isobologram lines, was constructed from the dose-response curves of MTA and paclitaxel. The concentrations which produced 80% cell growth inhibition are shown as 1.0 on the ordinate and the abscissa of all isobolograms for MCF7, PA1, and WiDr cells, while the concentrations which produced 50% cell growth inhibition are shown as 1.0 on the ordinate and the abscissa of all isobolograms for A549 cells. Combined data points Pa, Pb, Pc, and Pd show supraadditive, additive, subadditive, and protective effects, respectively

second agent under our experimental conditions could modulate the cytotoxicity of the first agent.

A combination that gives data points to the left of the envelope of additivity (i.e., the combined effect is caused by lower doses of the two agents than is predicted) can confidently be described as supraadditive (synergistic). A combination that gives data points to the right of the envelope of additivity, but within the square or on the line of the square can be described as subadditive (i.e., the combination is superior or equal to a single agent but is less than additive). A combination that gives data points outside the square can be described as protective (i.e., the combination is inferior in cytotoxic action to a single agent). A combination with both subadditive and/or protective interactions can confidently be described as antagonistic. The Steel and Peckham isobologram is generally more strict regarding synergism and antagonism than other methods.

Data analysis

The findings were analyzed as described previously [14]. When the observed data points of the combinations mainly fell in the area of supraadditivity or in the areas of subadditivity and protection, i.e., the mean value of the observed data was smaller than that of the predicted minimum values or larger than that of the predicted maximum values, the combinations were considered to have a synergistic or antagonistic effect, respectively. To determine whether the condition of synergism (or antagonism) truly existed, a statistical analysis was performed. The Wilcoxon signed-ranks test was used for comparing the observed data with the predicted minimum (or maximum) values for additive effects, which were closest to the observed data (i.e., the data on the boundary (mode I or mode II lines) between the additive area and supraadditive area (or subadditive and protective areas)). Probability (P) values < 0.05 were considered significant. Combinations with $P \geq 0.05$ were regarded as indicating additive to synergistic (or additive to antagonistic) effects. All statistical analyses were performed using the Stat View 4.01 software program (Abacus Concepts, Berkeley, Calif.).

Results

The IC_{80} values of pemetrexed for a 24-h exposure against MCF7, PA1, and WiDr cells were 3.3 ± 0.4 , 0.15 ± 0.02 , and $0.45 \pm 0.04 \mu M$, respectively, while those of paclitaxel against MCF7, PA1, and WiDr cells were 5.9 ± 0.4 , 2.5 ± 0.06 , and $5.8 \pm 0.06 nM$, respectively. The IC_{50} values of pemetrexed and paclitaxel for a 24-h exposure against A549 cells were $2.5 \pm 0.3 \mu M$ and $3.4 \pm 0.3 nM$, respectively.

Figure 2 shows the dose-response curves obtained from simultaneous exposure and sequential exposure to pemetrexed and paclitaxel for the MCF7 cells. The

