

TABLE 1—(Continued)

JCI No	Name	Abbreviation	Application/Target/Mechanism
-418	Acrylamide		Neurotoxin/carcinogenicity
-417	Hexachlorobenzene	BHC	Agricultural chemical/carcinogenicity
-346	2-Deoxyglucose	2-DG	Glycolytic pathway/glycosylation inhibitor
-325	Pentachlorophenol	PCP	Agricultural chemical/teratogenicity/carcinogenicity
-324	Aniline		Oxidative stress/methemoglobinemia/carcinogenicity
-323	Triazine		Agricultural chemical
-322	Edifenphos	EDDP	Agricultural chemical/antibiotics/choline esterase
-321	γ -1,2,3,4,5,6-Hexachlorocyclohexane	γ -BHC	Agricultural chemical/carcinogenicity
-320	Dichlorvos	DDVP	Agricultural chemical/teratogenicity/carcinogenicity
-319	O-Ethyl O-4-nitrophenyl phenylphosphonothioate	EPN	Agricultural chemical
-318	Cadmium chloride	CdCl ₂	Teratogenicity/carcinogenicity
-317	Phenylmercury acetate	PMA	Fungicides/mutagenicity
-316	Mercaptoacetic acid		Synthetic intermediate
-315	1,3-Diphenylguanidine	DPG	Vulcanizing agent
-314	3,4,4'-Trichlorocarbanilide	TCC	Cosmetics/antibacterial agent
-313	3-Iodo-2-propynyl butylcarbamate	IPBC	Antibacterial agent
-311	2,3,3,3'-2',3',3'-Octachlorodipropylether	S-421	Agricultural chemical/antibacterial agent
-310	1,2-Benzisothiazolin-3-one	BIT	Antibacterial agent
-309	Isobornylthiocyanacetate	IBTA	Antibacterial agent
-308	p-Chlorophenyl-3-iodopropargylformal	CPIP	Antibacterial agent
-307	Zinc butylxanthate	ZBX	Vulcanizing agent
-306	Polypropylene glycol	PG	Synthetic intermediate
-305	10,10'-Oxy-bis(phenoxyarsine)	OBPA	Antibacterial agent
-296	Snake venom from <i>Naja naja kaouthia</i>	SV-NNK	Snake venom
-295	Snake venom from <i>Naja nigricollis</i>	SV-NN	Snake venom
-294	2,5-di(tert-butyl)-1,4-Hydroquinone	DTBHQ	Oxidative stress
-293	Ibotenic Acid		Mushroom toxin/neurotoxin
-292	N-Methyl-4-phenyl-1,2,3,6-tetrahydropyridine	MPTP	Neurotoxin
-289	Tetrodotoxin		Natural product/Na ⁺ channel inhibitor
-288	ICI 182,780		Estrogen antagonist
-275	Benzophenone		Agricultural chemical
-274	1,2-Dibromo-3-chloropropane	DBCP	Antibacterial agent/insecticide/carcinogenicity
-273	Zineb		Agricultural chemical
-272	Dieldrin		Insecticide
-271	Hexachlorobenzene	HCB	Antibacterial agent/carcinogenicity
-270	Ziram		Antibacterial agent/vulcanizing agent
-269	Chlordane		Insecticide/carcinogenicity
-268	4,4'-Dichlorodiphenyltrichloroethane	p,p'-DDT	Insecticide/carcinogenicity/teratogenicity
-267	Bisphenol A	BPA	Estrogenic
-266	17- β -Estradiol	E2	Estrogenic
-265	Diethylstilbestrol	DES	Estrogenic
-261	Paraquat		Agricultural chemical/oxidative stress
-247	Ouabain		Cardiac glycosides
-245	Okadaic acid		Natural product/PP1, PP2A inhibitor
-242	Antimycin A1		Agricultural chemical
-232	Digoxin		Cardiac glycosides
-201	OH-Flutamide		Flutamide derivative/androgen antagonist
-200	Flutamide		Anticancer drugs/androgen antagonist
-185	30% H ₂ O ₂		Oxidative stress
-182	N-Acetyl-L-cysteine	NAC	Super oxydase scavenger
-181	L-Ascorbic acid		Food constituent
-179	Dopamine		Neurotransmitter
-177	Caffeine		Food constituent
-168	Cycloheximide		Protein synthesis inhibitor
-144	4-Hydroxyphenylretinamide	4-HPR	RAR
-137	Indomethacin		COX inhibitor
-99	SN-38		Irinotecan derivative/Topo I
-96	Toremifene		Anticancer drugs/estrogen antagonist
-95	Tamoxifen		Anticancer drugs/estrogen antagonist
-63	Cyclosporin A		Anticancer drugs/helper T cell
-46	HCFU		Anticancer drugs/antimetabolite(pyrimidine)
-36	Docetaxel		Anticancer drugs/tubulin
-35	Paclitaxel		Anticancer drugs/tubulin
-34	Colchicine		Antipodagric/tubulin
-33	Cisplatin		Anticancer drugs/DNA cross linker
-32	Carboplatin		Anticancer drugs/DNA cross linker
-31	Irinotecan		Anticancer drugs/Topo I
-30	Camptothecin	CPT	Anticancer drugs/Topo I
-24	Methotrexate		Anticancer drugs/DHFR
-19	Vincristine		Anticancer drugs/tubulin
-18	Vinblastine		Anticancer drugs/tubulin
-16	Mitomycin-C	MMC	Anticancer drugs/DNA alkylator
-9	Tegafur		Anticancer drugs/antimetabolite(pyrimidine)
-8	5-Fluorouracil	5-FU	Anticancer drugs/antimetabolite(pyrimidine)
-5	Cytarabine		Anticancer drugs/antimetabolite(pyrimidine)
-4	Nitrogen mustard		Anticancer drugs/DNA alkylator

RAR, retinoic acid receptor; RXR, retinoid X receptor.

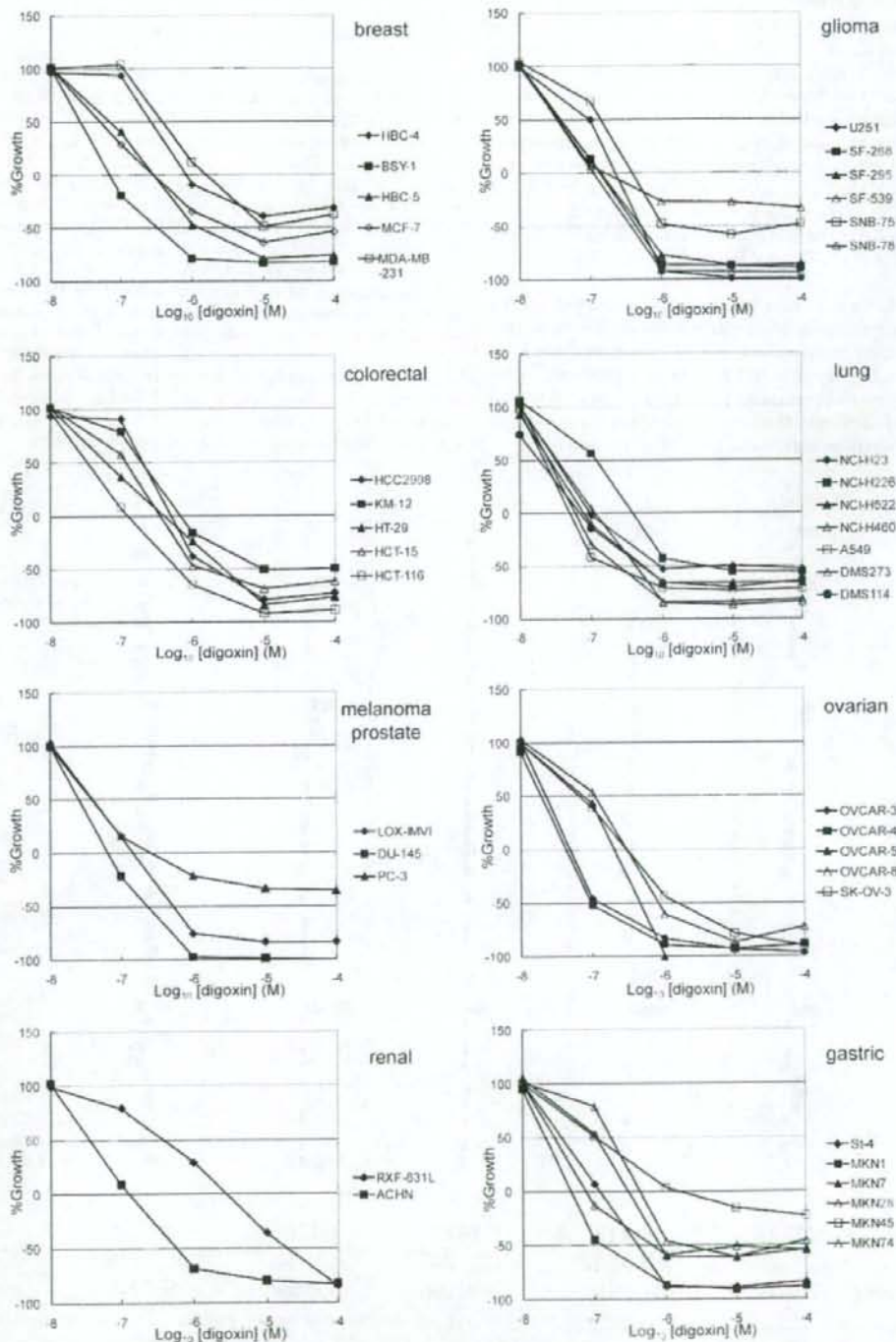


Fig. 1. Dose response curves of digoxin against growth of JFCR-39 cells. The x-axis represents concentration of digoxin and the y-axis represents percentage growth. The GI50 represents the concentration required to inhibit cell growth by 50% compared with untreated controls.

the standard anticancer drugs using the COMPARE algorithm (Yamori et al., 1999). We have used this system successfully and demonstrated that the molecular targets of the novel chemicals MS-274, FJ5002, and ZSTK474 were topoisomerases I and II (Yamori et al., 1999), telomerase (Naasani et al., 1999), and phosphatidylinositol 3-kinase (Yaguchi et al., 2006), respectively. Several other interesting studies, based on a panel of cancer cells, classified anticancer drugs according to their action mechanisms or molecular targets by cluster analysis of their GI50 values (Weinstein et al., 1992, 1997; Dan et al., 2002). Correlation analysis has also been used to explore the genes associated with the sensitivity of the cells in the panel to anticancer drugs (Scherf et al., 2000; Okutsu et al., 2002; Zembutsu et al., 2002; Nakatsu et al., 2005).

In this study, we have examined the potential of the JFCR39 system in classifying various chemicals, and predicted their action mechanisms. For this purpose, we have determined the fingerprints of 130 different types of chemicals including toxic chemicals, pesticides, drugs and synthetic intermediates, and then classified these chemicals according to the cluster analysis of their fingerprints.

Materials and Methods

Cell Lines and Cell Cultures. The panel of human cancer cell lines has been described previously (Yamori et al., 1999; Dan et al., 2002) and consists of the following 39 human cancer cell lines: lung cancer, NCI-H23, NCI-H226, NCI-H522, NCI-H460, A549, DMS273, and DMS114; colorectal cancer, HCC-2998, KM-12, HT-29, HCT-15, and HCT-116; gastric cancer, MKN-1, MKN-7, MKN-28, MKN-45, MKN-74, and St-4; ovarian cancer, OVCAR-3, OVCAR-4, OVCAR-5, OVCAR-8, and SK-OV-3; breast cancer, BSY-1, HBC-4, HBC-5, MDA-MB-231, and MCF-7; renal cancer, RXF-631L and ACHN; melanoma, LOX-IMVI; glioma, U251, SF-295, SF-539, SF-268, SNB-75, and SNB-78; and prostate cancer, DU-145 and PC-3. All cell lines were cultured in RPMI 1640 medium (Nissui Pharmaceutical, Tokyo, Japan) with 5% fetal bovine serum, penicillin (100 units/ml), and streptomycin (100 µg/ml) at 37°C under 5% CO₂.

