

Table 1-1. Medaka cell lines used in this study

Cell line	Species	Population	Strain	Tissue type	Inhabiting Prefecture, Province or Country
OLHNI-1	<i>Oryzias latipes</i>	Northern Japanese	HNI	Caudal fin	Niigata
OLHNI-2	<i>O. latipes</i>	Northern Japanese	HNI	Caudal fin	Niigata
OLHNI-e1	<i>O. latipes</i>	Northern Japanese	HNI	Embryo	Niigata
OLKaga-e2	<i>O. latipes</i>	Northern Japanese	Kaga	Embryo	Ishikawa
OLCAB-2	<i>O. latipes</i>	Southern Japanese	CAB	Caudal fin	Unknown
OLCAB-e1	<i>O. latipes</i>	Southern Japanese	CAB	Embryo	Unknown
OLCAB-e3	<i>O. latipes</i>	Southern Japanese	CAB	Embryo	Unknown
OLHdrR-e3	<i>O. latipes</i>	Southern Japanese	HdrR	Embryo	Unknown
OL32	<i>O. latipes</i>	Southern Japanese	HB32	Caudal fin	Chiba
OLSOK-e7	<i>O. latipes</i>	East Korean	SOK	Embryo	Kangwon
CE-1	<i>O. celebensis</i>	-	Wild type	Embryo	Indonesia

Table 2-1. Medaka OL libraries and numbers of cDNA clones used in this study

Library	RNA source	Number of clones used in this study
OLa	Adult whole body of HNI inbred strain (male and female)	-
OLb	OLHNI-1 culture cells, derived from caudal fin of adult male HNI inbred strain	1,233
OLc	OLHNI-1 culture cells, derived from caudal fin of adult male HNI inbred strain (20 J/m ² UV ± PR)	268
OLd	Ovary of HNI inbred strain	1,549
OLe	Liver of HNI inbred strain (male and female)	325
OLf	Gamma-irradiated OLHNI-1 culture cell, derived from caudal fin of adult male HNI inbred strain	174
Total		3,549

Table 3-1. Gene Ontology terms and number of clones the accumulated mRNA levels of which were significantly different in OLHNI-e1 cells cultured at 15, 25 and 33°C during 7 days, and between the cells cultured at 15 and 25°C for 7 days ($P < 0.05$ by Kruskal-Wallis ANOVA or Mann-Whitney test as appropriate)

GO term	P values by χ^2 test											
	25°C			15°C			33°C			25°C and 15°C		
	All	>0.5 in \log_2 ratio on day 7	<0.5 in \log_2 ratio on day 7	All	>0.5 in \log_2 ratio on day 7	<0.5 in \log_2 ratio on day 7	All	>0.5 in \log_2 ratio on day 7	<0.5 in \log_2 ratio on day 7	All	>0.5 in \log_2 ratio on day 7 at 15°C	<0.5 in \log_2 ratio on day 7 at 15°C
Molecular function	0.422	0.300	0.888	0.011	0.330	0.068	0.470	0.603	0.818	0.372	0.116	0.012
Binding	0.423	0.393	0.761	0.001	0.462	0.044	0.329	0.595	0.430	0.236	0.342	0.010
Glycosaminoglycan binding	-	-	-	0.015	-	-	-	-	-	-	-	-
Metal binding	0.296	-	-	0.080	0.476	0.182	0.611	-	-	0.111	0.426	0.082
Nucleic acid binding	0.633	0.498	0.813	0.008	0.441	0.137	0.519	0.659	0.639	0.451	0.196	0.104
Nucleotide binding	0.639	0.539	0.876	0.037	0.139	0.031	0.053	0.099	0.782	0.447	0.186	0.043
Protein binding	0.106	0.388	0.502	0.004	0.27	0.231	0.732	0.687	0.687	0.205	0.225	0.129
Catalytic activity	0.010	0.094	0.872	0.033	0.176	0.001	0.130	0.198	0.134	0.163	0.091	0.000
Hydrolase activity	0.159	0.301	0.834	0.067	0.452	0.020	0.069	0.015	-	0.174	0.422	0.017
Kinase activity	0.611	-	-	0.01	-	-	0.678	-	-	0.449	-	-
Ligase activity	0.576	-	-	0.102	-	-	0.703	-	-	0.030	-	-
Oxidoreductase activity	0.237	-	-	0.102	0.057	0.197	0.307	-	-	0.451	0.116	0.109
Transferase activity	0.637	-	-	0.010	0.452	0.165	0.737	-	-	0.267	0.389	-
Enzyme regulator activity	0.452	-	-	0.05	-	-	0.122	-	-	0.003	-	-
Enzyme activator activity	-	-	-	0.040	-	-	-	-	-	-	-	-
Transporter activity	0.425	0.534	0.591	0.102	0.234	0.203	0.582	0.568	-	0.040	0.053	0.096
Electron transporter activity	0.109	-	-	0.101	-	-	0.279	-	-	0.442	-	-
Transcription regulator activity	0.382	0.418	-	0.096	0.436	0.231	0.410	-	-	0.448	0.397	-
Transcription cofactor activity	0.616	-	-	0.040	-	-	-	-	-	-	-	-
Structural molecule activity	0.041	0.543	0.894	0.100	0.275	0.067	0.450	0.524	0.260	0.034	0.095	0.113
Structural constituent of ribosome	0.025	-	-	0.069	0.099	0.094	0.100	0.259	-	0.049	0.081	0.117
Biological process	0.371	0.478	0.870	0.013	0.403	0.077	0.450	0.545	0.846	0.306	0.172	0.033
Cellular process	0.642	0.441	0.880	0.004	0.450	0.016	0.514	0.196	0.485	0.439	0.269	0.022
Cell communication	0.255	0.309	0.032	0.007	0.186	0.164	0.572	0.371	-	0.162	0.285	0.128
Cellular physiological process	0.642	0.544	0.901	0.002	0.459	0.001	0.520	0.246	0.765	0.435	0.178	0.013
Physiological process	0.623	0.531	0.512	0.038	0.133	0.053	0.726	0.675	0.838	0.452	0.013	0.023
Cellular physiological process	0.642	0.544	0.901	0.002	0.459	0.001	0.520	0.246	0.765	0.435	0.178	0.013
Metabolism	0.595	0.528	0.100	0.076	0.091	0.082	0.735	0.251	0.507	0.450	0.013	0.008
Response to stimulus	0.056	-	-	0.003	0.444	0.109	0.135	-	-	0.168	0.428	0.109
Development	0.006	-	-	0.005	0.000	0.235	0.210	-	-	0.232	0.098	0.127
Morphogenesis	0.007	0.211	-	0.001	0.000	0.235	0.098	-	-	0.125	0.106	0.127
Cellular component	0.619	0.443	0.889	0.022	0.359	0.149	0.738	0.519	0.841	0.371	0.290	0.042
Cell	0.642	0.534	0.481	0.032	0.351	0.141	0.668	0.668	0.814	0.449	0.308	0.049
Intracellular	0.641	0.503	0.367	0.019	0.158	0.058	0.724	0.678	0.807	0.451	0.105	0.024
Membrane	0.193	0.347	0.465	0.102	0.322	0.235	0.584	0.653	0.729	0.448	0.434	0.125
Extracellular	0.056	-	-	0.066	0.003	0.189	0.549	-	-	0.076	-	-

Red and blue color boxes represent the GO terms the clone number of which was significantly more and less than the expectation values, respectively ($P < 0.05$). Hyphens indicate the GO terms the expectation values of which were too small for reliable analyses (See Supplementary Table 3-1 - 3-4).

Table 3-2. Genes which exhibited the accumulated mRNA levels on day 7 after temperature shift from 25°C to 15°C in OLHNI-e1 cells more than those of the cells successively cultured at 25°C for the same period

Clone ID	Gene name	Gene symbol	GenBank acc No.	Accumulated mRNA levels on day 7	
				25°C	15°C
OLb01.02c	Eukaryotic translation elongation factor 1 gamma	EEF1G	NM_001404	Down	Up
OLb01.08g	Collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital)	COL2A1	NM_001844	Down	Up
OLb28.11e	Cytokine-like 1	CYTL1	NM_018659	Down	Up
OLb32.06b	CD82 antigen	KAI1	NM_002231	Down	Up
OLc39.01e	EH-domain containing 2	EHD2	NM_014601	Down	Up
OLd70.02e	Homo sapiens arginine-glutamic acid dipeptide (RE) repeats	RERE	NM_012102	Down	Up
OLD77.01f	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	ID3	NM_002167	Down	Up
OLD77.05h	PREDICTED: similar to MGC86501 protein isoform 4 [<i>Danio rerio</i>]		XP_708570	Down	Up
OLF44.01a	MHC B-G antigen isoform 1 precursor		NM_001031810	Down	Up
OLF49.06c	Keratin 19	KRT19	NM_002276	Down	Up
OLb06.03c	TIMP metalloproteinase inhibitor 2	TIMP2	NM_003255	Down	
OLb09.01f	Decorin	DCN	NM_133503	Down	
OLb17.12c	Myocilin, trabecular meshwork inducible glucocorticoid response	MYOC	NM_000261	Down	
OLb21.05c	Homogentisate 1,2-dioxygenase (homogentisate oxidase)	HGD	NM_000187	Down	
OLb26.01g	Angiopoietin 4	ANGPT4	NM_015985	Down	
OLb01.07h	Serum deprivation response (phosphatidylserine binding protein)	SDPR	NM_004657		Up
OLb01.08f	Type I collagen alpha 2 chain		BAA25383		Up
OLb09.05h	High-mobility group box 1	HMGB1	NM_002128		Up
OLb09.12c	Ectodermal-neural cortex (with BTB-like domain)	ENC1	NM_003633		Up
OLb10.03e	Phosphatidylinositol glycan, class S	PIGS	NM_033198		Up
OLb11.11d	Amyloid beta (A4) precursor-like protein 2	APLP2	NM_001642		Up
OLb12.06b	Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	MYL6	NM_079423		Up
OLb12.11b	Monocyte to macrophage differentiation-associated	MMD	NM_012329		Up
OLb13.09a	Quinoid dihydropteridine reductase	QDPR	NM_000320		Up
OLb16.03a	Transgelin	TAGLN	NM_003186		Up
OLb18.10e	Keratin 18	KRT18	NM_000224		Up
OLb19.03a	Integral membrane protein 2B	ITM2B	NM_021999		Up
OLb21.11a	Guanine nucleotide binding protein (G protein), beta polypeptide 2	GNB2	NM_005273		Up
OLb22.05b	Glypican 6	GPC6	NM_005708		Up
OLb23.01e	PREDICTED: hypothetical protein XP_691710 [<i>Danio rerio</i>]		XP_696802		Up
OLb26.08g	Gelsolin (amyloidosis, Finnish type)	GSN	NM_000177		Up
OLb31.04e	Carboxypeptidase, vitellogenic-like	CPVL	NM_031311		Up
OLb32.04a	HtrA serine peptidase 1	HTRA1	NM_002775		Up
OLD06.01e	Spindlin	SPIN	NM_006717		Up
OLD06.06b	Zinc finger, FYVE domain containing 21	ZFYVE21	NM_024071		Up
OLD10.09h	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (I κ B α)	NFKBIA	NM_020529		Up
OLD70.09a	V-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian)	RELB	NM_006509		Up
OLD70.11a	Prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	PSAP	NM_002778		Up
OLD71.04c	Inhibitor of growth family, member 3	ING3	NM_019071		Up
OLD71.05e	Calcyclin binding protein	CACYBP	NM_014412		Up
OLD72.07g	RIO kinase 3 (yeast)	RIOK3	NM_003831		Up
OLD75.05e	Actin, gamma 1	ACTG1	NM_001614		Up
OLD79.06h	Thioredoxin interacting protein	TXNIP	NM_006472		Up
OLE09.11e	Signal peptide peptidase-like 2A	SPPL2A	NM_032802		Up
OLF47.12g	Sorting nexin 4	SNX4	NM_003794		Up
OLb07.07h	Cathepsin F	CTSF	NM_003793	Up	Up