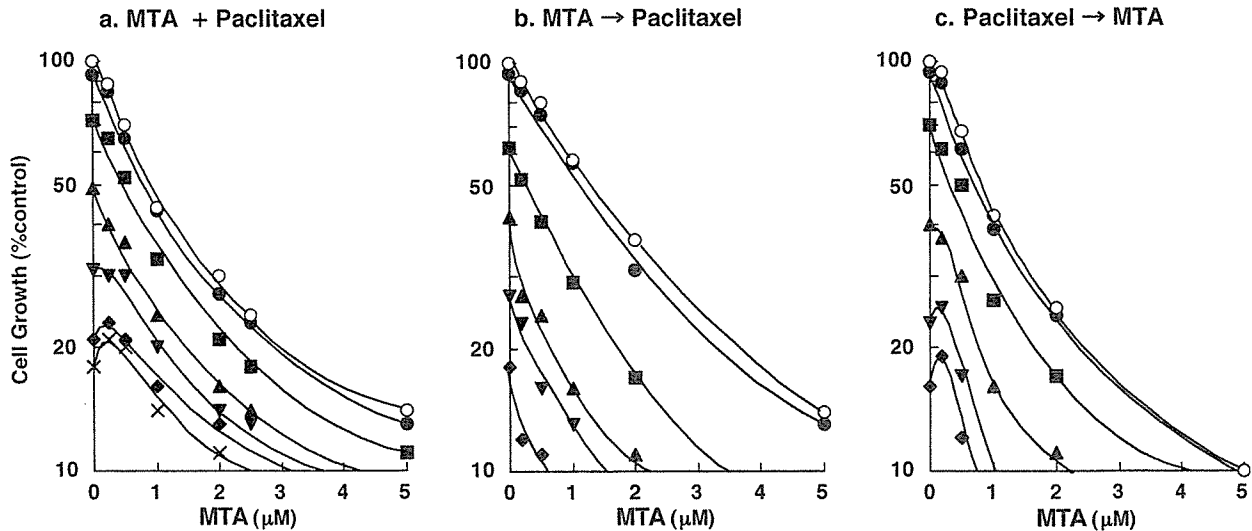


Fig. 2 Schedule dependence of the interaction between MTA and paclitaxel in MCF7 cells. Cells were exposed to (a) these two drugs simultaneously for 24 h, (b) MTA first for 24 h followed by paclitaxel for 24 h, or (c) the reverse sequence. The cell number after 5 days was measured using the MTT assay and was plotted as a percentage of the control (cells not exposed to drugs). The concentrations of MTA are shown on the abscissa. The concentrations of paclitaxel were 0 (*open circles*), 1 (*filled circles*), 2 (*filled squares*), 3 (*filled uptriangles*), 4 (*filled downtriangles*), 6 (*filled diamonds*), and 8 (*crosses*) nM, respectively. Data are the mean values for three independent experiments; SE was < 20%

dose-response curves were plotted on a semilog scale as a percentage of the control, the cell number of which was obtained from the samples not exposed to the drugs administered simultaneously. The pemetrexed concentrations are shown on the abscissa. Dose-response curves in which paclitaxel concentrations are shown on the abscissa could be made based on the same data (figure not shown).

Based upon the dose-response curves of pemetrexed alone and paclitaxel alone, three isoeffect curves (mode I and mode II lines) were constructed. Isobolograms at the IC_{80} and IC_{50} levels were generated based upon these dose-response curves for the combinations.

Simultaneous exposure to pemetrexed and paclitaxel for 24 h

Figure 3 shows the isobolograms of the A549, MCF7, PA1, and WiDr cells exposed to both agents simultaneously. For the A549 and PA1 cells, all or most combined data points fell in the areas of subadditivity and protection (Fig. 3a,c). The mean values of the data were larger than those of the predicted maximum data (Table 1). The differences were significant ($P < 0.05$ and $P < 0.05$), indicating antagonistic effects. For the MCF7 cells, the combined data points fell within the envelope of additivity and in the areas of subadditivity and protection (Fig. 3b; Table 1). The mean value of the data was larger than that of the predicted maximum data. The difference was not significant ($P \geq 0.05$), indicating

additive/antagonistic effects. For the WiDr cells, the combined data points fell mainly within the envelope of additivity (Fig. 3d). The mean value of the data was larger than that of the predicted minimum data and smaller than that of the predicted maximum data (Table 1), indicating additive effects. A quite similar tendency was observed in the IC_{50} isobologram of the MCF7, PA1, and WiDr cells (not shown).

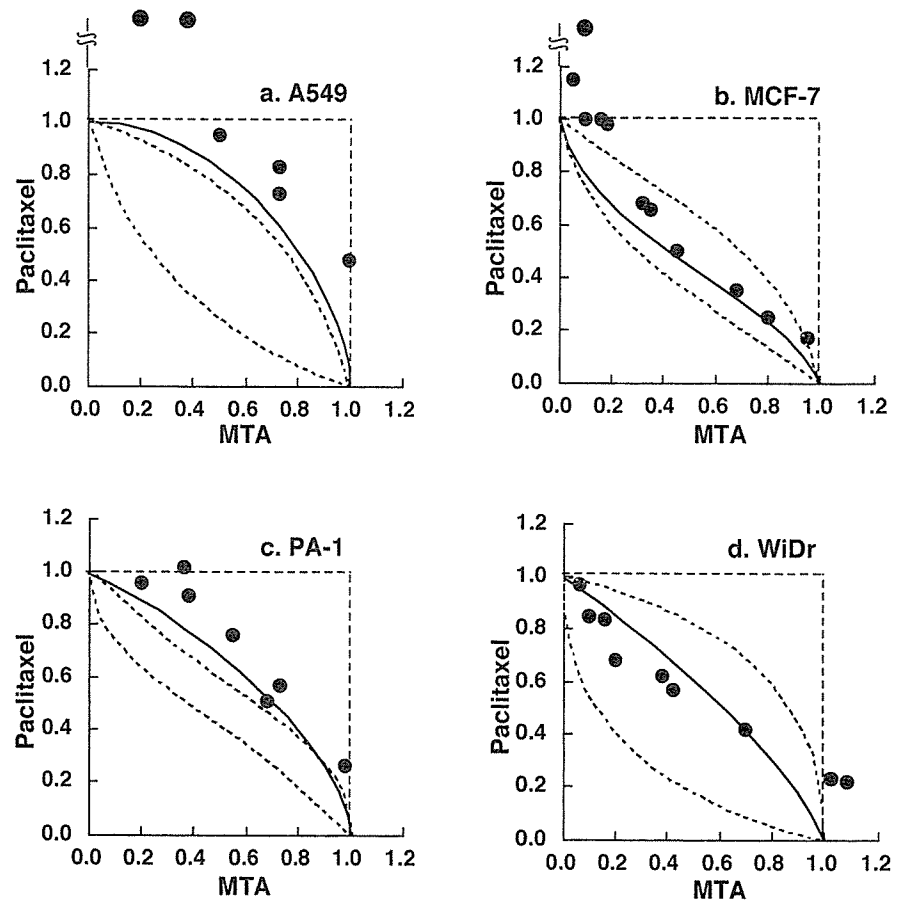
Sequential exposure to pemetrexed for 24 h followed by paclitaxel for 24 h