Determination of Cell Growth Inhibition Profiles. Growth inhibition experiments were performed to assess the sensitivity of the cells to various chemicals as described before (Yamori et al., 1999; Dan et al., 2002). Growth inhibition was measured by determining the changes in the amounts of total cellular protein after 48 h of chemical treatment using a sulforhodamine B assay. For each chemical, the growth assay was performed using a total of five different concentrations of the chemical (for example, 10⁻⁴, 10⁻⁵,

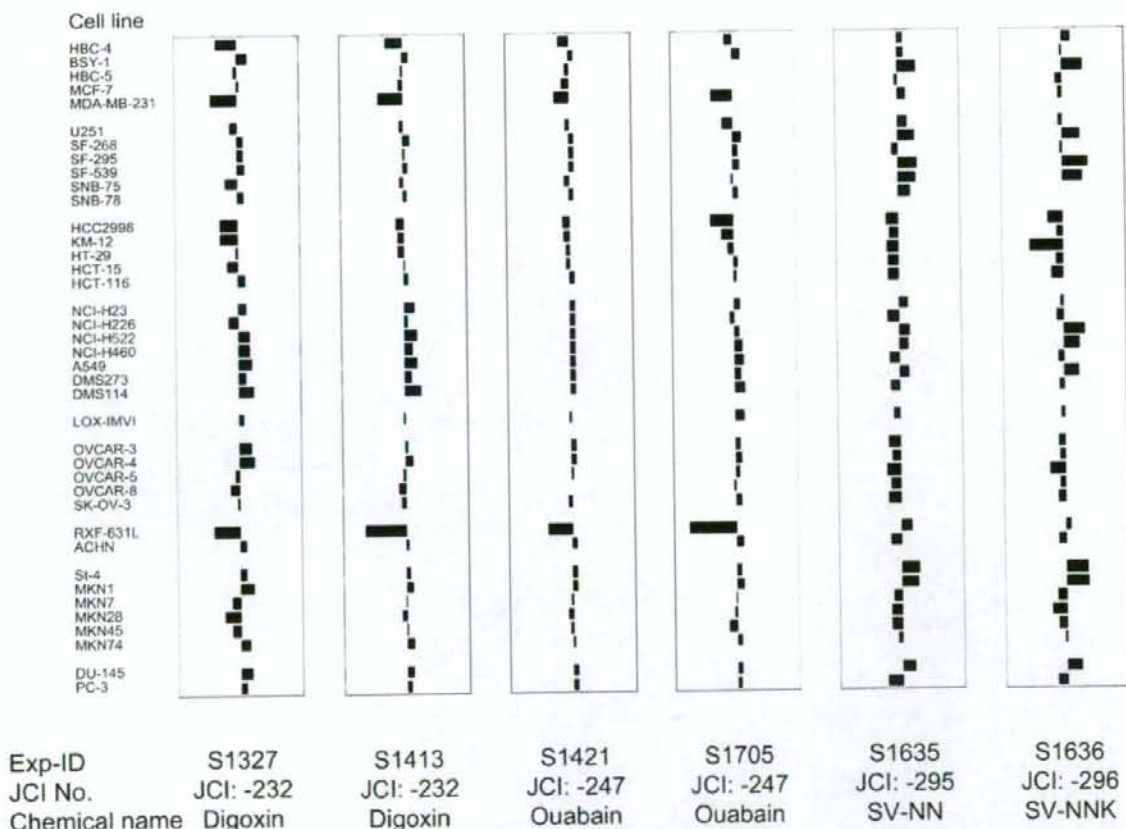


Fig. 2. Fingerprints of digoxin, ouabain, SV-NN, and SV-NNK. Fingerprint shows the differential growth inhibition pattern of the cells in the JFCR-39 panel against the test chemical. The X-axis represents relative value of GI50; $(-1) \times (\log \text{GI50} - \text{MG-MID})$; MG-MID is the mean value of the log GI50. Zero means the mean GI50 and one means the GI50 value is 10-fold more sensitive than the mean GI50. Exp-ID and JCI numbers are the ID for the experiment and ID for the chemical, respectively, in our database.

10^{-6} , 10^{-7} , and 10^{-8} M) and one negative control. All assays were performed in duplicate. This GI50 calculation method is well established and reliable through anticancer drug screen using NCI60 as well as JFCR39 (Paull et al., 1989; Yamori et al., 1999; Yamori, 2003). At each test concentration, the percentage growth was calculated using the following seven absorbance measurements: growth at time 0 (T_0), growth of the control cells (C), and test growth in the presence of five different concentrations (T) of a drug. The percentage growth inhibition was calculated as: % growth = $100 \times [(T - T_0)/(C - T_0)]$ when $T \geq T_0$, and % growth = $100 \times [(T - T_0)/T]$ when $T < T_0$. The GI50 values, which represent 50% growth inhibition concentration, were calculated as $100 \times [(T - T_0)/(C - T_0)] = 50$. When the GI50 of a chemical could not be calculated, the highest used concentration was assigned as its GI50 value. Absolute values of GI50 were then log transformed for further analysis. We certified the accuracy of measured GI50 data by using reference control chemicals, such as mitomycin-C, paclitaxel, and SN-38, in every experiment and by checking the dose response curves.

Chemicals. Spirolactone, *para*-aminoazobenzene, *para*-cresidine, neostigmine bromide, *para*-dichlorobenzene, phenytoin, *ortho*-toluidine, imipramine, cobalt chloride, atrazine, propylthiouracil, (D,L)-thalidomide, carbon tetrachloride, hydroquinone, monocrotaline, vinyl chloride, tributyl-tin chloride, valproic acid, benzene, acrylamide, pentachlorophenol, aniline, 1,3-diphenylguanidine, polypropylene glycol, 10,10'-oxy-bis(phenoxyarsine), testosterone propionate, carbaryl, acephate, bisphenol A, 17- β -estradiol, diethylstilbestrol, and α -bungarotoxin were purchased from Wako (Tokyo, Japan). Snake venoms from *Aghistrodon halys blomhoffii*, *Trimeresurus flavoviridis*, *Crotalus atrox*, *Naja nigricollis*, and *Naja kaouthia* were purchased from Latoxan (Valence, France).

TABLE 2

Log₁₀ GI50 values of chemicals for each cell line in the JFCR-39 panel

Hi-Cone means the highest concentration of the test chemical used. When the growth inhibition was over 50% at the Hi-Cone, GI₅₀ was assigned the Hi-Cone value.

Exp-ID	S3416	S3415	S3413	S3245	S3117	S3414	S3118	S3246	S3125	S3124	S3123	S1636	S1635	S1634	S1718
JCI No	-687	-686	-559	-559	-559	-560	-560	-560	-567	-566	-565	-296	-295	-294	-294
Name or Abbr.	TTNPB	13-cis	9-cis			ATRA			SV-TF	SV-CA	SV-AHB	SV-NNK	SV-NN	DTBHQ	
Hi-Cone	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4
HBC-4	-4.76	-4.00	-4.53	-4.40	-4.43	-4.42	-4.41	-4.41	-5.87	-5.80	-5.66	-7.25	-7.31	-4.72	-4.80
BSY-1	-4.78	-4.16	-4.60	-4.73	-4.73	-4.69	-4.70	-4.81	-6.31	-6.06	-5.76	-6.93	-7.34	-5.07	-4.93
HBC-5	-4.80	-4.41	-4.56	-4.57	-4.61	-4.61	-4.47	-4.51	-6.98	-6.45	-5.73	-7.64	-7.72	-4.89	-4.78
MCF-7	-4.73	-4.35	-4.40	-4.39	-4.48	-4.48	-4.54	-4.66	-5.87	-5.78	-5.68	-6.77	-7.06	-5.29	-5.25
MDA-MB-231	-4.75	-4.21	-4.70	-4.55	-4.69	-4.63	-4.53	-4.65	-5.90	-5.86	-5.84	-6.84	-7.39	-5.52	-5.30
U251	-4.77	-4.14	-4.61	-4.51	-4.61	-4.57	-4.45	-4.63	-6.45	-5.76	-5.70	-6.85	-7.44	-4.96	-5.11
SF-268	-4.75	-4.00	-4.24	-4.55	-4.40	-4.47	-4.48	-4.76	-5.90	-5.79	-5.70	-7.53	-7.67	-4.77	-4.81
SF-295	-4.80	-4.29	-4.54	-4.66	-4.60	-4.59	-4.48	-4.57	-6.19	-5.80	-5.74	-6.89	-6.97	-4.87	-4.97
SF-539	-4.95	-4.35	-4.75	-4.80	-4.79	-4.80	-4.71	-4.76	-6.39	-5.96	-5.81	-7.79	-7.75	-4.79	-4.86
SNB-76	-5.31	-5.28	-5.13	-5.19		-4.71	-4.69	-4.87	-6.41	-6.33	-5.93	-7.60	-7.70	-4.67	-4.80
SNB-78	-4.77	-4.25	-4.69	-4.78	-4.86	-4.49	-4.70	-4.68	-6.19	-6.00	-5.95	-6.97	-7.53	-4.75	-4.75
HCC2998	-4.68	-4.00	-4.48	-4.61	-4.62	-4.55	-4.62	-4.76	-5.91	-5.75	-5.67	-6.47	-6.77	-4.82	-4.75
KM-12	-4.70	-4.00	-4.46	-4.51	-4.48	-4.51	-4.47	-4.58	-5.93	-5.80	-5.65	-6.77	-6.87	-4.74	-4.77
HT-29	-4.73	-4.00	-4.47	-4.53	-4.50	-4.60	-4.52	-4.56	-5.90	-5.80	-5.66	-5.89	-6.78	-4.80	-4.89
HCT-15	-4.72	-4.25	-4.45	-4.49	-4.48	-4.52	-4.57	-4.53	-5.88	-5.76	-5.77	-6.73	-6.82	-4.72	-4.77
HCT-116	-4.77	-4.07	-4.67	-4.59	-4.67	-4.71	-4.61	-4.64	-6.46	-6.10	-5.77	-6.58	-6.82	-4.98	-5.13
NCI-H23	-4.74	-4.00	-4.47	-4.60	-4.59	-4.61	-4.55	-4.63	-6.11	-5.75	-5.72	-6.86	-7.42	-4.76	-4.90
NCI-H226	-4.72	-4.00	-4.61	-4.68	-4.78	-4.80	-4.54	-5.48	-5.95	-5.81	-5.76	-6.73	-6.78	-4.89	-4.91
NCI-H522	-4.72	-4.45	-4.68	-4.82	-4.77	-4.71	-4.71	-4.68	-6.45	-5.99	-5.78	-7.62	-7.46	-5.37	-5.37
NCI-H460	-4.70	-4.00	-4.55	-4.63	-4.58	-4.58	-4.55	-4.49	-5.96	-5.82	-5.72	-7.44	-7.42	-4.84	-4.84
A549	-4.79	-4.00	-4.72	-4.77	-4.78	-4.70	-4.62	-4.53	-5.91	-5.79	-5.71	-6.80	-6.83	-4.83	-4.87
DMS273	-4.57	-4.21	-4.50	-4.62	-4.55	-4.57	-4.51	-4.49	-6.20	-5.81	-5.72	-7.43	-7.44	-4.91	-4.98
DMS114	-4.77	-4.16	-4.33	-4.62	-4.49	-4.51	-4.53	-4.61	-6.66	-6.33	-5.77	-6.83	-6.88	-5.12	-5.21
LOX-IMVI	-4.77	-4.69	-4.68	-4.66	-4.70	-4.77	-4.74	-4.74	-6.75	-6.59	-5.76	-6.86	-6.94	-5.05	-5.15
OVCAR-3	-4.77	-4.38	-4.56	-4.67	-4.72	-4.64	-4.62	-4.71	-6.61	-6.13	-5.89	-6.77	-6.79	-4.89	-4.86
OVCAR-4	-4.72	-4.05	-4.63	-4.64	-4.64	-4.58	-4.39	-4.54	-6.73	-6.23	-5.80	-6.82	-6.90	-5.13	-4.90
OVCAR-5	-4.75	-4.00	-4.33	-4.39	-4.42	-4.44	-4.34	-4.44	-5.92	-5.74	-5.67	-6.46	-6.71	-5.22	-5.26
OVCAR-8	-4.75	-4.23	-4.50	-4.53	-4.59	-4.66	-4.67	-4.70	-5.95	-5.77	-5.69	-6.82	-6.84	-4.64	-4.70
SK-OV-3	-4.79	-4.00	-4.49	-4.51	-4.81	-4.82	-4.54	-4.50	-5.76	-5.64	-4.91	-6.75	-6.76	-4.64	-4.74
RXP-631L	-4.77	-4.00	-4.54	-4.58	-4.60	-4.72	-4.63	-4.61	-5.91	-5.80	-5.59	-7.13	-7.46	-4.81	-4.84
ACHN	-4.73	-4.00	-4.66	-4.66	-4.66	-4.56	-4.40	-4.76	-5.90	-5.79	-5.73	-6.74	-6.80	-4.71	-4.83
Se-4	-4.74	-4.00	-4.42	-4.54	-4.85	-4.53	-4.49	-4.57	-5.91	-5.81	-5.76	-7.65	-7.70	-4.68	-4.75
MKN1	-4.75	-4.33	-4.56	-4.63	-4.62	-4.56	-4.45	-4.48	-6.15	-5.81	-5.78	-7.67	-7.68	-4.59	-4.81
MKN7	-4.78	-4.40	-4.68	-4.59	-4.70	-4.73	-4.56	-4.65	-6.29	-5.85	-5.76	-6.70	-6.90	-4.79	-4.84
MKN28	-4.71	-4.28	-4.56	-4.59	-4.59	-4.65	-4.56	-4.60	-6.10	-5.93	-5.68	-6.51	-6.81	-4.72	-4.89
MKN45	-4.72	-4.00	-4.51	-4.41	-4.46	-4.73	-4.41	-4.43	-6.06	-5.90	-5.69	-6.71	-6.82	-4.71	-4.87
MKN74	-4.74	-4.40	-4.61	-4.63	-4.61	-4.73	-4.68	-4.67	-5.97	-5.92	-5.61	-6.92	-7.00	-5.10	-5.42
DU-145	-4.68	-4.00	-4.25	-4.78	-4.41	-4.42	-4.44	-4.54	-6.08	-5.82	-5.75	-7.43	-7.55	-4.89	-5.02
PC-3	-4.74	-4.00	-4.58	-4.65	-4.48	-4.74	-4.39	-4.51	-5.83	-5.77	-5.61	-6.67	-6.69	-4.89	-4.74

2-Aminomethylpyridine, 1H-1,2,4-triazole, 1H-1,2,3-triazole, 3,4,4'-trichlorocarbanilide, difenphos, dichlorvos, *O*-ethyl *O*-4-nitrophenyl phenylphosphonothioate, 2,4-dinitrophenol, *N*-methylaniline, 1,2-dichloro-3-nitrobenzene, 4-ethylnitrobenzene, 2-vinylpyridine, 3-amino-1H-1,2,4-triazole, *N*-ethyl-*N*-nitrosourea, 5-aza-2'-deoxycytidine, ethynyl estradiol, 3-methylcholanthrene, phenobarbital, acetaminophen, isoniazid, capsaicin, *N*-deacetyl-*N*-methylcolchicine (Colcemid), 2,4-dinitrochlorobenzene, and dexamethasone were from Sigma Chemicals (St. Louis, MO). Methoprene acid, methoprene, all-*trans* retinoic acid, and 9-*cis* retinoic acid were from BIOMOL International L.P. (Plymouth Meeting, PA). Levothyroxine was from MP Biomedicals (Irvine, CA). 3-Iodo-2-propynyl butylcarbamate was from Olin Japan Inc. (Tokyo, Japan), *p*-chlorophenyl-3-iodopropargylformal was from Nagase ChemteX (Osaka, Japan), and 2,3,3,3'-2',3',3',3'-octachlorodipropylether was from Sankyo Chemical Industries, Ltd. (Tokyo, Japan), 1,2-Benzisothiazolin-3-one was from Riverson (Osaka, Japan), zinc butylxanthate was from Ouchishinko Chemical Industrial Co., Ltd. (Tokyo, Japan), and 4-amino-2,6-dichlorophenol was from Tokyo Kasei Kogyo Co. Ltd. (Tokyo, Japan).