The first column lists the clone ID in MEBase. "Up" and "down" mean the accumulated mRNA levels of the gene were more than 0.5 or less than -0.5 in log₂ ratio on day 7 compared with those at 0 h, respectively.

Table 3-2. continued.

Clone ID	Gene name	Gene symbol	GenBank acc No.	Accumulated mRNA levels on day 7	
				25°C	15°C
OLb13.04f	CAP, adenylate cyclase-associated protein 1 (yeast)	CAP1	NM_006367		
OLb19.09c	Matrix-remodelling associated 8	MXRA8	NM_032348		
OLb23.11g	Myeloid leukemia factor 2	MLF2	NM_005439		
OLb26.06f	Fumarylacetoacetate hydrolase (fumarylacetoacetase)	FAH	NM_000137		
OLc37.07d	V-rat simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	RALB	NM_002881		
OLc56.05g	Rho GTPase activating protein 1	ARHGAP1	NM_004308		
OLd08.04f	Zinc finger, HIT type 1	ZNHIT1	NM_006349		
OLd59.01d	CD9 antigen (p24)	CD9	NM_001769		
OLd60.05b	Tetraspanin-7 (Tspan-7)		P41732		
OLd68.05c	Ring finger protein 185	FLJ38628	NM_152267		
OLd73.11c	P450 (cytochrome) oxidoreductase	POR	NM_000941		
OLd77.04f	SUB1 homolog (<i>S. cerevisiae</i>)	PC4	NM_006713		
OLe03.09e	Casein kinase 2, beta polypeptide	CSNK2B	NM_001320		
OLb21.07b	Unknown			Down	Up
OLc57.05g	Unknown			Down	Up
OLd56.03e	Unknown			Down	Up
OLd59.04a	Unknown			Down	Up
OLd66.12b	Unknown			Down	Up
OLd77.03f	Unknown			Down	Up
OLb02.01c	Unknown				Up
OLb02.01d	Unknown				Up
OLb11.07b	Unknown				Up
OLb13.05e	Unknown				Up
OLb21.11c	Unknown				Up
OLb27.04a	Unknown				Up
OLb30.08b	Unknown				Up
OLc35.08f	Unknown				Up
OLc57.12a	Unknown				Up
OLd06.01g	Unknown				Up
OLd09.05a	Unknown				Up
OLd50.09h	Unknown				Up
OLd54.05c	Unknown				Up
OLd58.03h	Unknown				Up
OLd60.08b	Unknown				Up
OLd79.01a	Unknown				Up
OLf46.08b	Unknown				Up
OLf48.02b	Unknown				Up
OLf48.09a	Unknown				Up
OLf49.01d	Unknown				Up
OLb04.01a	Unknown			Up	Up
OLc56.03b	Unknown			Up	Up
OLb07.04g	Unknown				Up
OLb32.04h	Unknown				Up
OLd56.09f	Unknown				Up
OLd76.03d	Unknown				Up
OLd77.03e	Unknown				Up
OLe05.09h	Unknown				Up
OLf48.11h	Unknown				Up

Table 3-3. Genes which exhibited the accumulated mRNA levels on day 7 after temperature shift from 25°C to 15°C in OLHNI-e1 cells less than those of the cells successively cultured at 25°C for the same period

Clone ID	Gene name	Gene symbol	GenBank acc No.	Accumulated mRNA levels on day 7	
				25°C	15°C
OLb29.01g	Aldolase C, fructose-bisphosphate	ALDOC	NM_005165	Up	Down
OLf48.06c	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide 1	P4HA1	NM_000917	Up	Down
OLb08.03h	Enolase 1, (alpha)	ENO1	NM_001428	Up	
OLc53.12e	Glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	GAPDS	NM_014364	Up	
OLd57.09c	Myosin, heavy polypeptide 4, skeletal muscle	MYH4	NM_017533	Up	
OLd68.03f	Sequestosome 1	SQSTM1	NM_003900	Up	
OLf44.01c	Scavenger receptor class B, member 2	SCARB2	NM_005506	Up	
OLb01.08a	Stearoyl-CoA desaturase (delta-9-desaturase)	SCD	NM_005063		Down
OLb04.10b	Isopentenyl-diphosphate delta isomerase 1	IDI1	NM_004508		Down
OLb07.01h	3-Hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	NM_000859		Down
OLb07.02g	Phosphoglycerate mutase 1 (brain)	PGAM1	NM_002629		Down
OLb07.04f	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	YWHAB	NM_139323		Down
OLb07.09h	H2A histone family, member V	H2AFV	NM_012412		Down
OLb07.12d	ADP-ribosylation factor 4	ARF4	NM_001660		Down
OLb08.02b	Nucleolar protein 5A (56kDa with KKE/D repeat)	NOL5A	NM_006392		Down
OLb09.05g	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	SMC4L1	NM_005496		Down
OLb11.08e	Extracellular matrix protein 2, female organ and adipocyte specific	ECM2	NM_001393		Down
OLb12.08h	Putative 28 kDa protein	LOC56902	NM_020143		Down
OLb15.04e	Lectin, mannose-binding, 1	LMAN1	NM_005570		Down
OLb15.09f	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methylenetetrahydrofolate cyclohydrolase	MTHFD2	NM_006636		Down
OLb22.06g	Nascent-polypeptide-associated complex alpha polypeptide	NACA	NM_005594		Down
OLb25.08e	ATPase, Na+/K+ transporting, beta 1 polypeptide, transcript variant 1	ATP1B1	NM_001677		Down
OLb25.11d	Phenylalanine-tRNA synthetase-like, alpha subunit	FARSLA	NM_004461		Down
OLb25.11e	RAN, member RAS oncogene family	RAN	NM_006325		Down
OLb26.04a	FK506 binding protein 11, 19 kDa	FKBP11	NM_016594		Down
OLb26.06d	Threonyl-tRNA synthetase	TARS	NM_152295		Down
OLb29.02c	Threonyl-tRNA synthetase	TARS	NM_152295		Down
OLb29.04b	H2A histone family, member X	H2AFX	NM_002105		Down
OLb29.06e	Integrin beta 1 binding protein 3	ITGB1BP3	NM_170678		Down
OLc37.07f	Kruppel-like factor 6	KLF6	NM_001300		Down
OLc56.03a	Mitochondrial ribosomal protein S6	MRPS6	NM_032476		Down
OLc58.02b	Ribosomal protein S27a	RPS27A	NM_002954		Down
OLd05.12e	Exosome component 4	EXOSC4	NM_019037		Down
OLd52.10b	Cytochrome c, somatic	CYCS	NM_018947		Down
OLd55.03g	Translocase of inner mitochondrial membrane 10 homolog (yeast)	TMM10	NM_012456		Down
OLd57.03a	Ribonucleotide reductase M2 polypeptide	RRM2	NM_001034		Down
OLd57.03e	PRP19/PSO4 pre-mRNA processing factor 19 homolog (<i>S. cerevisiae</i>)	PRP19	NM_014502		Down
OLd58.10c	Adaptor-related protein complex 1, sigma 2 subunit	AP1S2	NM_003916		Down
OLd61.07d	S-adenosylhomocysteine hydrolase	AHCY	NM_000687		Down
OLd67.02b	Ubiquitin-conjugating enzyme E2C	UBE2C	NM_007019		Down
OLd67.03c	Proliferation-associated 2G4, 38kDa	PA2G4	NM_006191		Down
OLd69.05e	Phosphoserine phosphatase	PSPH	NM_004577		Down
OLd72.06h	CD69 antigen (p60, early T-cell activation antigen)	CD69	NM_001781		Down
OLe09.05e	Heat shock 90kDa protein 1, alpha	HSPCA	NM_005348		Down
OLf43.05h	Nuclear factor (erythroid-derived 2)-like 2	NFE2L2	NM_006164		Down
OLf48.01g	Plastin 3 (T isoform)	PLS3	NM_005032		Down

The first column lists the clone ID in MEBase. "Up" and "down" mean the accumulated mRNA levels of the gene were more than 0.5 or less than -0.5 in log₂ ratio on day 7 compared with those at 0 h, respectively.