Figure 4 shows the isobolograms of the four cell lines exposed first to pemetrexed and then to paclitaxel. For the A549 and MCF7 cells, the combined data points fell in the area of supraadditivity and within the envelope of additivity (Fig. 4a,b). The mean values of the data were smaller than those of the predicted minimum data (Table 1). The differences were significant ($P < 0.05$ and $P < 0.05$), indicating synergistic effects. For the PA1 cells, the combined data points fell within the envelope of additivity (Fig. 4c), indicating additive effects (Table 1). For the WiDr cells, the combined data points fell within the envelope of additivity and in the area of supraadditivity (Fig. 4d). The mean value of the data was smaller than that of the predicted maximum data and larger than that of the predicted minimum data (Table 1), indicating additive effects. A quite similar tendency was observed in the IC_{50} isobologram of the MCF7, PA1, and WiDr cells (not shown).

Sequential exposure to paclitaxel for 24 h followed by pemetrexed for 24 h

Figure 5 shows the isobolograms of cells exposed first to paclitaxel and then to pemetrexed. For all four cell lines, all or most of the data points fell within the envelope of additivity, indicating additive effects (Table 1). A quite

Fig. 3 Isobolograms of simultaneous exposure to MTA and paclitaxel for 24 h in (a) A549, (b) MCF7, (c) PA1, and (d) WiDr cells. For the A549, and PA1 cells, all or most combined data points fell in the areas of subadditivity and protection. For the MCF7 cells, combined data points fell within the envelope of additivity and in the areas of subadditivity and protection. For the WiDr cells, combined data points fell mainly within the envelope of additivity. Data are the mean values for at least three independent experiments; SE was <30%



similar tendency was observed in the IC_{50} isobologram of the MCF7, PA1, and WiDr cells.

Discussion

We studied the cytotoxic activity of various schedules of pemetrexed in combination with paclitaxel in culture to investigate the optimal schedule of this combination. The analysis of the effects of drug–drug interaction was carried out using the isobologram method of Steel and

Peckham [32]. Among the solid tumor cell lines studied, PA1 was most sensitive to pemetrexed, while A549 was most resistant to pemetrexed. The pemetrexed concentrations required for IC_{80} and/or IC_{50} were well within the range that can be attained in human plasma using standard dosing regimens [23].

We demonstrated that cytotoxic interactions between pemetrexed and paclitaxel were schedule-dependent and cell line-dependent. Simultaneous exposure to pemetrexed and paclitaxel showed antagonistic effects in A549 and PA1 cells, additive/antagonistic effects in MCF7

Table 1 Mean values of observed data, predicted minimum, and predicted maximum values of MTA in combination with paclitaxel at IC_{80} for MCF7, PA1 and WiDr cells and at IC_{50} for A549 cells

Schedule	Cell line	n	Observed data	Predicted data for an additive effect		Effect
				Minimum	Maximum	
MTA + paclitaxel	A549	6	> 0.92	0.22	0.69	Antagonism ($P < 0.05$)
	MCF7	11	0.61	0.42	0.52	Additive/antagonism
	PA1	7	0.71	0.33	0.60	Antagonism ($P < 0.05$)
	WiDr	9	0.61	0.29	0.78	Additive
MTA → paclitaxel	A549	8	0.31	0.36	0.80	Synergism ($P < 0.05$)
	MCF7	8	0.45	0.60	0.66	Synergism ($P < 0.05$)
	PA1	7	0.41	0.32	0.70	Additive
	WiDr	10	0.34	0.33	0.83	Additive
Paclitaxel → MTA	A549	6	0.78	0.31	0.82	Additive
	MCF7	8	0.58	0.44	0.66	Additive
	PA1	6	0.55	0.44	0.67	Additive
	WiDr	9	0.64	0.25	0.93	Additive