Hierarchical Clustering. Hierarchical clustering analysis was carried out using the average linkage method and the "GeneSpring" software (Silicon Genetics, Inc., Redwood, CA). Pearson correlation coefficients were used to determine the degree of similarity.

Results

Sensitivity of JFCR39 to Chemicals. Sensitivity of the JFCR39 panel of cells to 130 chemicals was determined as described under *Materials and Methods*. Table 1 summarizes

abbreviations, applications, targets, and known mechanisms of 130 chemicals and 21 anticancer drugs. Approximately 15% of the chemicals were assessed twice or more. Approximately 40% of the chemicals tested had little effect on the growth of cells in the JFCR39 panel. However, the rest of the chemicals significantly inhibited the cell growth across the JFCR39 panel. For example, Fig. 1 shows the dose response curves of the cells in the JFCR39 panel against digoxin. The concentration at which the cell growth is inhibited by 50% represents GI50. Figure 2 shows the fingerprints of four chemicals [digoxin, ouabain, snake venom from *N. nigracollis* (SV-NN), and snake venom from *N. naja kaouthia* (SV-NNK)], which differentially inhibited the growth of cells in the JFCR39 panel; these fingerprints were drawn based on a calculation using a set of GI50s and clearly represented the GI50 pattern. These results were highly reproducible in that the Pearson correlation coefficient of the duplicate experiments for digoxin was 0.839 ($p < 0.001$) and that for ouabain was 0.864 ($p < 0.001$). It is noteworthy that, digoxin and ouabain, both of which are cardiac glycosides and inhibit Na-K ATPase, showed similar fingerprints. The fingerprints of SV-NNK and SV-NN, which belong to the elapidae, known as cobras, were also similar, but were different from the fingerprints of digoxin and ouabain. Table 2 summarizes only a portion of the GI50 values from 160 experiments involving 130 chemicals and 42 experiments involving 21 anticancer drugs. GI50 values from all experiments are described in the

Supplemental Data (Table S1). All these data were stored in a chemosensitivity database and used for further analysis.

Classification of the Chemicals by Hierarchical Clustering. Sixty-nine chemicals were selected for further analysis based on the following criteria: 1) GI50 values for the test chemical can be determined for at least 10 cell lines in the JFCR39 panel, and 2) the range of log GI50 for the test chemical is more than 0.6, suggesting differential growth inhibition. We analyzed the GI50 values of these 69 chemicals and 20 anticancer drugs by hierarchical clustering analysis (Fig. 3). We found approximately 12 clusters (threshold: $r = 0$, Fig. 3, clusters A-L), which were further divided into 49 subclusters (threshold: $r = 0.408$, Fig. 3, clusters A1-L6).

Analysis of Clusters. Most anticancer drugs we have tested belonged either to cluster A or cluster H, depending on their modes of action (Dan et al., 2002). The targets of the anticancer drugs belonging to the cluster A were related to DNA (Topo I, antimetabolite of pyridine, DNA alkylator) and the target of the anticancer drugs belonging to the cluster H was tubulin. We presently found that cisplatin exceptionally belonged to cluster F2, not cluster A, although it is known to cross-link DNA strands (Jamieson and Lippard, 1999; Wong and Giandomenico, 1999). We were also able to precisely group the clusters into several subclusters having similar characteristics. For example, the cardiac glycosides digoxin and ouabain were grouped in one cluster (cluster F3). SV-

S3243	S3244	S1534	S3237	S3238	S1525	S3236	S1928	S1421	S1705	S1327	S1413	S1413	S3408	S3409	S2421
-599	-599	-270	-270	-270	-261	-261	-261	-247	-247	-232	-232	-232	-421	-421	-421
Thiram		Ziram			Paraquat			Ouabain		Digoxin			TBT		
-4	-4	-4	-4	-4	-4	-3	-4	-4	-6	-4	-4	-4	-4	-4	-4
-4.71	-4.79	-5.80	-5.73	-5.70	-4.00	-3.61	-4.00	-7.54	-7.28	-6.57	-6.96	-6.96	-6.79	-6.77	-6.72
-6.97	-7.12	-6.85	-6.76	-6.80	-4.00	-4.45	-4.51	-8.00	-7.76	-7.58	-7.68	-7.68	-7.03	-7.01	-6.83
-7.41	-7.66	-7.18	-7.47	-7.47	-4.68	-4.70		-7.76	-7.51	-7.15	-7.44	-7.44	-6.76	-6.88	-6.83
-4.77	-4.80	-6.00	-5.84	-5.83	-4.06	-3.72	-4.00	-7.64	-7.51	-7.29	-7.39	-7.39	-6.86	-6.84	-6.79
-4.66	-4.68	-5.64	-5.75	-5.63	-4.00	-3.57	-4.00	-7.40	-6.81	-6.41	-6.72	-6.72	-6.83	-6.81	-6.70
-4.75	-4.78	-5.71	-5.79	-5.82	-4.00	-3.69	-4.00	-7.75	-7.16	-7.01	-7.40	-7.40	-6.79	-6.77	-6.72
-4.86	-4.96	-5.74	-5.83	-7.01	-4.00	-4.08	-4.00	-8.00	-7.77	-7.42	-7.70	-7.70	-6.84	-6.85	-6.71
-4.77	-4.89	-5.71	-5.70	-5.79	-4.47	-4.37	-4.20	-8.00	-7.64	-7.42	-7.55	-7.55	-6.75	-6.75	-6.76
-4.75	-4.88	-5.73	-5.75	-5.77	-4.00	-4.03	-4.00	-8.00	-7.70	-7.46	-7.63	-7.63	-6.77	-6.72	-6.67
-4.71	-4.96	-5.79	-5.92	-5.80	-4.00	-3.94	-4.00	-7.70	-7.45	-6.86	-7.40	-7.40	-6.99	-6.95	-7.05
-4.70	-4.78	-5.69	-5.64	-5.69	-4.00	-3.78	-4.00	-7.98	-7.64	-7.45	-7.60	-7.60	-6.72	-6.79	-6.70
-4.82	-4.69	-5.76	-5.79	-5.81	-4.00	-3.70	-4.00	-7.64	-6.77	-6.68	-7.25	-7.25	-6.77	-6.79	-6.72
-4.80	-4.80	-5.43	-5.74	-5.73	-4.00	-3.58	-4.00	-7.67	-7.12	-6.69	-7.34	-7.34	-7.00	-6.98	-6.74
-4.68	-4.85	-5.75	-5.77	-5.76	-4.10	-4.03	-4.07	-7.75	-7.31	-7.20	-7.34	-7.34	-6.89	-6.84	-6.66
-4.68	-4.75	-5.70	-5.72	-5.83	-4.00	-3.64	-4.00	-7.74	-7.63	-6.92	-7.54	-7.54	-6.88	-6.84	-6.70
-4.72	-4.72	-5.74	-5.68	-5.77	-4.00	-3.60	-4.00	-8.00	-7.87	-7.47	-7.62	-7.62	-6.90	-6.85	-6.74
-4.69	-4.78	-5.96	-5.85	-5.84	-4.19	-4.18	-4.00	-8.00	-7.67	-7.50	-7.84	-7.84	-6.90	-6.85	-6.76
-6.33	-6.74	-5.63	-5.96	-6.12	-4.41	-4.41	-4.00	-8.00	-7.37	-6.93	-7.61	-7.61	-6.99	-6.91	-6.74
-7.49	-7.50	-7.44	-7.66	-8.00	-4.49	-4.71	-4.59	-8.00	-7.64	-7.59	-7.91	-7.91	-6.83	-6.80	-6.25
-6.14	-6.16	-6.30	-6.10	-6.15	-4.30	-4.45	-4.37	-8.00	-7.74	-7.60	-7.77	-7.77	-6.98	-6.98	-6.56
-4.84	-4.82	-5.97	-5.91	-5.91	-4.49	-4.49	-4.41	-8.00	-7.80	-7.66	-7.91	-7.91	-6.82	-6.87	-6.73
-6.64	-6.58	-6.43	-6.84	-6.82	-4.25	-4.43	-4.30	-8.00	-7.71	-7.48	-7.72	-7.72	-6.74	-6.75	-6.70
-7.18	-7.39	-7.37	-7.38	-7.43	-4.50	-4.63	-4.27	-8.00	-7.84	-7.73	-8.00	-8.00	-7.11	-7.12	-7.02
-4.68	-4.71	-5.66	-5.71	-5.70	-4.00	-3.51	-4.00	-7.80	-7.80	-7.39	-7.46	-7.46	-6.93	-6.94	-6.76
-4.86	-6.25	-6.07	-6.35	-6.32	-4.00	-4.46	-4.28	-8.00	-7.66	-7.64	-7.59	-7.59	-6.80	-6.82	-6.74
-4.77	-6.67	-5.90	-5.91	-5.87	-4.00	-4.21	-4.48	-8.00	-7.71	-7.71	-7.72	-7.72	-6.91	-7.20	-6.80
-4.90	-6.00	-6.11	-6.91	-6.74	-4.00	-3.98	-4.00	-7.89	-7.62	-7.12	-7.42	-7.42	-6.90	-6.93	-6.75
-4.62	-4.74	-5.59	-5.68	-5.67	-4.00	-3.84	-4.00	-7.85	-7.44	-6.97	-7.29	-7.29	-6.73	-6.67	-6.57
-4.39	-4.38	-4.92	-5.49	-5.53	-4.00	-3.39	-4.00	-7.74	-7.67	-7.18	-7.38	-7.38	-6.73	-6.77	-6.68
-4.75	-4.65	-5.57	-5.63	-5.60	-4.00	-3.60	-4.00	-7.10	-6.00	-6.42	-6.20	-6.20	-6.78	-6.76	-6.68
-4.52	-4.60	-5.84	-5.68	-5.69	-4.00	-3.51	-4.00	-8.00	-7.72	-7.44	-7.59	-7.59	-6.78	-6.77	-6.76
-4.59	-4.72	-5.99	-5.73	-5.81	-4.00	-3.58	-4.00	-8.00	-7.65	-7.45	-7.60	-7.60	-6.80	-6.80	-6.72
-4.80	-4.85	-6.82	-5.84	-5.92	-4.41	-4.61	-4.48	-8.00	-7.72	-7.68	-7.72	-7.72	-7.25	-7.15	-6.87
-4.79	-4.82	-6.55	-5.84	-5.82	-4.08	-4.29	-4.32	-7.80	-7.48	-6.98	-7.47	-7.47	-7.34	-7.07	-6.86
-7.18	-7.21	-5.82	-7.09	-7.13	-4.00	-4.40	-4.18	-7.70	-7.42	-6.77	-7.37	-7.37	-6.84	-6.82	-6.87
-6.65	-6.71	-6.05	-7.18	-6.86	-4.00	-4.29	-4.35	-7.77	-7.25	-6.99	-7.52	-7.52	-6.96	-6.97	-6.87
-7.05	-7.08	-6.35	-5.86	-7.05	-4.00	-4.47	-4.06	-7.91	-7.65	-7.55	-7.74	-7.74	-6.97	-7.37	-7.05
-4.47	-4.70	-5.68	-5.68	-5.65	-4.00	-3.57	-4.00	-8.00	-7.64	-7.59	-7.71	-7.71	-6.90	-6.89	-6.70
-4.42	-4.77	-5.61	-5.53	-5.56	-4.00	-3.64	-4.37	-8.00	-7.62	-7.41	-7.62	-7.62	-6.77	-6.78	-6.73