Table 3-3. continued

Clone ID	Gene name	Gene symbol	GenBank acc No.	Accumulated mRNA levels on day 7	
				25°C	15°C
OLb04.10g	GTP binding protein 4	GTPBP4	NM_012341		
OLb08.12b	Ribosomal protein L36a	RPL36A	NM_021029		
OLb10.02b	Influenza virus NS1A binding protein	IVNS1ABP	NM_006469		
OLb15.10a	YY1 transcription factor	YY1	NM_003403		
OLb19.06c	Eukaryotic translation elongation factor 2	EEF2	NM_001961		
OLb25.06h	RAE1 RNA export 1 homolog (<i>S. pombe</i>)	RAE1	NM_003610		
OLb26.11e	Heat shock 27kDa protein 1	HSPB1	NM_001540		
OLc35.08d	Eukaryotic translation elongation factor 1 gamma	EEF1G	NM_001404		
OLc57.09h	GDP dissociation inhibitor 2	GDI2	NM_001494		
OLd52.06d	Dentin sialophosphoprotein	DSPP	NM_014208		
OLb07.04h	Unknown			Up	Down
OLc57.10h	Unknown			Up	
OLd70.10g	Unknown			Up	
OLb06.08f	Unknown				Down
OLb09.07a	Unknown				Down
OLb20.06f	Unknown				Down
OLb21.10a	Unknown				Down
OLb31.04g	Unknown				Down
OLc38.09g	Unknown				Down
OLd07.06h	Unknown				Down
OLd11.02d	Unknown				Down
OLd11.06c	Unknown				Down
OLd54.03e	Unknown				Down
OLd55.09e	Unknown				Down
OLd60.10e	Unknown				Down
OLd66.02b	Unknown				Down
OLd70.11d	Unknown				Down
OLe02.10b	Unknown				Down
OLf44.09a	Unknown				Down
OLd68.07e	Unknown			Down	Down
OLd77.04g	Unknown			Down	Down
OLb07.10g	Unknown				
OLb31.03d	Unknown				
OLc56.08a	Unknown				
OLd52.01c	Unknown				
OLf44.01b	Unknown				

Table 3-4. Gene Ontology terms and number of clones the accumulated mRNA levels of which were significantly different in OLHdrR-e3 cells cultured at 15 and 25°C during 7 days, and between OLHNI-e1 and OLHdrR-e3 cells cultured at 15°C for 7 days ($P < 0.05$ by Kruskal-Wallis ANOVA or Mann-Whitney test as appropriate)

GO term	P values by χ^2 test					
	25°C			15°C		
	All	>0.5 in log ₂ ratio on day 3	<-0.5 in log ₂ ratio on day 3	All	>0.5 in log ₂ ratio on day 3	<-0.5 in log ₂ ratio on day 3
Molecular function						
Binding						
Glycosaminoglycan binding	0.321	0.126	0.611	0.230	0.388	0.840
Metal binding	0.449	0.139	0.531	0.215	0.575	0.245
Nucleic acid binding	0.449	0.139	0.531	0.361	0.552	0.273
Nucleotide binding	0.245	0.095	0.612	0.358	0.499	0.217
Protein binding	0.479	0.066	0.635	0.349	0.534	0.633
Catalytic activity	0.482	0.240	0.585	0.361	0.361	0.889
Hydrolase activity	0.481	0.230	0.613	0.361	0.536	0.581
Kinase activity	0.481	0.235	-	0.330	0.386	0.708
Ligase activity	0.061	-	-	0.218	-	-
Oxidoreductase activity	0.478	-	-	0.115	-	-
Transferase activity	0.293	0.002	-	0.249	0.552	0.400
Enzyme regulator activity	0.388	0.214	-	0.263	0.403	0.896
Enzyme activator activity	0.472	-	-	0.218	-	-
Transporter activity	0.480	0.238	-	0.352	0.562	0.534
Electron transporter activity	0.407	-	-	0.360	-	0.456
Transcription regulator activity	0.479	0.228	-	0.292	0.085	0.933
Transcription cofactor activity	-	-	-	-	-	-
Structural molecule activity	0.039	0.027	0.547	0.362	0.574	0.666
Structural constituent of ribosome	0.049	0.030	-	0.054	0.070	0.938
Biological process						
Cellular process	0.482	0.143	0.260	0.362	0.457	0.403
Cell communication	0.216	0.124	0.547	0.362	0.391	0.587
Cellular physiological process	0.352	0.205	0.200	0.359	0.495	0.129
Physiological process	0.399	0.200	0.320	0.307	0.526	0.685
Cellular physiological process	0.391	0.090	0.363	0.352	0.459	0.794
Metabolism	0.399	0.200	0.320	0.307	0.526	0.685
Response to stimulus	0.431	0.086	0.618	0.213	0.191	0.963
Development	0.110	0.172	-	0.198	0.158	0.331
Morphogenesis	0.256	0.055	-	0.117	0.224	0.063
Cell component	0.311	0.106	-	0.195	0.463	0.074
Cell	0.251	0.058	0.227	0.221	0.575	0.950
Intracellular	0.151	0.019	0.154	0.165	0.561	0.770
Membrane	0.193	0.019	0.120	0.320	0.573	0.937
Extracellular	0.200	0.199	0.400	0.117	0.131	0.396
All	0.468	0.033	-	0.080	-	0.010
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.862	0.915	0.114	0.862	0.915	0.114
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.339	0.853	0.239	0.339	0.853	0.239
All	0.425	-	-	0.425	-	-
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.882	0.398	0.236	0.882	0.398	0.236
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.648	0.847	0.222	0.648	0.847	0.222
All	0.973	0.501	0.196	0.973	0.501	0.196
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.229	0.260	0.114	0.229	0.260	0.114
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.956	0.823	0.151	0.956	0.823	0.151
All	0.289	-	-	0.289	-	-
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.724	-	-	0.724	-	-
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.961	-	-	0.961	-	-
All	0.413	-	-	0.413	-	-
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.738	0.395	0.076	0.738	0.395	0.076
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.219	-	-	0.219	-	-
All	0.037	-	-	0.037	-	-
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.640	0.458	0.018	0.640	0.458	0.018
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.915	0.277	0.037	0.915	0.277	0.037
All	0.846	0.848	0.140	0.846	0.848	0.140
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.825	0.917	0.072	0.825	0.917	0.072
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.971	0.719	0.237	0.971	0.719	0.237
All	0.495	0.583	0.065	0.495	0.583	0.065
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.787	0.836	0.055	0.787	0.836	0.055
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.495	0.583	0.065	0.495	0.583	0.065
All	0.480	0.818	0.061	0.480	0.818	0.061
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.248	0.177	0.177	0.248	0.177	0.177
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.273	-	-	0.273	-	-
All	0.280	-	-	0.280	-	-
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.550	0.859	0.035	0.550	0.859	0.035
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.197	0.904	0.005	0.197	0.904	0.005
All	0.499	0.836	0.015	0.499	0.836	0.015
>0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.349	0.488	0.033	0.349	0.488	0.033
<-0.5 in log ₂ ratio on day 3 in OLHNI-e1	0.275	-	-	0.275	-	-

Red and blue color boxes represent the GO terms the clone numbers of which were significantly more and less than the expectation values, respectively ($P < 0.05$). Hyphens indicate the GO terms the expectation values of which were too small for reliable analyses (See Supplementary Table 3-5 - 3-7).

Table 3-5. Genes which exhibited the accumulated mRNA levels on day 3 after temperature shift from 25°C to 15°C in OLHNI-e1 cells more than those of OLHDrR-e3 cells

Clone ID	Gene name	Gene symbol	GenBank acc No.	Accumulated mRNA levels on day 3	
				OLHNI-e1	OLHDrR-e3
OLd69.05c	Ribosomal protein L22	RPL22	NM_000983	Up	Down
OLb07.07h	Cathepsin F	CTSF	NM_003793	Up	
OLb09.12c	Ectodermal-neural cortex (with BTB-like domain)	ENC1	NM_003633	Up	
OLb26.09c	Nuclear factor (erythroid-derived 2)-like 2	NFE2L2	NM_006164	Up	
OLd54.02c	B-cell receptor-associated protein 31	BAP31	NM_005745	Up	
OLb01.08f	Type I collagen alpha 2 chain		BAA25383.1		Down
OLb01.11d	Bone morphogenetic protein 4	BMP4	NM_130851		Down
OLb04.06g	Porin 31HM		AAB20246.1		Down
OLb06.04d	Membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1	MTCBP-1	NM_018269		Down
OLb08.03h	Enolase 1, (alpha)	ENO1	NM_001428		Down
OLb09.01f	Decorin	DCN	NM_133503		Down
OLb11.04a	Sterol regulatory element binding transcription factor 2	SRBP2	NM_004599		Down
OLb11.11h	Ubiquitin-like 7 (bone marrow stromal cell-derived)	UBL7	NM_032907		Down
OLb16.02c	Tudor domain containing 3	TDRD3	NM_030794		Down
OLb19.06c	Eukaryotic translation elongation factor 2	EEF2	NM_001961		Down
OLb21.09a	Follistatin-like 1	FSTL1	NM_007085		Down
OLb26.08g	Gelsolin (amyloidosis, Finnish type)	GEL	NM_000177		Down
OLb31.11d	Hexosaminidase B (beta polypeptide)	HEXB	NM_000521		Down
OLc57.12f	Sad1 unc-84 domain protein 1	SUN1	AAF15888.1		Down
OLd04.09e	FYN oncogene related to SRC, FGR, YES	FYN	NM_002037		Down
OLd50.09g	Ribose 5-phosphate isomerase A	RPIA	NM_144563		Down
OLd54.05f	KH domain containing, RNA binding, signal transduction associated 2	KHDRBS2	NM_152688		Down
OLd56.07c	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 23	SLC25A23	NM_024103		Down
OLd57.02d	Tudor domain containing 7	TDRD7	NM_014290		Down
OLd58.02b	Zinc finger protein 207	ZFP207	NM_003457		Down
OLd58.08d	Chromosome 16 open reading frame 34		NM_144570		Down
OLd59.02f	PREDICTED: similar to extracellular matrix protein 1 isoform 1 precursor		XP_692703		Down
OLd60.02e	Coronin, actin binding protein, 1C	COR1C	NM_014325		Down
OLd65.01d	Pyruvate kinase, muscle	PKM2	NM_002654		Down
OLd69.03f	Zinc finger, A20 domain containing 2	ZA20D2	NM_006007		Down
OLd69.07a	Probable RNA-dependent helicase p68	DDX5	P17844		Down
OLd69.09b	Myosin, light polypeptide kinase, transcript variant 6	MYLK	NM_005965		Down
OLd72.07f	Zinc finger protein 91	ZNF91	NM_003430		Down
OLd72.07g	RIO kinase 3 (yeast)	RIOK3	NM_003831		Down
OLd72.11d	Unnamed protein product [<i>Tetraodon nigroviridis</i>]		CAG03027.1		Down
OLd73.04a	Eukaryotic translation elongation factor 2	EEF2	NM_001961		Down
OLd79.09d	Hypothetical protein LOC196463		NM_173542		Down
OLe05.11f	Coagulation factor V precursor	FA5	P12259		Down
OLe07.01c	Cytochrome P450, family 2, subfamily J, polypeptide 2	CYP2J2	NM_000775		Down
OLe07.01f	Complement component 3	C3	NM_000064		Down
OLe07.01h	Toxin-1		AAM21198.1		Down
OLe07.04g	Kallikrein B, plasma (Fletcher factor) 1	KLKB1	NM_000892		Down
OLe09.04g	Glyoxalase I	GLO1	NM_006708		Down
OLf46.12e	Alpha 2 type V collagen preproprotein	COL5A2	NM_000393		Down
OLf49.06c	Keratin 19	KRT19	NM_002276		Down
OLb04.09d	Keratin 18	KRT18	NM_000224	Down	Down
OLb09.04b	Alpha 1 type I collagen preproprotein	COL1A1	NM_000088	Down	Down
OLb26.01g	Angiopoietin 4	ANGPT4	NM_015985	Down	Down
OLb04.11e	Hypothetical protein LOC144871		NM_006260		
OLb06.02g	Papillary renal cell carcinoma (translocation-associated)	PRCC	NM_005973		
OLb09.07f	Eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa	EIF3S2	NM_003757		
OLb11.11d	Amyloid beta (A4) precursor-like protein 2	APLP2	NM_001642		
OLb15.04e	Lectin, mannose-binding, 1	LMAN1	NM_005570		
OLb30.01e	GTP binding protein 4	ARAC5	NM_012341		
OLb31.04e	Carboxypeptidase, vitellogenic-like	CPV1	NM_031311		
OLb32.01e	Reticulon 4 interacting protein 1	RTN4IP1	NM_032730		
OLd59.01d	CD9 antigen (p24)	CD9	NM_001769		
OLd06.01f	Unknown				Down
OLd50.04g	Unknown				Down
OLd50.07f	Unknown				Down
OLd51.06c	Unknown				Down
OLd52.08a	Unknown				Down
OLd58.08c	Unknown				Down
OLd61.11a	Unknown				Down
OLd69.07c	Unknown				Down
OLd69.11a	Unknown				Down
OLd70.06f	Unknown				Down
OLd70.07a	Unknown				Down
OLd80.09b	Unknown				Down
OLf44.06h	Unknown				Down
OLb13.11b	Unknown				
OLd76.07a	Unknown				
OLe01.01e	Unknown				
OLf49.01d	Unknown				

The first column lists the clone ID in MEBase. "Up" and "down" mean the accumulated mRNA levels of the gene were more than 0.5 or less than -0.5 in log₂ ratio on day 3 compared with those at 0 h, respectively.

Table 3-6. Genes which exhibited the accumulated mRNA levels on day 3 after temperature shift from 25°C to 15°C in OLHNI-e1 cells less than those of OLHDrR-e3 cells

Clone ID	Gene name	Gene symbol	GenBank acc No.	Accumulated mRNA levels on day 3	
				OLHNI-e1	OLHDrR-e3
OLb24.02d	CD82 antigen	CD82	NM_212663	Down	Up
OLf45.05h	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NDUFA8	NM_005004	Down	Up
OLb06.12e	Peptidylprolyl isomerase D (cyclophilin D)	PPID	NM_005038	Down	
OLb13.03b	Peroxisredoxin 1	PRDX1	NM_002574	Down	
OLb25.06h	RAE1 RNA export 1 homolog (<i>S. pombe</i>)	RAE1	NM_003610	Down	
OLb25.07g	Casein kinase 2, alpha 1 polypeptide	CSNK2A1	NM_001895	Down	
OLd52.10b	Cytochrome c, somatic	CYCS	NM_018947	Down	
OLd61.06f	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	NDUFA9	NM_005002	Down	
OLb05.05g	Ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	NM_003336		Up
OLb07.09e	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	ID1	NM_002165		Up
OLb09.07g	Guanine nucleotide binding protein-like 3 (nucleolar)	GNL3	NM_014366		Up
OLb10.10h	Tubulin-specific chaperone a	TBCA	NM_004607		Up
OLb16.02g	Retinol binding protein 3, interstitial	RBP3	NM_002900		Up
OLb17.12c	Myocilin, trabecular meshwork inducible glucocorticoid response	MYOC	NM_000261		Up
OLb21.03a	Cold inducible RNA binding protein	CIBP	NM_001280		Up
OLb26.01c	ARP3 actin-related protein 3 homolog (yeast)	ACTR3	NM_005721		Up
OLb32.03e	Peroxisredoxin 5	PRDX5	NM_012094		Up
OLb32.12c	ATP-binding cassette, sub-family F (GCN20), member 2	ABCF2	NM_005692		Up
OLc35.10b	Ubiquinol-cytochrome c reductase core protein I	UQCRC1	NM_003365		Up
OLc37.11e	Four and a half LIM domains 1	FHL1	NM_001449		Up
OLd11.12a	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	UBE2D2	NM_003339		Up
OLd57.09c	Myosin, heavy polypeptide 4, skeletal muscle	MYH4	NM_017533		Up
OLd69.05e	Phosphoserine phosphatase	PSPH	NM_004577		Up
OLd77.04f	SUB1 homolog (<i>S. cerevisiae</i>)	SUB1	NM_006713		Up
OLf48.12a	Cysteine-rich, angiogenic inducer, 61	CYR61	NM_001554		Up
OLd77.01f	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	ID3	NM_002167	Up	Up
OLd77.05h	PREDICTED: similar to MGC86501 protein isoform 4 [<i>Danio rerio</i>]	XP_708570		Up	Up
OLb01.02b	FK506 binding protein 2, 13kDa	FKBP2	NM_057092		
OLb02.01g	Small nuclear ribonucleoprotein polypeptide F	SNRPF	NM_003095		
OLb11.06a	Tubulin, alpha 1 (testis specific)	TUBA1	NM_006000		
OLb12.08h	Putative 28 kDa protein		NM_020143		
OLb15.06g	Eukaryotic translation initiation factor 3, subunit 6 48kDa	EIF3S6	NM_001568		
OLb22.04c	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	NDUFA8	NM_014222		
OLb22.10f	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	NDUFA9	NM_005002		
OLb25.02a	Cytoglobin	CYGB	NM_134268		
OLb25.11e	RAN, member RAS oncogene family	RAN	NM_006325		
OLc38.02g	Cytochrome b5 reductase 3	CYB5R3	NM_000398		
OLe12.07a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	DDX48	NM_014740		
OLd60.10e	Unknown			Down	Up
OLb17.07d	Unknown			Down	
OLb20.06f	Unknown			Down	
OLc56.08a	Unknown			Down	
OLb12.10c	Unknown				Up
OLb27.11g	Unknown				Up
OLd49.07g	Unknown				Up
OLd51.02b	Unknown				Up
OLd55.07h	Unknown				Up
OLe05.07b	Unknown				Up
OLf44.03g	Unknown				Up
OLf46.04c	Unknown				Up
OLb31.03d	Unknown				Up
OLd11.12c	Unknown				
OLf49.01e	Unknown				

The first column lists the clone ID in MEBase. "Up" and "down" mean the accumulated mRNA levels of the gene were more than 0.5 or less than -0.5 in log₂ ratio on day 3 compared with those at 0 h, respectively.