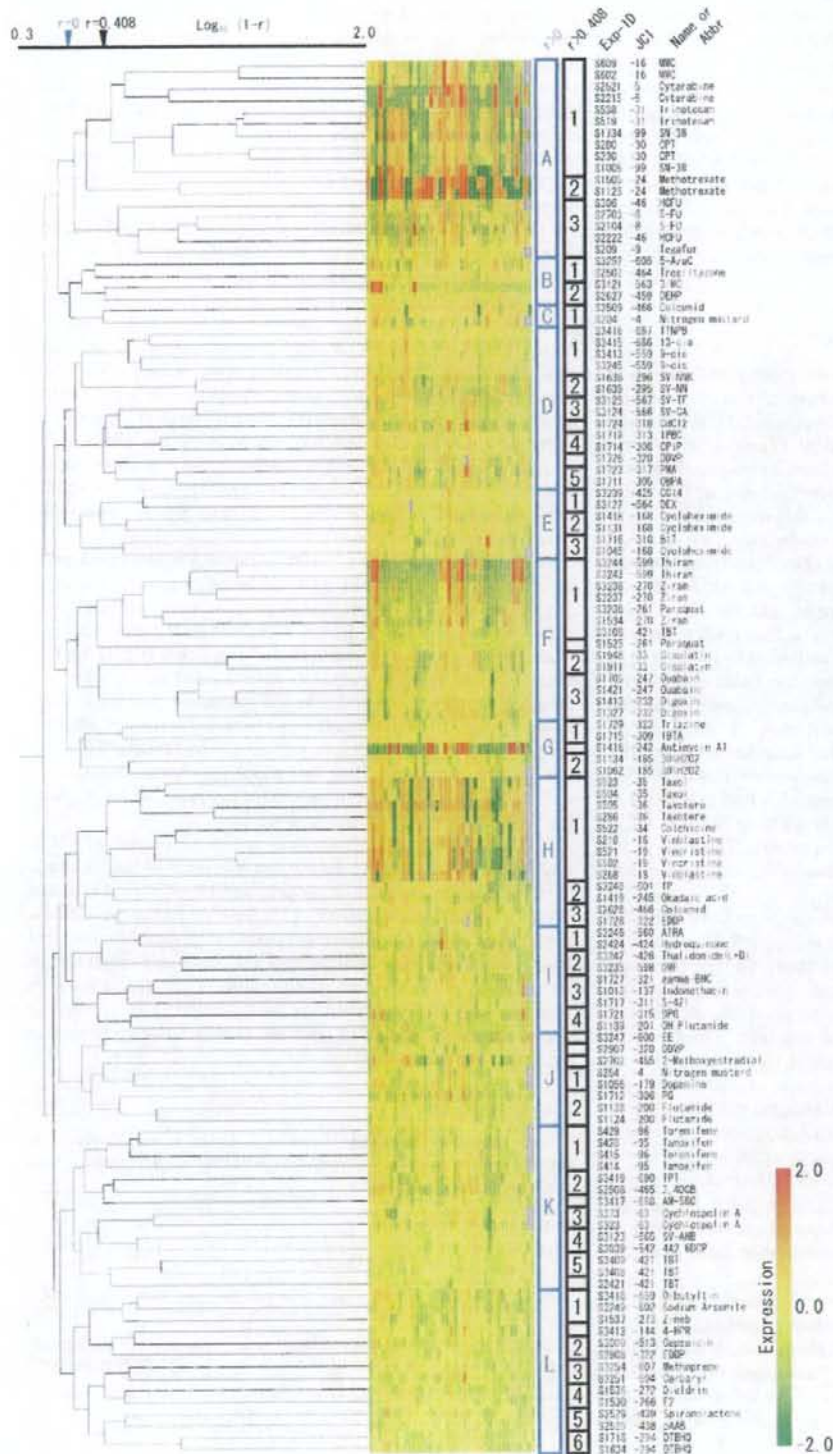


Fig. 3. Hierarchical clustering of 69 test chemicals and 20 anticancer drugs based on their GI50 values. Hierarchical clustering method was an "average linkage method" using the Pearson correlation as distance. We classified the chemicals into two kinds of clusters; their threshold values were $r = 0$ and $r = 0.408$ ($p < 0.01$), respectively. Gradient color indicates relative level (log transformed) of GI50. Red, more sensitive than the mean GI50 (2.0); yellow, mean GI50 (0.0); and green, less sensitive than the mean GI50 (-2.0). On the color scale, red represents the GI50 value that is 100-fold higher than the mean GI50.

NNK and SV-NN, on the other hand, belonged to the cluster D2. These results are in accordance with the similar fingerprints shown in Fig. 2. It is noteworthy that the snake venoms from the *C. atrox* and *T. flavoviridis*, species belonging to the viperidae family of snakes, formed another cluster (cluster D3), which was different from that of the elapidae family of snakes, *N. naja kaouthia* and *N. nigricollis*. 9-*cis* Retinoic acid, 13-*cis* retinoic acid, and 4-[*E*-2-(5,6,7,8-tetrahydro-5,5,8,8-tetra-methyl-2-naphthalenyl)-1-propenyl]benzoic acid, which are RAR agonists (Aström et al., 1990), also formed a separate cluster (cluster D1). Likewise, agricultural chemicals paraquat, ziram, and thiram formed a single cluster (cluster F1).

Discussion

The JFCR39 system coupled to a drug activity database is a good model for investigating the diversity of chemosensitivity in cancer cells. We have previously established panels of human cancer cell lines [JFCR39 (Yamori, 2003) and JFCR45 (Nakatsu et al., 2005)]. We used these panels of cells to demonstrate that they provide powerful means to predict the action mechanisms of drugs, and also used them to identify new target compounds. In this manuscript, we used the JFCR39 system to evaluate various chemicals (such as toxic chemicals, agricultural chemicals, and synthetic intermediates), which are not anticancer drugs, and classified them according to their molecular target or action mechanism. As a result, these chemicals were classified into a number of clusters. Our results also suggested that each cluster consisted of chemicals sharing a common action mechanism.

We determined the growth inhibition of cells in the JFCR39 panel by 130 chemicals and calculated their GI50 values. Some of the chemicals were assessed twice or more to confirm the reproducibility of the assay. We had to exclude 61 chemicals from further analysis because they did not inhibit the cells in the JFCR39 panel significantly. The rest of the chemicals (69 of 130, ~60%) met our selection criteria and were evaluated by cluster analysis.

First, we found that the chemicals tested in duplicate formed tight clusters, showing high reproducibility. Next, we investigated the difference between these 69 test chemicals and the anticancer drugs. Sixty-nine chemicals, which are not anticancer drugs, formed several clusters, which were different from the anticancer drug clusters. These results suggest that the action mechanisms of these chemicals are different from the action mechanisms of the anticancer drugs. However, we found that cisplatin did not belong to the cluster A, which consisted of DNA-targeting anticancer drugs. We do not understand the reason at present. However, there is a possibility that cisplatin has other action mechanisms, which may have made the fingerprint of cisplatin different from those of other DNA-targeting drugs. Indeed, cisplatin is known to form DNA-protein cross-links (Zwelling et al., 1979; Chválová et al., 2007).

Our analysis also identified several interesting clusters. For example, the cluster F3 consisted of cardiac glycosides digoxin and ouabain, both of which inhibit Na-K ATPase (Reuter et al., 2002). The cluster D1 consisted of 9-*cis* retinoic acid, 13-*cis* retinoic acid, and 4-[*E*-2-(5,6,7,8-tetrahydro-5,5,8,8-tetra-methyl-2-naphthalenyl)-1-propenyl]benzoic acid, which are RAR agonists. These results suggest that chemicals other

than the anticancer drugs also form clusters when they share the same action mechanisms. It is noteworthy that SV-NNK and SV-NN, from snakes that belonged to the elapidae family, formed one cluster (cluster D2). In contrast, the snake venoms from the *C. atrox* and *T. flavoviridis*, which belonged to the viperidae family, formed a cluster (cluster D3) different from the elapidae cluster. These results are reasonable because snake venoms from different snake families are known to differ not only in composition but also in levels of toxicity and mechanisms of action.

The agricultural chemicals paraquat, ziram, and thiram were also classified into a single cluster (cluster F1). Among these agricultural chemicals, the action mechanism of ziram is not known. However, both paraquat and thiram are known to induce oxidative stress (Cereser et al., 2001; Suntres, 2002). Therefore, based on our observations, we could suggest that ziram also acted by inducing oxidative stress. The agricultural chemicals methoprene (insect growth regulator) and carbaryl (choline esterase inhibitor) formed cluster L3, although their common mechanism is unknown. Cluster D4 and D5 consist of the antibacterial agents or fungicides. 3-Iodo-2-propynyl-butylcarbamate and *p*-chlorophenyl-3'-iodopropargylformal, belonging to cluster D4, are the iodotype antibacterial agents.

Thus, cluster analysis of GI50 values of various chemicals, determined using the JFCR39 cell panel, suggests that the JFCR39 system could, at least in part, allow classification of chemical compounds on the basis of their action mechanisms. Our analysis also suggests that the chemicals belonging to the same cluster share a common action mechanism. We are going to develop a larger library of reference chemicals with known action mechanisms (i.e., various inhibitors of biological pathways), and expand our database by integrating their GI50 measurements, which will make the cluster analysis as well as the COMPARE analysis more informative for predicting the mechanism of test chemicals.

In conclusion, to evaluate the potential of the JFCR39 system in predicting the action mechanisms of toxic chemicals, we investigated the fingerprints of 130 different types of chemical compounds including toxic chemicals, pesticides, drugs, and synthetic intermediates. Using the hierarchical clustering analysis, we classified 69 chemicals, at least in part, based on their action mechanisms. Thus, this approach using the JFCR39 cell panel is useful not only in predicting the action mechanisms of toxic chemicals but also in evaluating their toxicity.

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Address correspondence to: Takao Yamori, Division of Molecular Pharmacology, Cancer Chemotherapy Center, Japanese Foundation for Cancer Research, 3-10-6, Ariake, Koto-ku, Tokyo 135-8550, Japan. E-mail: yamori@jfccr.or.jp, 07a@jfccr.or.jp

Effects of aromatase inhibitors on human osteoblast and osteoblast-like cells: A possible androgenic bone protective effects induced by exemestane

Yasuhiro Miki^a, Takashi Suzuki^a, Masahito Hatori^b, Katsuhide Igarashi^c, Ken-ich Aisaki^c,
Jun Kanno^c, Yasuhiro Nakamura^a, Miwa Uzuki^d, Takashi Sawai^c, Hironobu Sasano^{a,*}

^a Department of Pathology, Tohoku University Graduate School of Medicine, 2-1 Seiryō-machi, Aoba-ku, Sendai, Miyagi, 980-8575, Japan

^b Department of Orthopedic Surgery, Tohoku University Graduate School of Medicine, Sendai, Japan

^c Division of Toxicology, National Institute of Health Sciences, Biological Safety Research Center, Setagaya, Tokyo, Japan

^d Department of Pathology, Iwate Medical College, Morioka, Japan

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Abstract

Effects of aromatase inhibitors (AIs) on the human skeletal system due to systemic estrogen depletion are becoming clinically important due to their increasing use as an adjuvant therapy in postmenopausal women with breast cancer. However, possible effects of AIs on human bone cells have remained largely unknown. We therefore studied effects of AIs including the steroidal AI, exemestane (EXE), and non-steroidal AIs, Aromatase Inhibitor I (AI-I) and aminoglutethimide (AGM), on a human osteoblast. We employed a human osteoblast cell line, hFOB, which maintains relatively physiological status of estrogen and androgen pathways of human osteoblasts, i.e., expression of aromatase, androgen receptor (AR), and estrogen receptor (ER) β . We also employed osteoblast-like cell lines, Saos-2 and MG-63 which expressed aromatase, AR, and ER α/β in order to further evaluate the mechanisms of effects of AIs on osteoblasts. There was a significant increment in the number of the cells following 72 h treatment with EXE in hFOB and Saos-2 but not in MG-63, in which the level of AR mRNA was lower than that in hFOB and Saos-2. Alkaline phosphatase activity was also increased by EXE treatment in hFOB and Saos-2. Pretreatment with the AR blocker, flutamide, partially inhibited the effect of EXE. AI-I exerted no effects on osteoblast cell proliferation and AGM diminished the number of the cells. hFOB converted androstenedione into E2 and testosterone (TST). Both EXE and AI-I decreased E2 level and increased TST level. In a microarray analysis, gene profile patterns following treatment with EXE demonstrated similar patterns as with DHT but not with E2 treatment. The genes induced by EXE treatment were related to cell proliferation, differentiation which includes genes encoding cytoskeleton proteins. We also examined the expression levels of these genes using quantitative RT-PCR in hFOB and Saos-2 treated with EXE and DHT and with/without flutamide. HOXD11 gene known as bone morphogenesis factor and osteoblast growth-related genes were induced by EXE treatment as well as DHT treatment in both hFOB and Saos-2. These results indicated that the steroidal aromatase inhibitor, EXE, stimulated hFOB cell proliferation via both AR dependent and independent pathways.

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Keywords: Osteoblast; Aromatase inhibitor; Androgen; Estrogen; Exemestane

Introduction

Results in various epidemiological or clinical studies demonstrated that estrogens play important protective roles in human skeletal as well as cardiovascular systems, and estrogen deficiency resulted in accelerating the development of osteoporosis in postmenopausal women [1–3]. In breast cancer of

postmenopausal women, hormone therapies without any clinically deleterious effects due to estrogen deficiency on bone metabolism as well as lipid metabolisms are preferable. Estrogen deficiency has been generally detected in the patients with breast cancer following chemotherapy induced ovarian failure, gonadotropin analogue, and aromatase inhibitors (AIs) therapy [4]. Aromatase is the pivotal enzyme of *in situ* or intratumoral estrogen biosynthesis in postmenopausal breast cancer patients, and catalyzes the conversion from androgens into estrogens (Fig. 1A). AIs therefore play an important role in

* Corresponding author. Fax: +81 22 273 5976.

E-mail address: hsasano@patholo2.med.tohoku.ac.jp (H. Sasano).