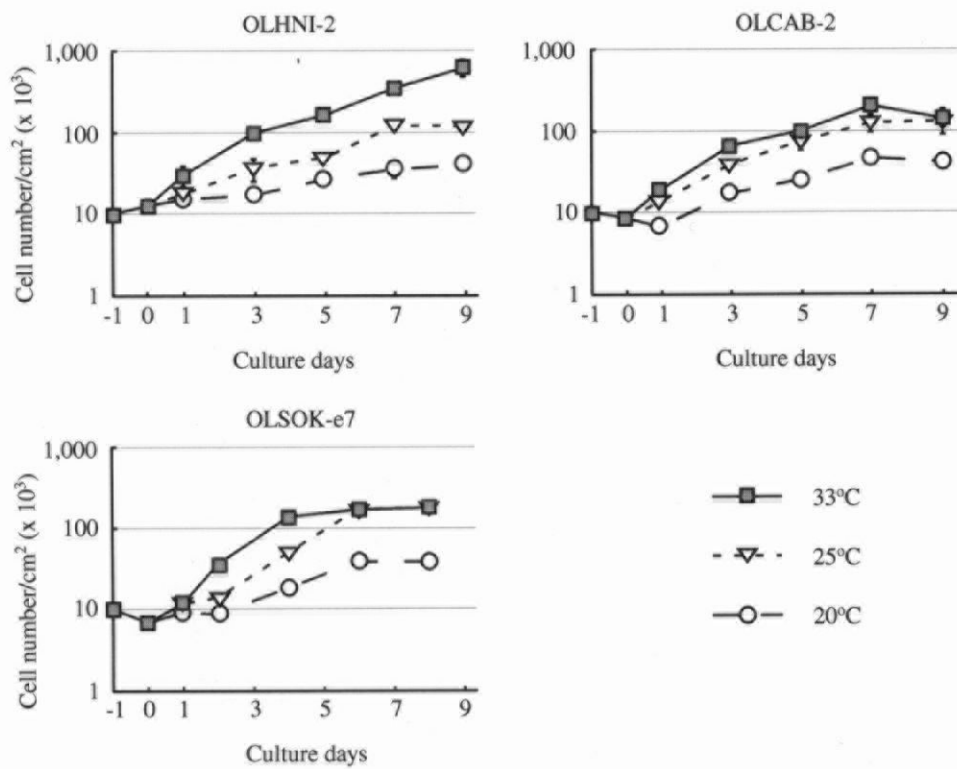


Fig. 1-1. Warm temperature-dependent growth of medaka cell lines from different populations. OLHNI-2, OLCAB-2 and OLSOK-e7 cell lines from the Northern Japanese, Southern Japanese and East Korean populations, respectively, were cultured at 20, 25 and 33°C. Cells, which had been cultured at 33°C, were adjusted their numbers to 1×10^4 cells/cm² and transferred to the indicated temperatures or successively maintained at 33°C. The number of cells per cm² was determined in three different plates on indicated days. Data are given as means \pm SD and marks without vertical lines of SD indicate that these lines are within the sizes of the marks.

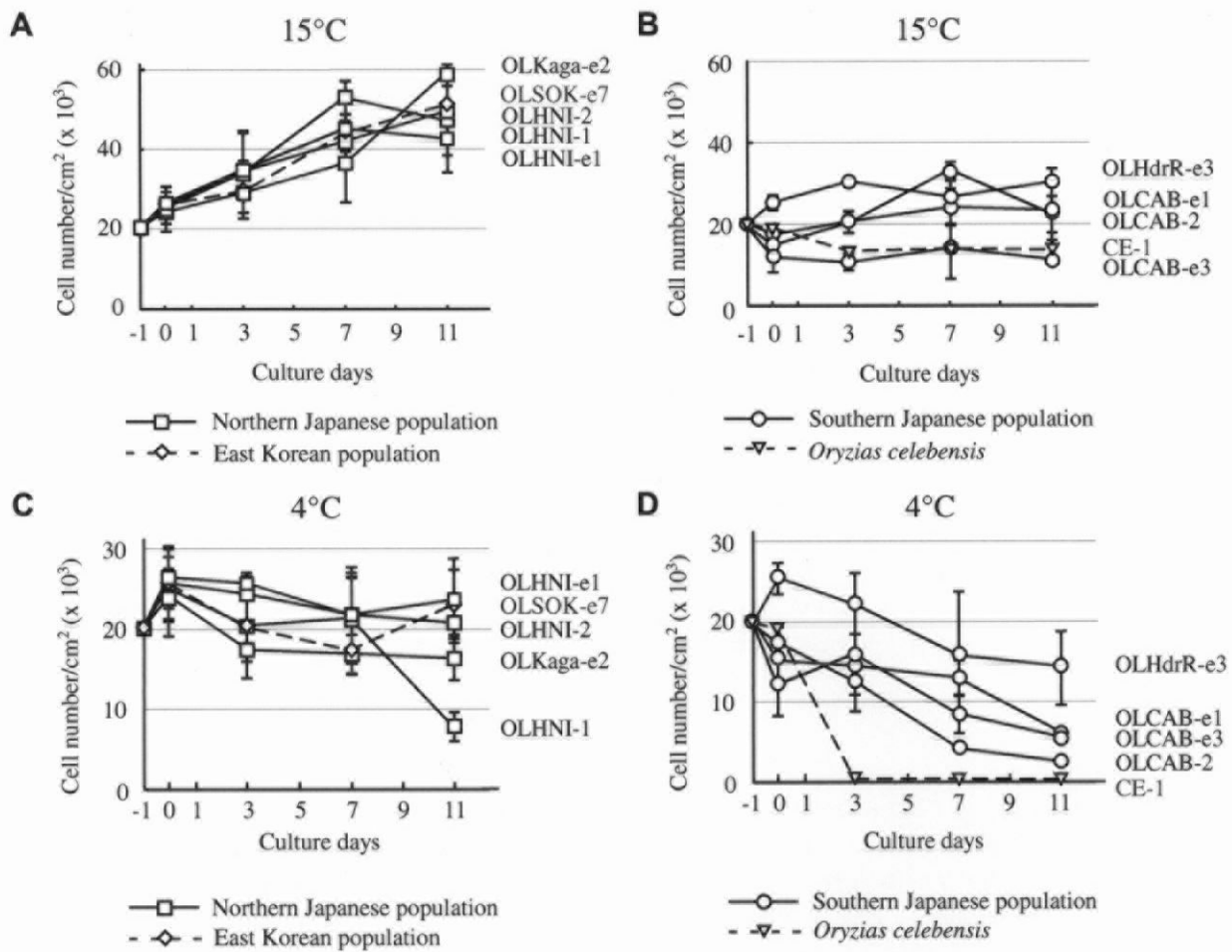


Fig. 1-2. Cold temperature-dependent growth of medaka cell lines from different populations. **A**, OLHNI-1, OLHNI-2, OLHNI-e1 and OLKaga-e2 cell lines from the Northern Japanese population and OLSOK-e7 cell line from the East Korean population were cultured at 15°C. **B**, OLCAB-2, OLCAB-e1, OLCAB-e3 and OLHdrR-e3 cell lines from the Southern Japanese population and CE-1 cell line from *Oryzias celebensis* were cultured at 15°C. **C**, all cell lines in panel **A** were cultured at 4°C. **D**, all cell lines in panel **B** were cultured at 4°C. Cells, which had been cultured at 33°C, were adjusted their numbers to 2×10^4 cells/cm² and transferred to the indicated temperatures. The number of cells per cm² was determined in three different plates on indicated days. Data are given as means \pm SD and marks without vertical lines of SD indicate that these lines are within the sizes of the marks.

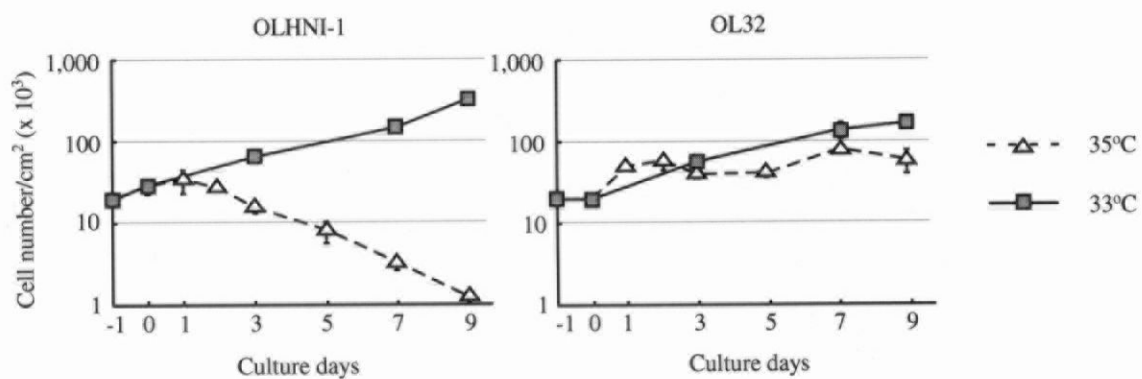
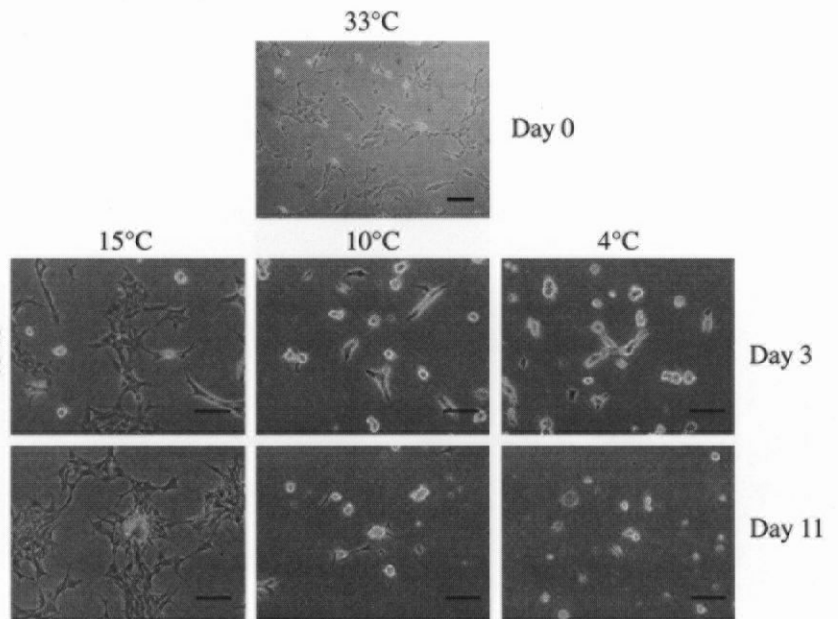
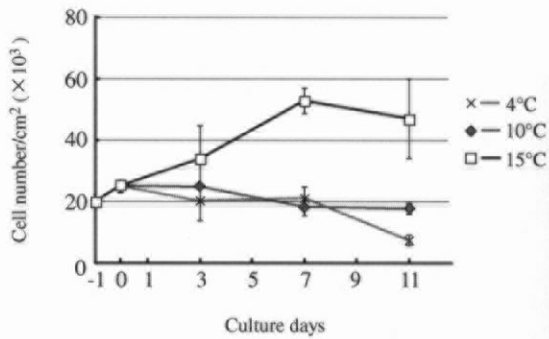


Fig. 1-3. High temperature-dependent growth of medaka cell lines from different populations. OLHNI-1 and OL32 cell lines from the Northern Japanese and Southern Japanese populations, respectively, were cultured at 33 and 35°C. Cells, which had been cultured at 33°C, were adjusted their numbers to 2×10^4 cells/cm² and transferred to the indicated temperatures or successively maintained at 33°C. The number of cells per cm² was determined in three different plates on indicated days. Data are given as means \pm SD and marks without vertical lines of SD indicate that these lines are within the sizes of the marks.