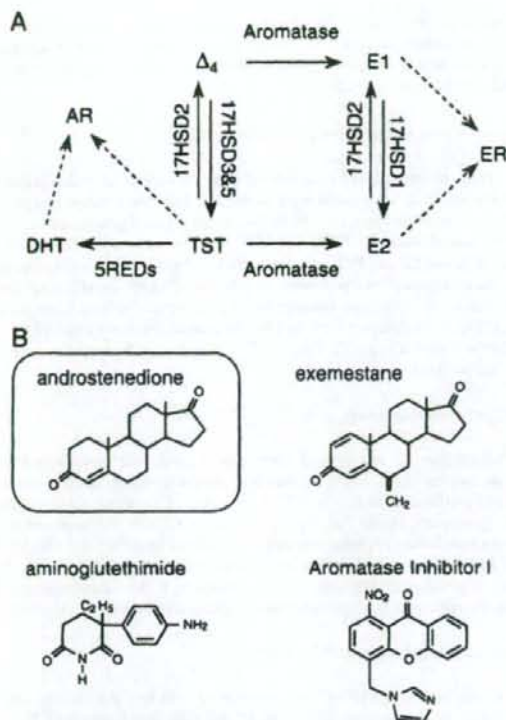


Fig. 1. (A) Summary of the pathway of estrogens and androgens production. Aromatase catalyzes the change from androstenedione (Δ_4) and testosterone (TST) into estrone (E1) and estradiol (E2), respectively. 17HSD, 17 β -hydroxysteroid dehydrogenase; 5REDs, 5 α -reductase types 1 and 2; AR, androgen receptor; DHT, 5 α -dihydrotestosterone; ER, estrogen receptor. (B) Structure of aromatase inhibitors used in this study. Androstenedione is a natural substrate of aromatase. Steroidal aromatase inhibitor, exemestane has an androstenedione-like structure.

clinical management of both primary and advanced breast cancer in postmenopausal women [5]. AIs are classified into two classes according to their modes of action. Type I AIs are steroidal inhibitions and one of them, exemestane (EXE) inhibits aromatase irreversibly and has an androstenedione (Δ_4)-like structure (Fig. 1B) [5–7]. Type II AIs are non-steroidal inhibitions and include aminoglutethimide (AGM), anastrozole, and letrozole [5].

Results of *in vivo* study using ovariectomized (OVX) rats demonstrated that EXE and its principal metabolite form, 17-hydroxexemestane (17H-EXE) but not letrozole significantly prevented bone loss in OVX rats [8,9]. EXE and its principal metabolite, 17H-EXE, are structurally related to Δ_4 and bind to androgen receptor (AR) with relatively low affinity compared to 5 α -dihydrotestosterone (DHT) [7]. These findings suggest that EXE may demonstrate protective effects toward bone tissues through its androgenic actions. However, detailed mechanisms of effects of EXE or androgen itself on human bone cells have remained largely unknown.

Various studies using human or animal bone tissues [10,11] and osteoblast cell culture using osteosarcoma cells [12,13] demonstrated that aromatase mRNA or protein was detected in osteoblast cells, which play an important role in bone remodeling. Therefore, in this study, we focused on effects of EXE in human osteoblast in an initial attempt to evaluate the effects of these AIs (summarized in Table 1 and Fig. 1B) [5–7,14], including AGM, EXE, and an experimental compound for inhibition of aromatase, Aromatase Inhibitor I (AI-I) [14] on human osteoblast and osteoblast-like cell lines. In our present study, we employed normal human cell line, hFOB, which maintains native characteristics of sex steroid hormone pathway of human osteoblasts, i.e., expression of AR, ER β but not ER α , and aromatase. We also employed other osteoblast-like cell lines, Saos-2 and MG-63 which expressed ER α as well as ER β in order to further study the mechanisms of effects of AI on human osteoblasts. We first examined the effects of estradiol (E2), DHT, progesterone (Prg), and AIs described above on cell proliferation of these cell lines, because the status of cell proliferation is important in the maintenance of homeostasis of bone tissue [15]. In addition, the effects of AIs on the conversion ratio of Δ_4 into E2 or testosterone (TST) in hFOB cultured medium were examined. We then screened E2, DHT, and EXE responsive genes using a microarray analysis in these cells, in order to further characterize the possible genomic effects of EXE on cell proliferation of osteoblasts. In this microarray analysis, hFOB was employed in order to examine the effects of E2, DHT, and EXE on native status of human osteoblasts but not on pathological status of osteoblasts such as osteosarcomas.

Materials and methods

Chemicals

Exemestane (EXE; FCE24304; 6-methyleneandrost-1,4-diene-3,17-dione) and 17-hydroxexemestane (17H-EXE; FCE25071; 6-methyleneandrost-1,4-diene-17 β -ol-3-one) were obtained from Pfizer, Inc. (ML, USA). Aminoglutethimide (AGM) and Aromatase Inhibitor I [AI-I; 4-(imidazolymethyl)-1-nitro-9H-xanthone] were obtained from Sigma-Aldrich Co. (MO, USA) and EMD Biosciences, Inc. (CA, USA), respectively. Estradiol (E2), progesterone (Prg), and RU38,486 (RU; mifepristone), spironolactone were obtained from Sigma-Aldrich. ICI 182,780 (ICI; fulvestrant) and hydroxyflutamide (OHF) were obtained from Tocris Cookson Inc. (MO, USA) and Toronto Research Chemicals, Inc. (Ontario, Canada), respectively. 5 α -dihydrotestosterone (DHT) was obtained from Wako Pure Chemical industries, Ltd. (Osaka, Japan).

Table 1
Aromatase inhibitors used in this study

	Aminoglutethimide	Exemestane	Aromatase inhibitor I
Trademark ^a	Cytadren [®]	Aromasin [®]	–
Type ^b	Type II	Type I	Type II
Generation	First	Third	–
IC50 (nM) ^c	3000	50	40

^a Cytadren[®] is trademark of Novartis Pharmaceutical Corporation. Aromasin[®] is trademark of Pfizer Inc. Aromatase Inhibitor I is non-clinical compound of Calbiochem[®].

^b Type I is steroidal compound. Type II is a non-steroidal compound.

^c Refs, Aminoglutethimide and Exemestane are Miller et al. [5]; Aromatase Inhibitor I is Recanatini et al. [14].

These materials were dissolved in pure ethanol (Wako Pure Chemical industries) and serially diluted (final concentrations: 10^{-12} M to 10^{-5} M), respectively. AGM was dissolved in DMSO (Wako Pure Chemical industries). The final concentration of ethanol and DMSO used in this study did not exceed 0.05%.

Osteoblast cell and osteoblast-like cell lines and culture conditions

Human normal osteoblast cell, hFOB 1.19 cell line (CRL-11372) was obtained from American Type Culture Collection (VA, USA). hFOB 1.19 cell was cultured according to the protocol previously described [16]. The cell line was maintained in a mixture of Dulbecco's Modified Eagle Medium and Ham's F12 medium (1:1) without phenol red (Invitrogen Corporation, CA, USA) supplemented with 10% fetal bovine serum (FBS; JRH Biosciences, KS, USA) and 50 mg/mL G 418 sulfate (EMD Biosciences). Human osteosarcoma cell lines Saos-2 and MG-63 were provided from the Cell Resource Center for Biomedical Research, Tohoku University (Sendai, Japan) and were maintained in a RPMI-1640 (Sigma-Aldrich) with 10% FBS. These cells were pre-incubated for 24 h with FBS-free medium prior to examination in order to remove exo-/endogenous steroid hormones from the culture medium and study the effects of various compounds in the absence of steroids and also to synchronize the cell cycle. Different concentrations of test compounds were added, and the assay was terminated after 3 or 5 days by removing the medium from wells. Steroid blockers were added simultaneously.

Characteristics of hFOB, Saos-2, and MG-63

Expressions of relevant steroid receptors, i.e., ER α , ER β , and AR were determined using quantitative RT-PCR methods in hFOB, Saos-2, and MG-63 cell lines. mRNA transcripts of steroid synthesis/metabolite enzymes, aromatase, 17 β -hydroxysteroid dehydrogenase (17 β -HSD) types 1, 2, 3, 4, and 5, and 5 α -reductase (5 α -Red) types 1 and 2 were all evaluated using RT-PCR methods. The details of quantitative RT-PCR including primer sets employed were previously described in detail [17,18]. Positive controls for these receptors and enzymes were cell lines of human breast cancer, T-47D, and

human prostate cancer, LNCaP obtained from Cell Resource Center for Biomedical Research, Tohoku University (Sendai, Japan). Alkaline phosphatase (ALP), an osteoblast-specific marker, was also studied using RT-PCR for characterization of these cell lines.

Estradiol and testosterone production assay

hFOB cells were plated in 10 mm dishes at a density of 10^6 viable cells and cultured for 48 h. Then media were changed to FBS-free medium, and hFOB cells were incubated with 10^{-7} M androstenedione (Δ_4 ; Sigma-Aldrich) in the presence or absence of EXE or A1-I (10^{-7} M). The media were then collected after 24 h, and E2 and TST were measured by solid-phase radioimmunoassay. Radioimmunoassay was performed in SRL Inc. (Tokyo, Japan) using DPC estradiol kit and DPC total testosterone kit (Diagnostic Products Corporation, LA, USA). In addition, we confirmed that the concentrations of E2 and TST were under the detection limits (E2, 5 pg/mL; TST, 30 pg/mL) in the serum- and phenol red-free medium.

Cell proliferation assay

hFOB, Saos-2, and MG-63 cells were treated with steroids and test compounds for 24, 48, and 72 h, when specimens were harvested and evaluated for cell proliferation using the WST-8 method (Cell Counting Kit-8; Dojindo Inc., Kumamoto, Japan) [18]. Optical densities (OD, 450 nm) were evaluated using a SpectraMax 190 microplate reader (Molecular Devices, Corp., CA, USA) and Softmax Pro 4.3 microplate analysis software (Molecular Devices). The status of proliferation (%) was calculated according to the following equation: (cell OD value after test materials treated/vehicle control cell OD value) \times 100.

Alkaline phosphatase activity assay

hFOB, Saos-2, and MG-63 cells were plated in 48 well plate at a density of 10^6 viable cells and cultured for 48 h. All cell lines were treated with 10^{-9} to 10^{-7} M exemestane for 72 h, when cells were lysed with 0.05% Triton X-100 (Wako Pure Chemical industries) and evaluated for alkaline phosphatase activity

Table 2
Primer sequences used in quantitative RT-PCR analysis

cDNA	GB#	Sequence	cDNA position	Size (bp)
MYBL2	NM_002466	Forward 5'-GTAACAGCCTCAGCCCAAGA-3' Reverse 5'-TCCAATGTGCTCTGTTTGTCCA-3'	1522–1615	94
OSTM1	NM_014028	Forward 5'-TTGAGAATAAGGCTGAACCTGGAAAC-3' Reverse 5'-TTACAGGCACTGTGCTCACTGCAAG-3'	801–926	126
HOXD11*	NM_021192	Forward 5'-CAC TGT CCT TGG GTT TAA TG-3' Reverse 5'-GGT AAA ATT GTA ACG GGA CG-3'	1091–1245	174
GPC2	NM_152742	Forward 5'-AGA AAT GTG GTC AGC GAA GC-3' Reverse 5'-ACA CCT TCG CAC TGT TTT CC-3'	871–1183	313
ADCYAP1R1	NM_001118	Forward 5'-CAG CAA AAG GGA AAG ACT CG-3' Reverse 5'-GAG CTG CTC TTG CTC AGG AT-3'	1351–1584	234
COL1A1	NM_000088	Forward 5'-GGT GGT GGT TAT GAC TTT GGT T-3' Reverse 5'-CTT GGC TGG GAT GTT TTC AGG T-3'	3784–4092	309
SMAD1*	NM_005900	Forward 5'-GGT TCA CCT CAT AAT CCT-3' Reverse 5'-CCT TTG TCA GTT CTC AAT C-3'	1779–1887	127
SMAD5*	NM_005903	Forward 5'-AGC TAA AGC CGT TGG ATA-3' Reverse 5'-AGG CAC TAA TAC TGG AGG T-3'	668–768	119
RUNX2	NM_004348	Forward 5'-GTG GAC GAG GCA AGA GTT T-3' Reverse 5'-TAC TGG GAT GAG GAA TGC G-3'	782–961	198
SPARC	NM_003118	Forward 5'-CCT GTA CAC TGG CAG TTC-3' Reverse 5'-CCA GGG CGA TGT ACT TGT C-3'	793–937	163
ALP	NM_000478	Forward 5'-ACC ATT CCC ACG TCT TCA CA-3' Reverse 5'-AGA CAT TCT CTC GTT CAC CGC C-3'	1379–1540	162
RPL13A	NM_012423	Forward 5'-CCT GGA GGA GAA GAG GAA AGA GA-3' Reverse 5'-TTG AGG ACC TCT GTG TAT TTG TCA A-3'	487–612	126

GB#, GeneBank accession number.

All primer sets were designed using OLIGO Primer Analysis Software (TAKARA Bio Inc., Shiga, Japan).

* Forward and reverse primers were located in same exon.