A OLHNI-1
(Northern Japanese population)



B OLHNI-2
(Northern Japanese population)

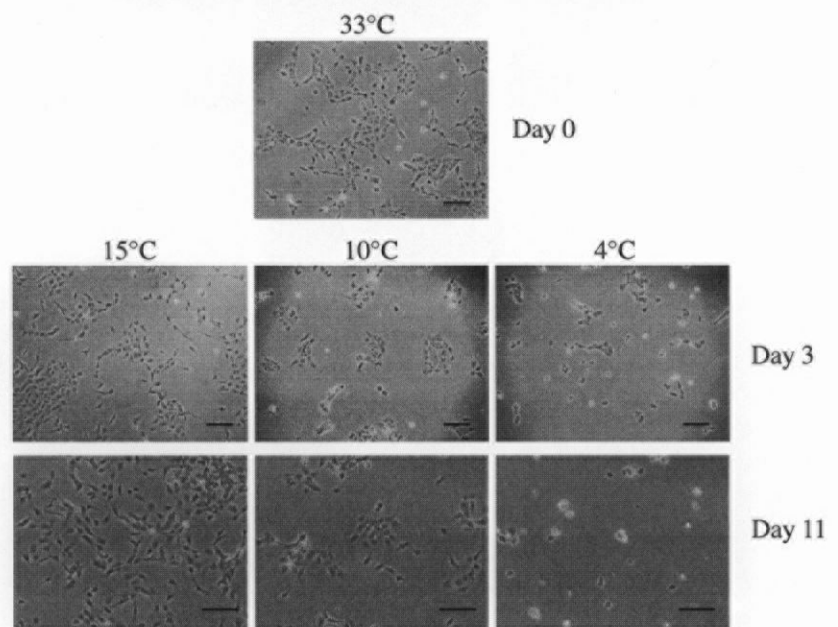
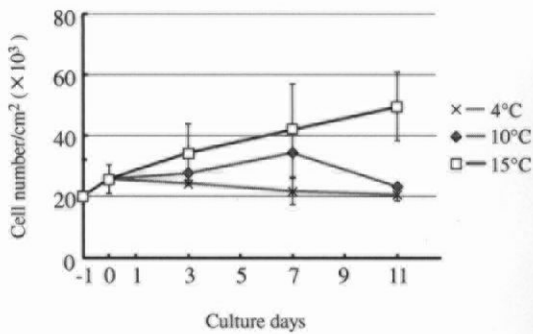
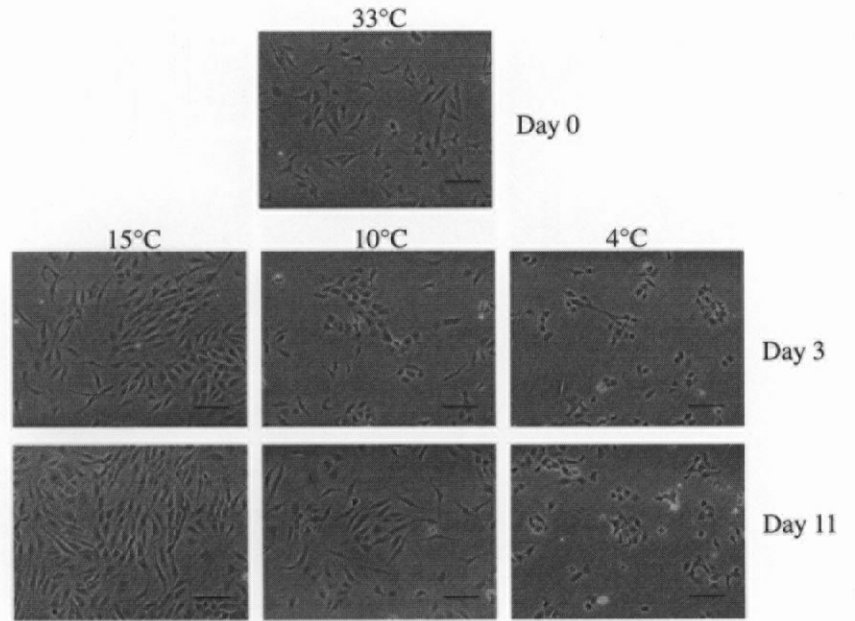
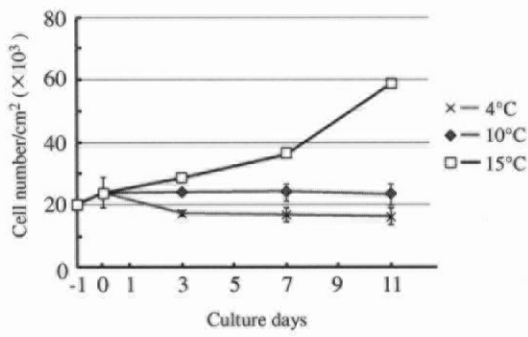


Fig.1-4. Cold temperature-dependent growth and morphological changes of medaka cell lines from different populations. OLHNI-1 (A), OLHNI-2 (B) and OLKaga-e2 (C) cell lines from the Northern Japanese population, OLSOK-e7 (D) cell line from the East Korean population, OLHdrR-e3 (E), OLCAB-2 (F), OLCAB-e1 (G) and OLCAB-e3 (H) from the Southern Japanese population, and CE-1 (I) cell line from *Oryzias celebensis* were cultured at 15, 10 and 4°C. Cells, which had been cultured at 33°C were adjusted their numbers to 2×10^4 cells/cm² and transferred to the indicated temperatures. The number of cells per cm² was determined in three different plates on indicated days. Data are given as means \pm SD and marks without vertical lines of SD indicate these lines are within the sizes of the marks. Bars indicate 100 μ m.

C OLKaga-e2
(Northern Japanese population)



D OLSOK-e7
(East Korean population)

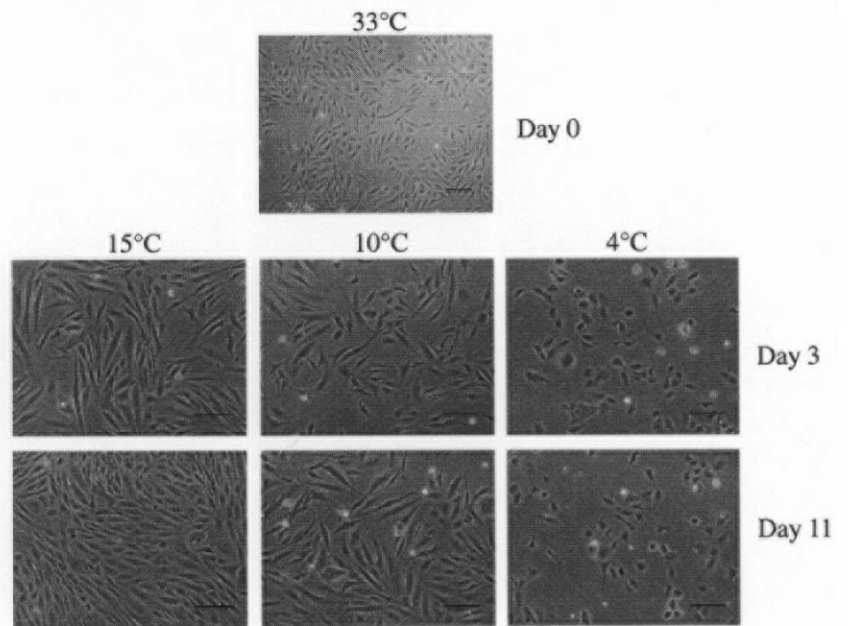
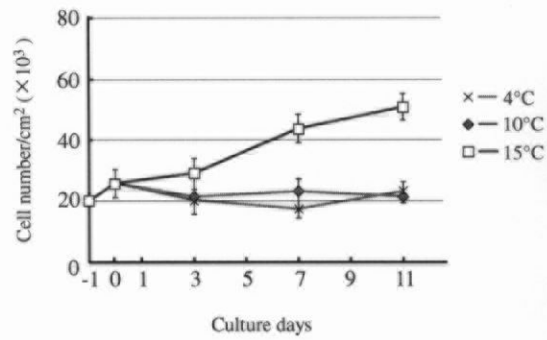
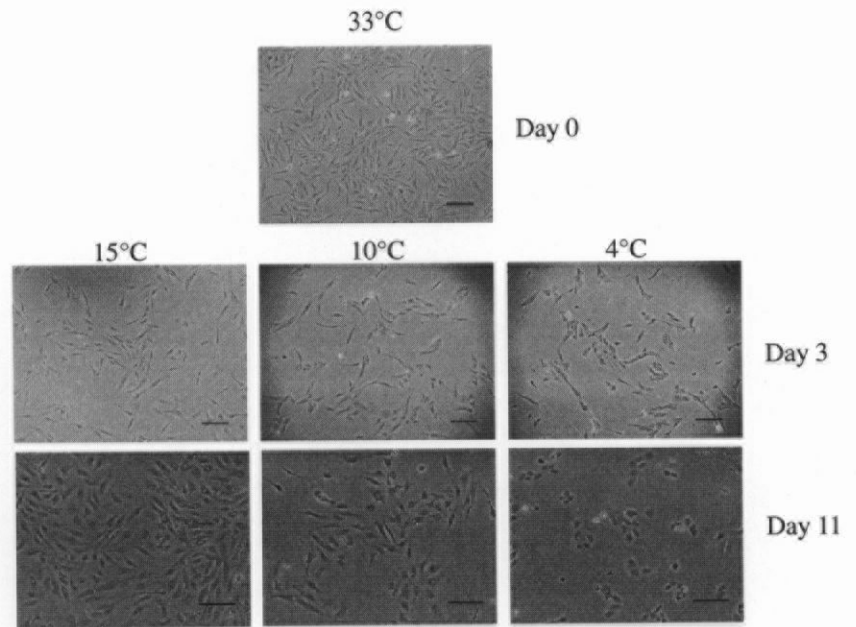
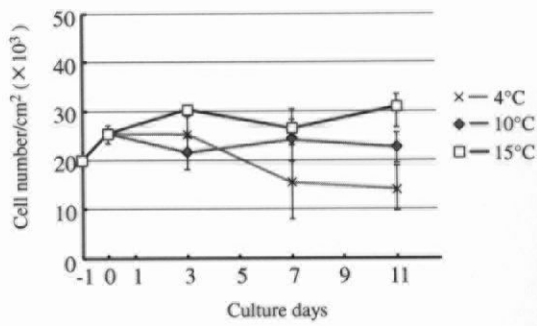
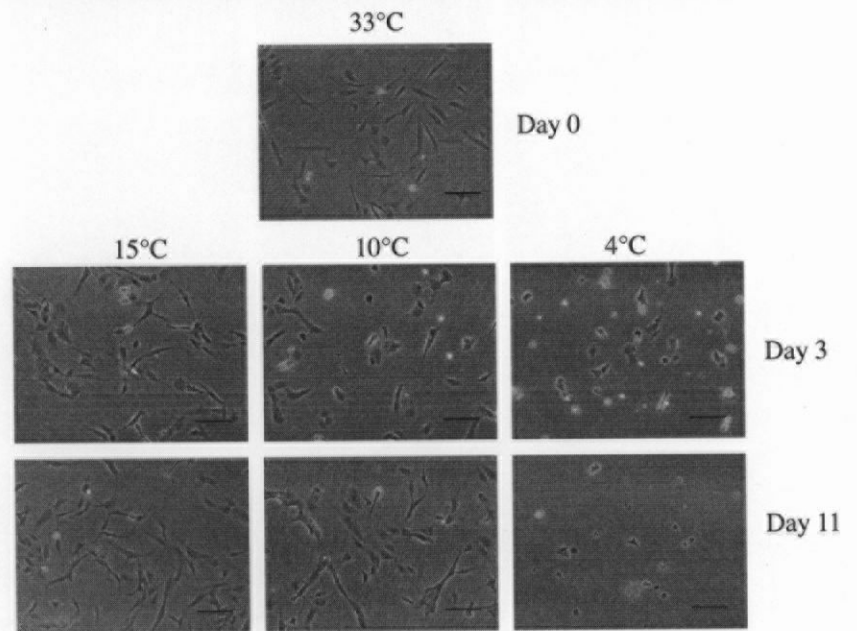
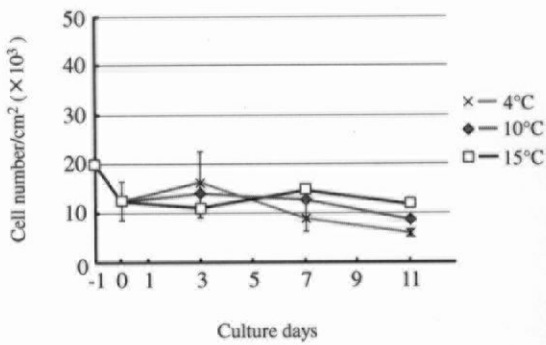


Fig. 1-4. continued

E OLHdrR-e3
(Southern Japanese population)



F OLCAB-e3
(Southern Japanese population)



G OLCAB-e1
(Southern Japanese population)

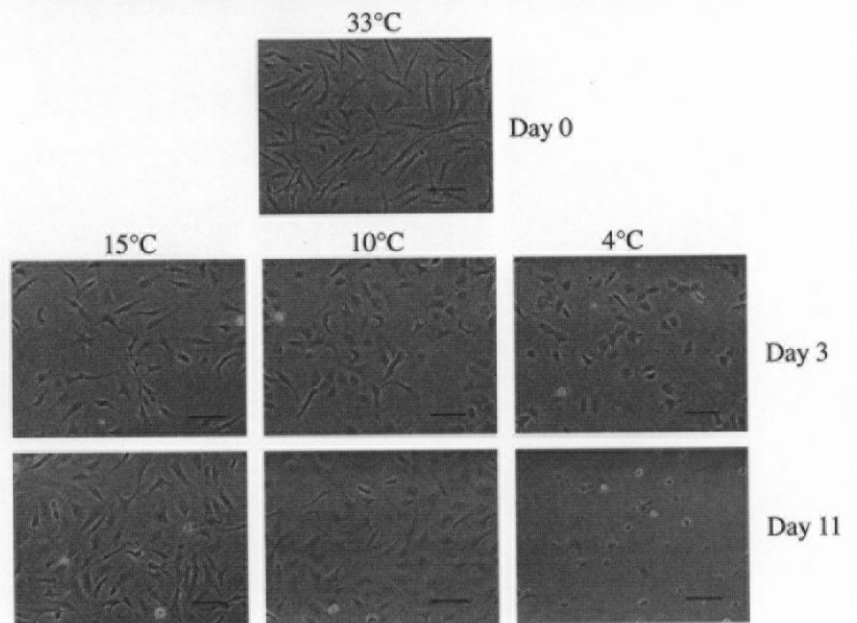
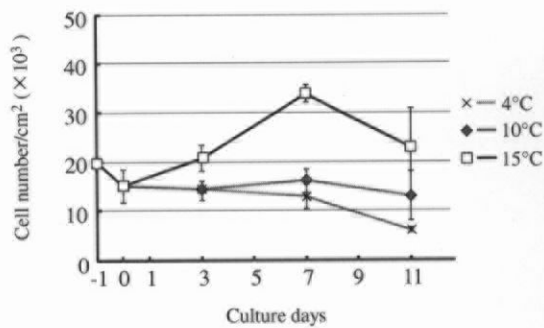
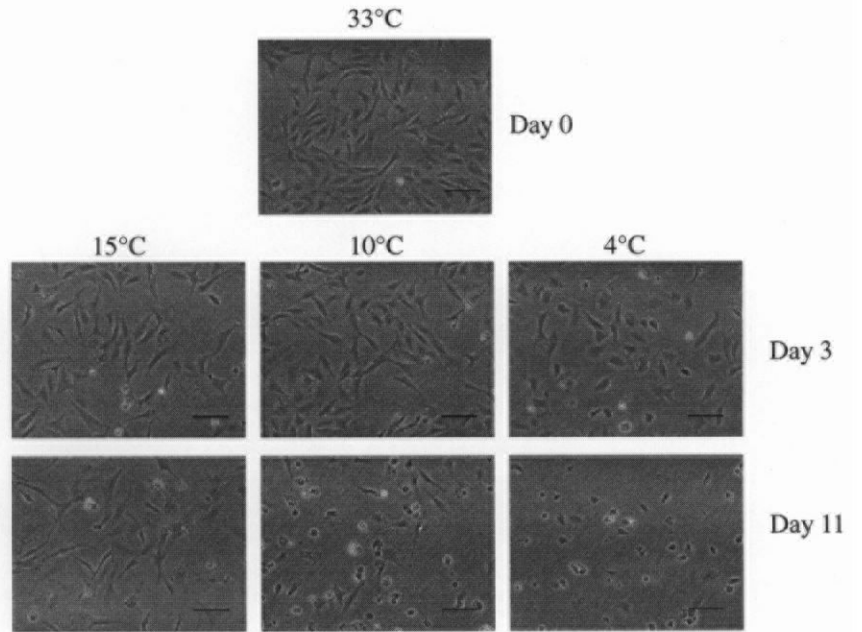
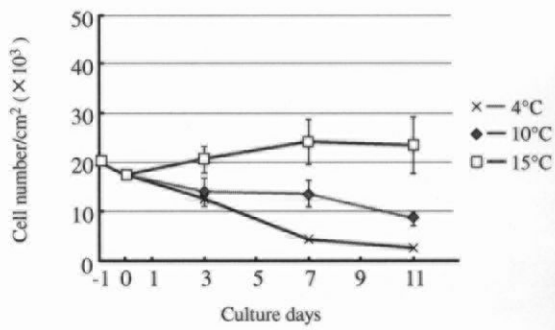


Fig. 1-4. continued

H OLCAB-2
(Southern Japanese population)



I CE-1
(*Oryzias celebensis*)