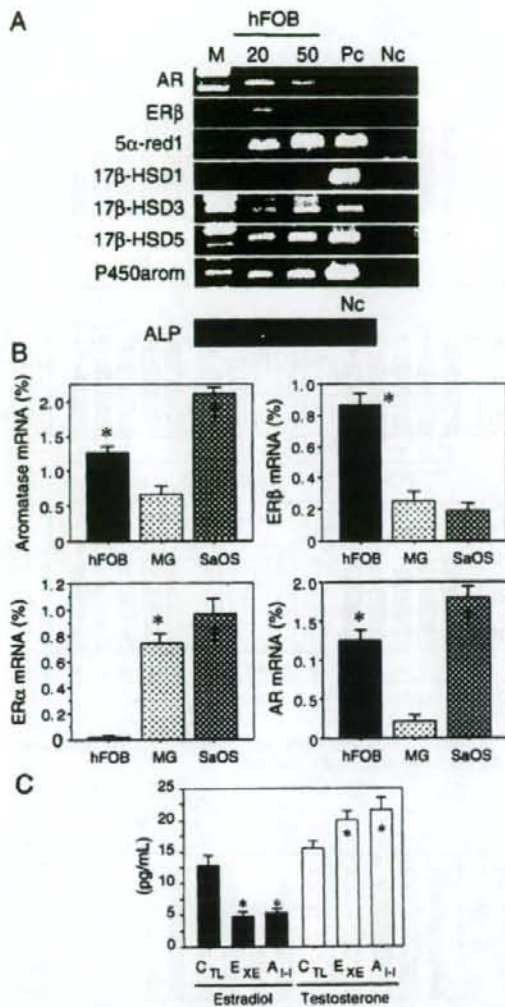


Fig. 2. (A) Results of RT-PCR analysis of steroid hormone receptors and steroid-related enzymes. Both 20 and 50 ng/ μ L cDNA of hFOB were used for PCR (ALP was 20 ng/ μ L alone). AR, androgen receptor; ER, estrogen receptor; 5 α -red1, 5 α -reductase type 1; 17 β -HSD, 17 β -hydroxysteroid dehydrogenase; P450arom, aromatase; M, molecular marker; Pc, positive control; Nc, negative control. (B) Expression levels of aromatase, AR, ER α , and ER β in hFOB, Saos-2, and MG-63. * p <0.05 vs. MG-63 (aromatase and AR), vs. MG-63 and Saos-2 (ER β), vs. hFOB (ER α); [†] p <0.05 vs. hFOB and MG-63 (aromatase and AR), vs. MG-63 and hFOB (ER α). (C) Estradiol and testosterone productions in hFOB cells. The data are expressed as the mean SD ($n=3$). * p <0.05 vs. control cells (CTL). EXE, 10^{-7} M exemestane; A-I, 10^{-7} M aromatase inhibitor I.

using the *p*-nitrophenylphosphate method (LabAssay ALP; Wako Pure Chemical industries) [19]. Optical densities (OD, 405 nm) were evaluated using a SpectraMax 190 microplate reader (Molecular Devices) and Softmax Pro 4.3 microplate analysis software (Molecular Devices). ALP activity (units/ μ L)=(concentration of *p*-nitrophenol/15 min) \times 1 (dilution factor of sample). The ALP activities were presented as units/ μ L/ 10^6 cells. The ALP activity levels in each case were represented as a ratio of vehicle control (%).

Microarray analysis

The procedure was based on a previously reported study [20]. Cell lysates were prepared using RLT buffer (QIAGEN GmbH, Hilden, Germany). Total RNA was extracted using RNeasy Mini Kit (QIAGEN). First-strand cDNA was synthesized by incubating 5 μ g of total RNA with 200 U SuperScript II reverse transcriptase (Invitrogen), 100 pmol T7-(dT)₂₄ primer (Invitrogen). Ten units of T4 DNA polymerase (Invitrogen) were then added, and the dsDNA was mixed with T7 RNA polymerase (Invitrogen). The purified cRNA was fragmented at 300–500 bp as target solution. Hybridization was performed with the GeneChip Human Genome 133 ver. 2.0 (Affymetrix, Inc., CA, USA). The reacted arrays were then scanned as digital image files and scanned data were analyzed with GeneChip software (Affymetrix). Relative levels of gene expression were calculated by global normalization.

Data were subjected to hierarchical clustering analysis and visualization using the Cluster and TreeView programs (Stanford University) in order to generate tree structures based on the degree of similarity, as well as matrices comparing the levels of expression of individual genes in each sample [21].

Real-time PCR

Real-time PCR was carried out using the LightCycler System and the FastStart DNA Master SYBR Green I (Roche Diagnostics GmbH, Mannheim, Germany). The primer sequences used in this study are summarized in Table 2. An initial denaturing step of 95 $^{\circ}$ C for 10 min was followed by 35 cycles, respectively, at 95 $^{\circ}$ C for 10 min; 15 s annealing at 65 $^{\circ}$ C (ALP, COL1A1), 64 $^{\circ}$ C (MYBL2, OSTM1, RPL13A), 62 $^{\circ}$ C (SMAD1, SMAD5, SPARC, RUNX2), or 60 $^{\circ}$ C (HOXD11); and extension for 15 s at 72 $^{\circ}$ C. Negative control experiments included those lacking cDNA substrates to confirm the presence of exogenous contaminant DNA. No amplified products were detected under these conditions. The mRNA levels in each case were represented as a ratio of RPL13A (%) [22].

Immunohistochemistry of AR

Five non-pathological bone tissues were retrieved from surgical pathology files (two females and three males, 17 to 55 years old) of Department of Pathology, Tohoku University Hospital (Sendai, Japan).

Tissue sections were immunostained using a biotin-streptavidin method with Histofine kit (Nichirei Co. Ltd., Tokyo, Japan). The monoclonal antibody for AR (AR411) [23] was obtained from DakoCytomation (Kyoto, Japan). Experimental procedures employed in our present study have been previously described in detail [22,23]. The dilutions of primary AR antibody were 1:100. The antigen-antibody complex was then visualized with 3,3'-diaminobenzidine solution, and counterstained with hematoxylin. Prostate cancer was used as a positive control for AR. Normal mouse IgG was used as a negative control for immunostaining and no specific immunoreactivity was detected.

Statistical analysis

Results were expressed as mean \pm SD. Statistical analysis was performed with the StatView 5.0 J software (SAS Institute Inc., NC, USA). All data were analyzed by analysis of variance (ANOVA) followed by post hoc Bonferroni/Dunnett multiple comparison test. A p -value<0.05 was considered to indicate statistical significance.

Results

Characteristics of hFOB, MG-63, and Saos-2 cell line

Characteristics of osteoblast and osteoblast-like cell lines are summarized in Figs. 2A and B. hFOB cells expressed mRNA transcripts of AR and ER β . Relatively low level of ER α mRNA transcript was detected in hFOB cells. Aromatase, 17 β -HSD type 1, 3, and 5, and 5 α -Red types 1 and 2 mRNA transcripts were all detected in hFOB cells by

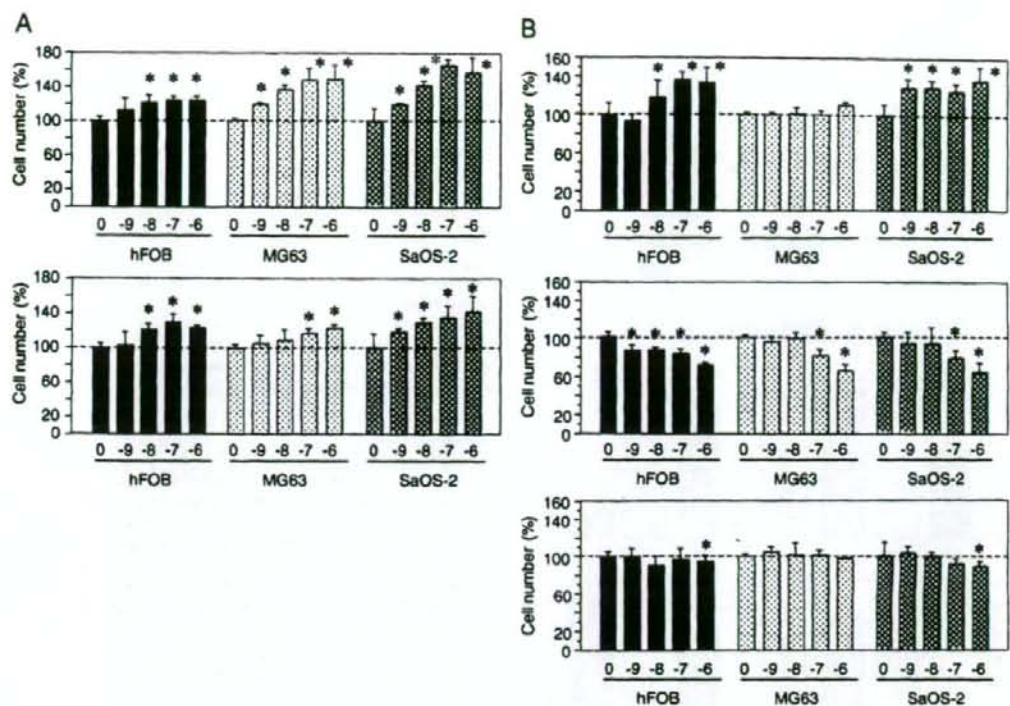


Fig. 3. (A) Proliferation of hFOB cells treated by estradiol (top) and 5 α -DHT (bottom). * $p < 0.05$ vs. vehicle control (0). (B) Proliferation of hFOB cells treated by exemestane (top), aminoglutethimide (middle), and Aromatase Inhibitor-I (bottom). * $p < 0.05$ vs. vehicle control (0). $n = 5$.

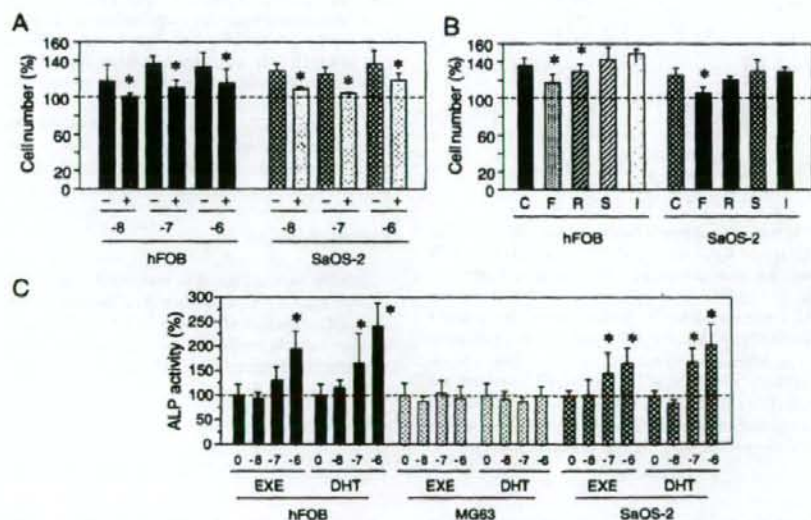


Fig. 4. (A) Effects of hydroxyflutamide on exemestane (10 $^{-8}$ to 10 $^{-6}$ M) stimulated the cell proliferation of both hFOB and Saos-2. With (+) or without (-) hydroxyflutamide, $p < 0.05$ vs. without hydroxyflutamide (*). (B) Effects of steroid blockers on exemestane (10 $^{-7}$ M) stimulated cell proliferation of hFOB and Saos-2. C, 10 $^{-7}$ M exemestane; F, hydroxyflutamide (5 \times 10 $^{-6}$ M); R, RU38,486 (5 \times 10 $^{-6}$ M); S, spironolactone (5 \times 10 $^{-6}$ M); I, ICI182,720 (5 \times 10 $^{-6}$ M). * $p < 0.05$ vs. C. (C) ALP activity in hFOB, Saos-2, MG-63 treated with exemestane (EXE, 10 $^{-8}$ to 10 $^{-6}$ M), or 5 α -DHT (DHT, 10 $^{-8}$ to 10 $^{-6}$ M). * $p < 0.05$ vs. vehicle control (0).

RT-PCR. Aromatase, ER α , ER β , and AR were all detected in osteoblast-like cell lines, Saos-2 and MG-63 (Fig. 2B). In hFOB cell, expression of ER β mRNA was more predominant than that of ER α mRNA. ER α mRNA as well as ER β mRNA was detected in Saos-2 and MG-63 cells. The levels of AR mRNA expression in both hFOB and Saos-2 were significantly higher ($p=0.01$) than that in MG-63. ALP mRNA was also detected in intact hFOB, Saos-2, and MG-63 cells (data not present), respectively.

Estradiol and testosterone production

Results were summarized in Fig. 2C. The E2 levels in the medium of hFOB supplemented with Δ_4 treated with EXE or

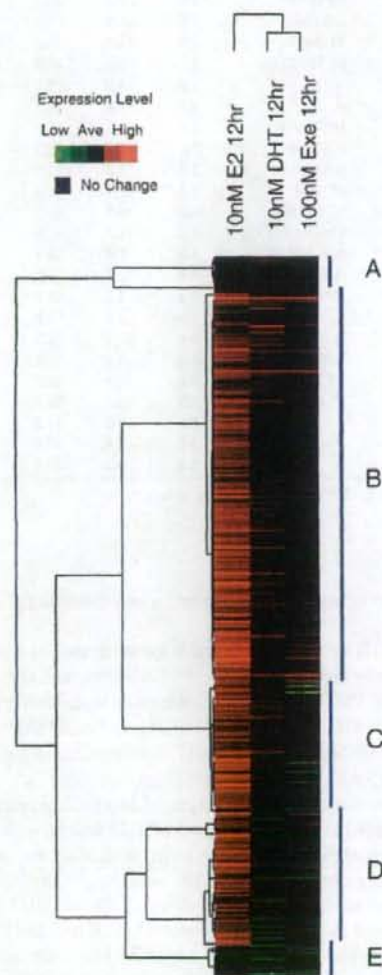


Fig. 5. In clustering analysis of the expression levels of each gene in hFOB cells treated with estradiol (E2), 5 α -dihydrotestosterone (DHT), and exemestane (Exe).

AI-I were significantly lower than that of cells without AIs. The levels of TST in the medium of hFOB supplemented with Δ_4 treated with EXE or AI-I were significantly higher than that of cells without AIs.

Cell proliferation

Results of the cell proliferation assays are summarized in Figs. 3 and 4. There was a significant increment in the number of the cells after 72 h in hFOB, Saos-2, and MG-63 cells treated with 10^{-9} M (Saos-2 and MG-63) or 10^{-8} M (hFOB) to 10^{-6} M E2 (Fig. 3A). The cell number of hFOB and Saos-2 cells treated by 10^{-9} M (Saos-2) or 10^{-8} M (hFOB) to 10^{-6} M DHT for 72 h was also significantly higher than control (Fig. 3A). The number of MG-63 cells was significantly increased only by high dose of DHT (10^{-7} M and 10^{-6} M) treatments (Fig. 3A). Prg (10^{-9} M to 10^{-6} M) treatments did not change the number of cells even after 72 h in all three cell lines examined (data not present).

Both EXE (Fig. 3B) and 17H-EXE (data not present) treatments of 10^{-8} M to 10^{-6} M, which were comparable to pharmacological inhibition doses of aromatization (Table 1), significantly increased the hFOB cell number for 72 h, respectively. In Saos-2 cells treated with relatively low dose, 10^{-9} to 10^{-6} M EXE, there was a significant increment in the number of the cells after 72 h (Fig. 3B). However, all the dose (10^{-9} M to 10^{-6} M) of EXE employed did not result in the change of cell number of MG-63 even after 72 h of treatment (Fig. 3B). The cell number of both hFOB and Saos-2 cells treated by both 10^{-6} M EXE and/or 17H-EXE for 48 h was also significantly higher than that treated for 24 h (data not present).

AGM treatment [10^{-9} (hFOB) or 10^{-7} (Saos-2 and MG-63) to 10^{-6} M] diminished the number of these three cells (Fig. 3B) and morphological changes in these cells were consistent with those caused by cytotoxic effects (data not present). AI-I treatment (10^{-9} to 10^{-7} M) was not associated with significant increment of the cell number in these cell lines (Fig. 3B). Only high dose (10^{-6} M) of AI-I significantly diminished the cell numbers of hFOB and Saos-2 but not of MG-63 (Fig. 3B).

The androgen receptor antagonist OHF (5×10^{-6} M) diminished the effects of EXE on these increments of both hFOB and Saos-2 cells (Figs. 4A and B). Treatment with RU but not spironolactone and ICI also inhibited EXE effects on hFOB cells (Fig. 4B).

ALP activity assay

Results of the ALP activity assay were summarized in Fig. 4C. There was a significant increment in the ALP activity of both hFOB and Saos-2 cells treated with 10^{-7} M (Saos-2) and/or 10^{-6} M (hFOB and Saos-2) EXE. Both 10^{-7} M and 10^{-6} M DHT treatment also increased the ALP activity in hFOB and Saos-2 cells, respectively. There were no changes of ALP activity in MG-63 treated with 10^{-8} M to 10^{-6} M of EXE and DHT, respectively.

Table 3a
Genes induced by exemestane treatment in hFOB cells—2.0 higher

	Gene title	Gene symbol	Raw data			Ratio	
			C	D	Ex	D	Ex
NM_002466	V-myb myeloblastosis viral oncogene homolog (avian)-like 2	MYBL2	70.9	156.9	150.3	2.2	2.1
AW444985	–	–	57.8	124.7	127.1	2.2	2.2
AF143684	Myosin IXB	MYO9B	48.3	64.4	122.2	1.3	2.5
NM_024682	TBC1 domain family, member 17	TBC1D17	31.7	37.6	64.8	1.2	2.0
BE965311	Chromosome 16 open reading frame 23	C16orf23	29.2	44.2	64.0	1.5	2.2
NM_004233	CD83 antigen (activated B lymphocytes, immunoglobulin superfamily)	CD83	29.0	66.5	60.9	2.3	2.1
AI806031	Skeletal muscle and kidney enriched inositol phosphatase	SKIP	27.7	48.6	55.4	1.8	2.0
AL136729	Ring finger protein 123	RNF123	20.0	23.7	41.3	1.2	2.1
NM_015254	Kinesin family member 13B	KIF13B	13.0	24.5	39.4	1.9	3.0
AL110249	Chromosome 20 open reading frame 194	C20orf194	13.4	39.0	29.7	2.9	2.2
AF208502	Early B-cell factor	EBF	12.5	21.1	28.5	1.7	2.3
AW007221	Solute carrier family 13 (sodium/sulfate symporters), member 4	SLC13A4	12.3	9.6	27.8	0.8	2.3
AB007458	TP53 activated protein 1	TP53AP1	12.6	22.2	26.2	1.8	2.1
AV713913	Osteopetrosis associated transmembrane protein 1	OSTM1	9.8	16.5	21.3	1.7	2.2
BF339201	THAP domain containing 6	THAP6	6.0	14.0	20.6	2.3	3.4
AK000455	Hypothetical gene MGC16733 similar to CG12113	MGC16733	7.3	16.6	18.8	2.3	2.6
AW974816	–	–	2.2	16.0	17.2	7.2	7.7
AK025325	Transcribed locus, moderately similar to NP_689573.2 zinc finger protein 573	–	7.3	11.4	16.2	1.6	2.2
NM_021192	Homeo box D11	HOXD11	5.3	16.2	15.8	3.0	3.0
NM_022169	ATP-binding cassette, sub-family G (WHITE), member 4	ABCG4	7.0	10.5	15.7	1.5	2.2
R62907	Disabled homolog 2, mitogen-responsive phosphoprotein (<i>Drosophila</i>)	DAB2	7.7	13.0	15.5	1.7	2.0
NM_002661	Phospholipase C, gamma 2 (phosphatidylinositol-specific)	PLCG2	7.3	12.3	15.3	1.7	2.1
BG393032	Solute carrier family 13 (sodium/sulfate symporters), member 4	SLC13A4	6.4	6.7	15.1	1.0	2.3
BC002794	Tumor necrosis factor receptor superfamily, member 14	TNFRSF14	6.2	11.3	13.6	1.8	2.2
BC042908	KIAA0690	KIAA0690	5.6	7.4	13.5	1.3	2.4
AW451961	Adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1	ADCYAP1R1	4.3	11.7	13.2	2.7	3.1
AI863264	Glypican 2 (cerebroglycan)	GPC2	5.3	7.2	13.2	1.3	2.5
AF130050	ACA47 scRNA gene	–	5.6	9.5	12.9	1.7	2.3
AK022326	Hypothetical gene supported by AK022326	–	6.1	12.7	12.9	2.1	2.1
AK021807	Low density lipoprotein receptor-related protein 11	LRP11	5.9	6.2	12.8	1.0	2.2
AU155415	Kallikrein 7 (chymotryptic, stratum corneum)	KLK7	5.6	13.5	12.7	2.4	2.3
BF673779	Hypothetical protein FLJ30834	FLJ30834	5.5	6.3	12.3	1.1	2.2
AV646335	–	–	2.6	13.0	11.2	5.0	4.3
BC040600	–	–	5.0	5.4	10.6	1.1	2.1
AI131035	–	–	5.1	9.2	10.5	1.8	2.1

C, vehicle control; D, 5 α -dihydrotestosterone; Ex, exemestane. Genes that performed quantitative RT-PCR were described in bold style.

Microarray/clustering analysis

In hFOB cells, the hierarchical clustering analysis contains 430 genes which demonstrated expression ratios above 2.0-fold and below 0.5-fold compared with vehicle control cells after 12 h of each gene treated with 10⁻⁸ M E2, 10⁻⁸ M DHT, or 10⁻⁷ M EXE. The expression profiles of EXE treated cells were closely related to those of DHT (Fig. 5). In this study, we focused on 35 genes (Table 3a), which were all up-regulated twice or more than control. In this group, we further focused on 5 genes, B-Myb 2 (MYBL2), osteopetrosis associated transmembrane protein 1 (OSTM1), homeo box D 11 (HOXD11), adenylate cyclase activating polypeptide 1 receptor (ADCYAP1R1), and glypican 2 (GPC2) which are all considered to play important roles in EXE or DHT induced cell proliferation. We therefore examined whether these 5 genes were increased by EXE or DHT treatments using quantitative RT-PCR in hFOB cells. We also examined the validation of results of microarray analysis obtained in hFOB cells in Saos-2 and MG-63 cells.

Validation of microarray analysis using quantitative RT-PCR

In hFOB cells, all of these 5 genes described above were significantly increased by 10⁻⁷ M EXE treatment, and 3/5 genes (except for OSTM1 and GPC2) were also significantly increased by 10⁻⁸ M DHT treatment. HOXD11 and ADCYAP1R1 genes increased by both EXE and DHT were significantly diminished by OHF (5 \times 10⁻⁶ M) treatment (Figs. 6A–C).

The similar results of changes of MYBL2 expression were also obtained in both Saos-2 and MG-63 treated with EXE and DHT, respectively (Fig. 6A). In addition, the results of HOXD11 expression in hFOB were equivalent to those in Saos-2 but not in MG-63 treated with EXE and DHT (Fig. 6B). Other genes induced by treatment of EXE and DHT in hFOB such as OSTM1, GPC2, and ADCYAP1R1 were not changed in both Saos-2 and MG-63 cells treated with EXE and DHT, respectively (data not present). AI-I or AGM treatment did not increase all of these genes expression in hFOB (data not present).

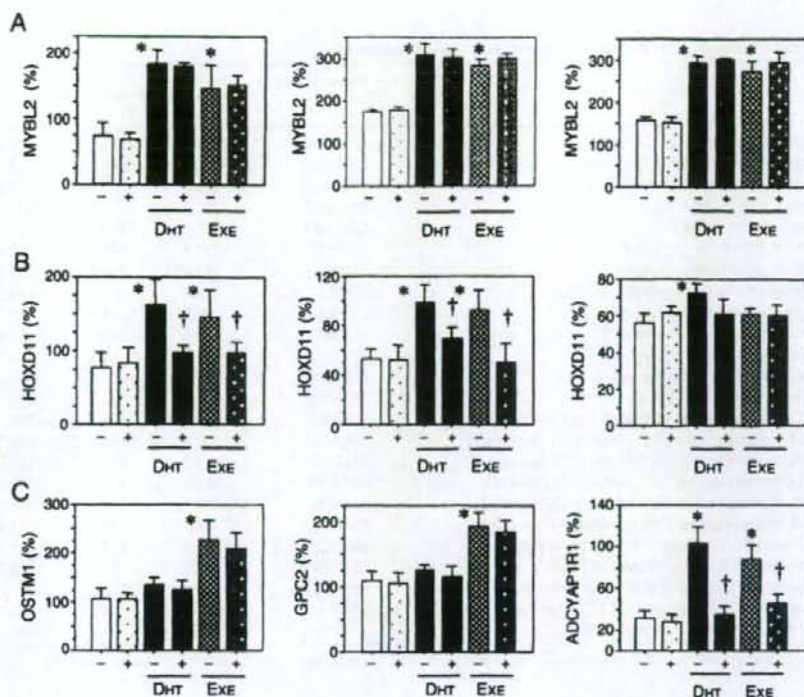


Fig. 6. Validation of microarray analysis. (A) Expression levels of MYBL2 in hFOB (left), Saos-2 (middle), and MG-63 (right). (B) Expression levels of HOXD11 in hFOB (left), Saos-2 (middle), and MG-63 (right). (C) Expression levels of OSTM1, GPC2, and ADCYAP1R1 in hFOB. DHT: 10^{-8} M 5 α -dihydrotestosterone, EXE: 10^{-7} M Exemestane, with (+) or without (-) hydroxyflutamide, $p < 0.05$ vs. control (*) or without hydroxyflutamide (†).

Analysis of osteoblast growth-related genes

Results of microarray analysis in hFOB cell demonstrated that osteoblast growth-related genes [24,25] such as COL1A1, SMAD1, SMAD5, SPARC, and RUNX2 were all up-regulated by exemestane (10^{-7} M) treatment but the degrees of increment were all under 2-fold (Table 3b). In this microarray analysis, other expression levels of previously reported osteoblast-related genes were not altered.

In hFOB cells, the validation analysis of these genes described above using quantitative RT-PCR (Fig. 7) demonstrated that 4/5 genes (except for COL1A1) were significantly increased by 10^{-7} M EXE treatment, and 4/5 genes (except for SMAD1) were also significantly increased by 10^{-8} M DHT treatment. The increased expression of the SMAD1, SMAD5, and SPARC genes by EXE or DHT, was significantly diminished by OHF (5×10^{-6} M) treatment. There were no effects of OHF pretreatment on the increased expression levels of RUNX2 that had occurred after both EXE and DHT treatments. Both AI-1 and AGM treatment could not increase all of these genes expression in hFOB (data not present).

In Saos-2 cells, 4/5 genes (except for RUNX2) were significantly increased by 10^{-7} M EXE treatment, and 3/5 genes (except for RUNX2 and SMAD1) were also significantly increased by 10^{-8} M DHT treatment. The increment of the

COL1A1, SMAD5, and SPARC genes expression by EXE or DHT, was significantly diminished by OHF (5×10^{-6} M) treatment. All of these 5 genes did not change in MG-63 cells treated with EXE or DHT, respectively (data not present).

Immunohistochemistry of AR

Marked AR immunoreactivity was detected in the nuclei of osteoblasts or lining cells but not in osteoclasts in four cases (Fig. 8). In these four cases, AR immunoreactivity was also detected in osteocytes and chondrocytes. In one case, there was no immunoreactivity in all types of bone cells.

Discussion

In the clinical study of EXE compared to placebo administered for two years [26,27], EXE modestly enhanced bone loss from the femoral neck without significant influence on lumbar bone loss despite a marked systemic estrogen depletion. Furthermore, the risks of clinical bone fractures are considered to be lower with EXE treatment than that seen with non steroidal AIs [27,28], though it is also important to recognize that EXE has not been shown to significantly increase the amount of bone mass in various clinical studies of breast cancer patients [26,27]. The relative protective effect of EXE, a

Table 3b
Genes induced by exemestane treatment in hFOB cells—the osteoblast growth-related genes

Gene title	Gene symbol	Raw data			Ratio		
		C	D	Ex	D	Ex	
K01228	Collagen, type I, alpha 1	COL1A1	2797.2	3240.9	3058.5	1.2	1.1
BE221212	Collagen, type I, alpha 1	COL1A1	2741.1	3048.3	3052.2	1.1	1.1
A1743621	Collagen, type I, alpha 1	COL1A1	228.0	241.6	242.5	1.1	1.1
AA788711	Collagen, type I, alpha 2	COL1A2	2250.6	2474.3	2375.4	1.1	1.1
NM_000089	Collagen, type I, alpha 2	COL1A2	1749.1	1848.7	1787.6	1.1	1.0
M60485	Fibroblast growth factor receptor 1	FGFR1	178.9	185.7	198.6	1.0	1.1
BE467261	Fibroblast growth factor receptor 1	FGFR1	165.4	208.6	189.7	1.3	1.1
M63889	Fibroblast growth factor receptor 1	FGFR1	119.3	111.6	140.5	0.9	1.2
NM_023110	Fibroblast growth factor receptor 1	FGFR1	60.5	84.0	70.2	1.4	1.2
AU145411	Fibroblast growth factor receptor 1	FGFR1	29.2	44.1	37.5	1.5	1.3
AI359368	Fibroblast growth factor receptor 3	FGFR3	41.4	65.5	58.7	1.6	1.4
NM_001552	Insulin-like growth factor binding protein 4	IGFBP4	809.1	1027.5	1040.4	1.3	1.3
AL353944	Runt-related transcription factor 2	RUNX2	192.9	226.3	216.3	1.2	1.1
AU146891	SMAD, mothers against DPP homolog 1 (<i>Drosophila</i>)	SMAD1	161.2	195.6	204.6	1.2	1.3
NM_005901	SMAD, mothers against DPP homolog 2 (<i>Drosophila</i>)	SMAD2	100.3	108.2	113.7	1.1	1.1
NM_005902	SMAD, mothers against DPP homolog 3 (<i>Drosophila</i>)	SMAD3	110.2	106.5	127.7	1.0	1.2
BF526175	SMAD, mothers against DPP homolog 5 (<i>Drosophila</i>)	SMAD5	361.0	488.3	514.2	1.4	1.4
AI478523	SMAD, mothers against DPP homolog 5 (<i>Drosophila</i>)	SMAD5	300.7	384.9	346.9	1.3	1.2
AF010601	SMAD, mothers against DPP homolog 5 (<i>Drosophila</i>)	SMAD5	79.2	99.7	87.6	1.3	1.1
AY014180	SMAD-specific E3 ubiquitin protein ligase 2	SMURF2	804.2	844.7	851.8	1.1	1.1
AU157259	SMAD-specific E3 ubiquitin protein ligase 2	SMURF2	77.1	81.5	86.3	1.1	1.1
AL575922	Secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	1702.1	1935.5	1925.8	1.1	1.1
BF508662	Sprouty homolog 1, antagonist of FGF signaling (<i>Drosophila</i>)	SPRY1	31.9	46.3	45.4	1.5	1.4
NM_014886	TGF beta-inducible nuclear protein 1	TNFP1	1185.7	1259.5	1241.1	1.1	1.0

C, vehicle control; D, 5 α -dihydrotestosterone; Ex, exemestane. Genes that performed quantitative RT-PCR were described in bold style.

steroidal aromatase inhibitor, has been therefore attributed to its actions through AR in osteoblasts. Systemic androgenic effects such as hypertrichosis, hair loss, hoarseness, and acne have been reported only in 4% [6] of the patients treated with EXE (25 mg/day) and the frequency of these effects increases to approximately 10% in those treated with higher dose 200 mg/day of EXE [6]. This finding suggests that the patients treated with EXE are under relatively weak systemic androgenic effects. Androgen sensitivity has been well-known to be subject to great individual variation caused by AR gene CAG polymorphism in women as well as men [29,30]. Therefore, this 5 to 10% of the patients who manifested clinical androgenic effects by EXE treatment may be individuals associated with relatively enhanced androgenic sensitivity. Replacement therapy with TST is generally effective at restoring bone in hypogonadal men [31]. In female-to-male, genetic female transsexual subjects, high-dose TST therapy generally increased BMD at the femoral neck, despite decrement of E2 to postmenopausal levels [32,33]. Therefore, androgens may play an important role in bone protection in women as well as men.

The results of cell proliferation assay demonstrated that the cell number of MG-63 was increased by both E2 and DHT treatments, but the dose of DHT was relatively higher than that in two other cells. MG-63 expressed higher levels of ER α / β mRNA, but the level of AR mRNA was lower than that in both Saos-2 and hFOB. Both cell proliferation and ALP activity of MG-63 could not be stimulated by EXE treatment. Molecular mechanisms of androgen actions on osteoblasts have remained largely unknown. Androgen is well-known to stimulate

osteoblast proliferation [34] and differentiation [35]. For instance, osteoprotegerin mRNA was increased by TST as well as DHT treatments in mouse 3T3-E1 cells [36].

AR and ER β but not ER α are predominantly detected in osteoblasts located on human cancellous bone using immunohistochemical analysis [37]. Therefore, hFOB examined in this study is considered to maintain relatively native status of sex steroids pathways in human osteoblasts. Therefore, we employed hFOB for further examination of EXE effects on osteoblast gene expression pattern using microarray analysis. In this study, we demonstrated that the genes MYBL2 [38], OSTM1 [39], HOXD11 [40], ADCYAP1R1 [41], and GPC2 [42] were target genes of EXE alone or both EXE and DHT in hFOB using microarray/PCR analysis. These genes were demonstrated to be involved in regulation of cell cycle, differentiation, and transcription. In EXE or DHT treatment in hFOB and Saos-2, in which cells proliferations were stimulated, an increased expression of HOXD11 gene was detected. The product of the mouse Hoxd11 gene was reported to play a role in forelimb morphogenesis [40,43]. Therefore, these finding suggest that osteoblast cell proliferation stimulated by EXE treatment may depend on HOXD11 gene expression through AR. In this study, the cell proliferation of MG-63, which expressed relatively low level of AR, was not stimulated by EXE. In addition, HOXD11 gene expression was not up-regulated by EXE treatment in MG-63 cells. These results were also consistent with the protective effects of EXE through potential androgen-HOXD11 pathway in osteoblast cells. In this study, we also examined the effects of EXE and DHT on osteoblast growth-related genes using micro-

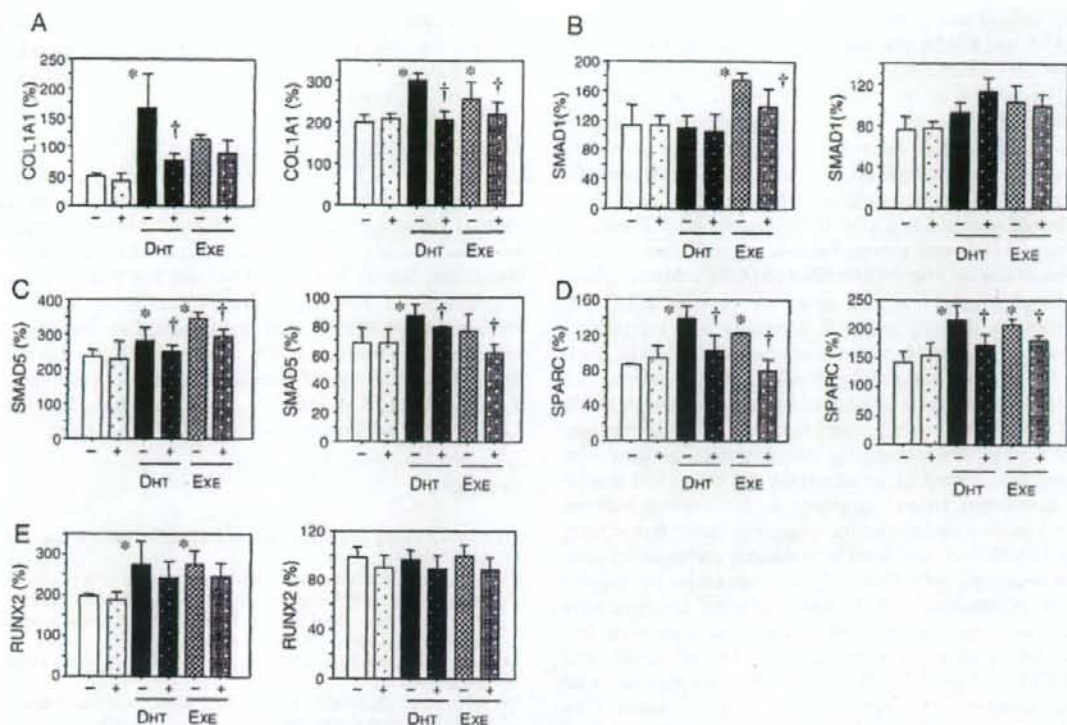


Fig. 7. Expression levels of osteoblast growth-related genes in hFOB (left) and Saos-2 (right). DHT: 10^{-8} M 5α -dihydrotestosterone, EXE: 10^{-7} M Exemestane, with (+) or without (-) hydroxyflutamide, $p < 0.05$ vs. control (*) or without hydroxyflutamide (†).

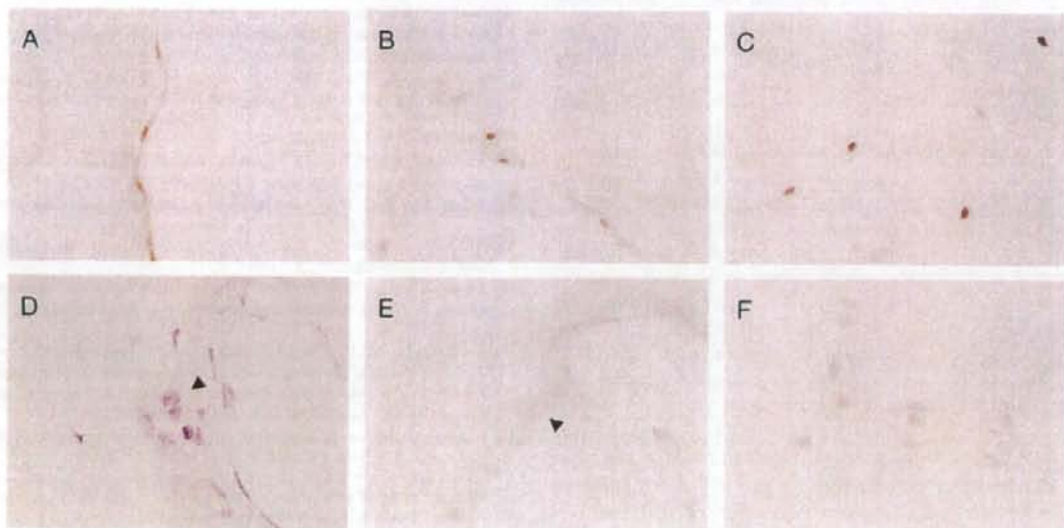


Fig. 8. Immunohistochemistry of androgen receptor in human bone tissues. Immunoreactivity of androgen receptor was detected in nuclei of osteoblasts/liner cells (A, B) but not in osteoclasts (D, E; arrowheads). Immunoreactivity of androgen receptor was also detected in nuclei of osteocytes (C) and condrocytes (F).

array analysis and following quantitative RT-PCR. COL1A1, SMAD5, and SPARC (osteonection) were up-regulated by EXE and/or DHT treatments in both hFOB and Saos-2 cells. EXE or DHT treatments in both hFOB and Saos-2 also resulted in increased ALP activity. There have been, however, no studies reported on whether these genes are primary or secondary androgen responsive genes in osteoblasts. The AR-specific antagonist, OHF demonstrated no inhibitory effects on RUNX2 expression increased by EXE or DHT treatment in hFOB cells. In addition, hFOB cell growth induced by high dose of EXE treatment was not completely inhibited by OHF treatment. These results all suggest that EXE also may stimulate hFOB cell proliferation through both AR dependent and independent pathways. From our data of steroid production in hFOB, EXE may have an additional androgenic effect through increased TST levels in conjunction with inhibition of aromatization in hFOB cells. However, it awaits further investigations for clarification.

In normal bone remodeling, bone formation by osteoblasts follows bone resorption by osteoclasts and occurs in a precise and quantitative manner (coupling). In this coupling between bone formation and resorption, a coupling factor that induces bone formation is considered to be released during osteoclastic bone resorption [44]. This study has focused on the specific effects on osteoblast cells. However, it is true that there were significant increases in both serum bone formation and resorption markers in postmenopausal women administered with EXE for 2 years [26]. Osteoclasts, which are responsible for bone resorption, are target cells for many anti-osteoporosis therapeutic agents such as bisphosphonate of postmenopausal women [45]. However, it is unclear whether EXE acts on osteoclast directly. Chen et al. [46] reported that testosterone inhibited osteoclast formation stimulated by parathyroid hormone through the AR but not through the production of intrinsic estrogen using primary mouse osteoclast cells. In both human and rodent bone tissues, AR is expressed in both osteoblasts and osteocytes [47,48]. However, AR is detected in osteoclasts of rodent but not in human cells [31,47,48]. Therefore, in humans, androgens are considered to exert their effects on bone through osteoblasts. EXE may therefore exert its possible androgenic effects on human bone through osteoblasts but not osteoclasts. Results of our present study also suggest the possible roles of EXE on osteoblast cells through AR independent manner. Results of clinical studies suggest that the combination therapy of AI and COX-2 inhibitors could provide more effective aromatase inhibition than single therapy in hormone-sensitive postmenopausal breast cancer [49]. Bone resorption induced by IL-1 and IL-6 was also reported to occur via stimulation of COX-2 dependent PGE₂ production in osteoblasts *in vitro* [50]. Therefore, further investigations are required to clarify the effects of AI including EXE on human bone tissues.

In summary, this study using osteoblast and osteoblast-like cell lines suggested the potential protective effect of steroidal AI, EXE on osteoblasts occurred through both AR dependent and independent pathways. HOXD11 gene known as bone morphogenesis factor and osteoblast growth-related genes were induced by EXE treatment as well as DHT treatment in both hFOB and Saos-2. Damages of bone tissues by estrogen

depletion caused by AI administration are considered unavoidable but the selection of potential hormone therapies which could minimize the damages or injuries of bone tissues is considered important.

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