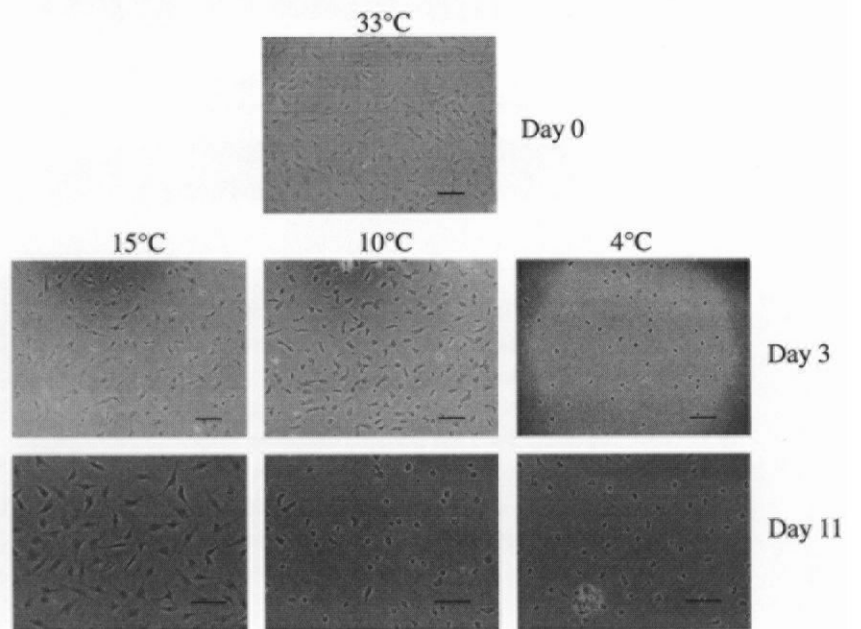
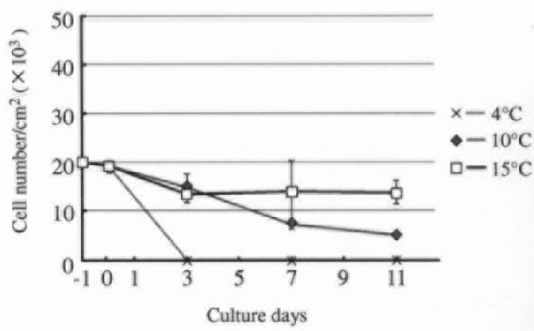


Fig. 1-4. continued

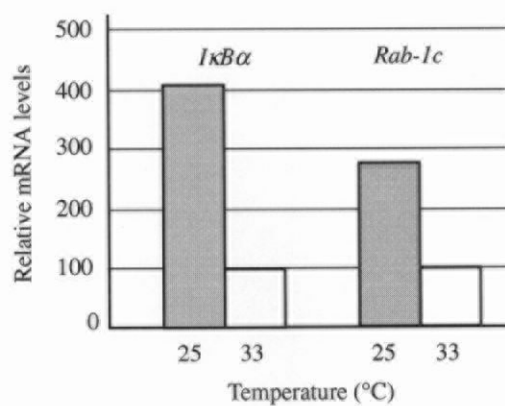


Fig. 1-6. The accumulated mRNA levels as revealed by quantitative real-time PCR for *IkBα* and *Rab-1c* in medaka OLHNI-1 cell line at 25 and 33°C. Real-time PCR was performed using cDNA samples No. 1 shown in Fig. 1-4 as templates. The relative levels were determined using *EF-1α* as the internal standard and the value at 33°C was accounted for 100.

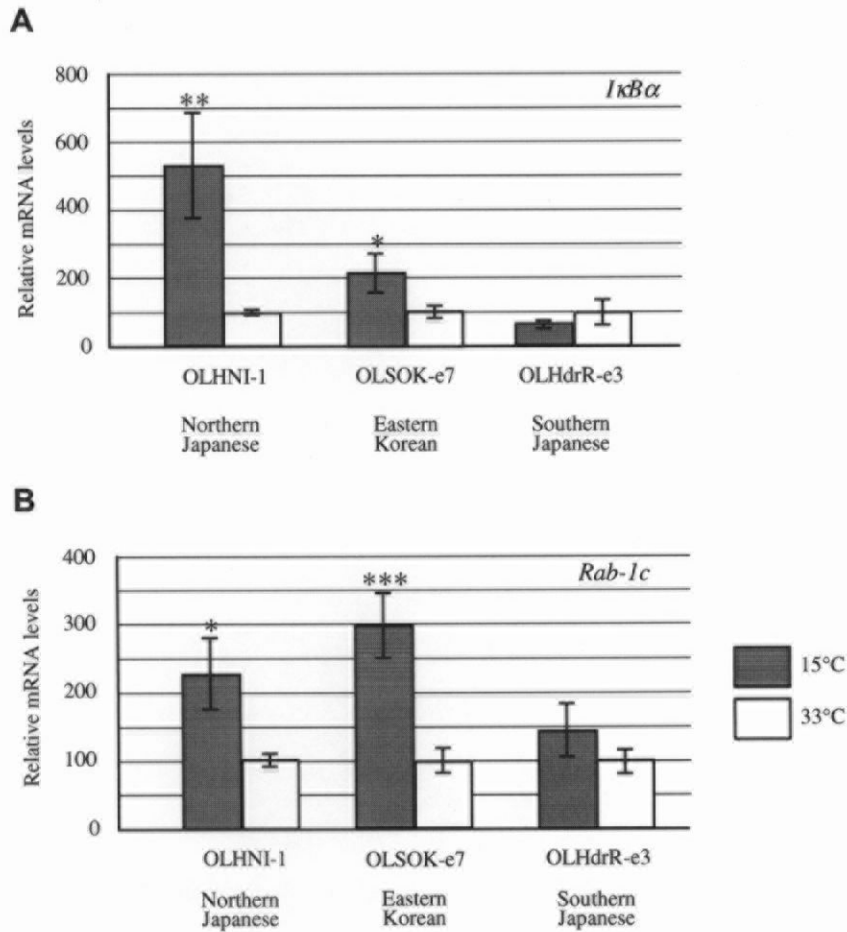


Fig. 1-7. The accumulated mRNA levels as revealed by quantitative real-time PCR for *IkBα* (A) and *Rab-1c* (B) in medaka OLHNI-1, OLSOK-e7 and OLHdrR-e3 cell lines at 15 and 33°C. OLHNI-1, OLSOK-e7 and OLHdrR-e3 were derived from the Northern Japanese, East Korean, and Southern Japanese populations, respectively. Total RNAs were isolated from cells incubated at 33°C throughout for 7 days, and from those incubated at 33°C and subsequently at 15°C for 7 days. The relative levels were determined using *EF-1α* as the internal standard and the value at 33°C was accounted for 100. Student's *t*-test was employed for statistical comparison between the levels at 15 and 33°C (* $P < 0.01$, ** $P < 0.005$, *** $P < 0.0005$). Three experiments were performed for each cell line and data are given as means \pm SD.

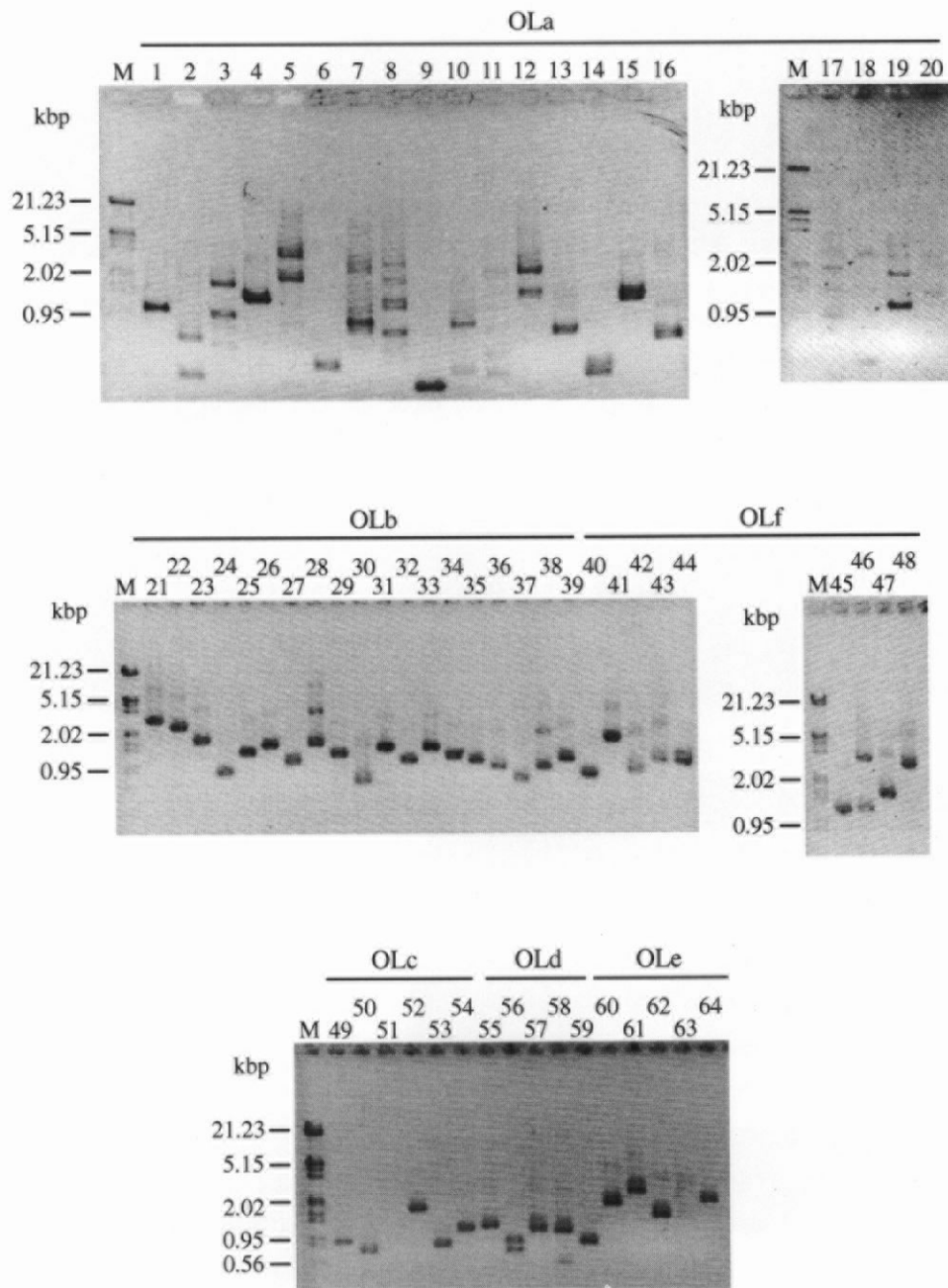


Fig. 2-1. PCR amplification of inserts in clones from various medaka libraries. PCR was performed using universal primer sets for each vector. M; molecular marker.

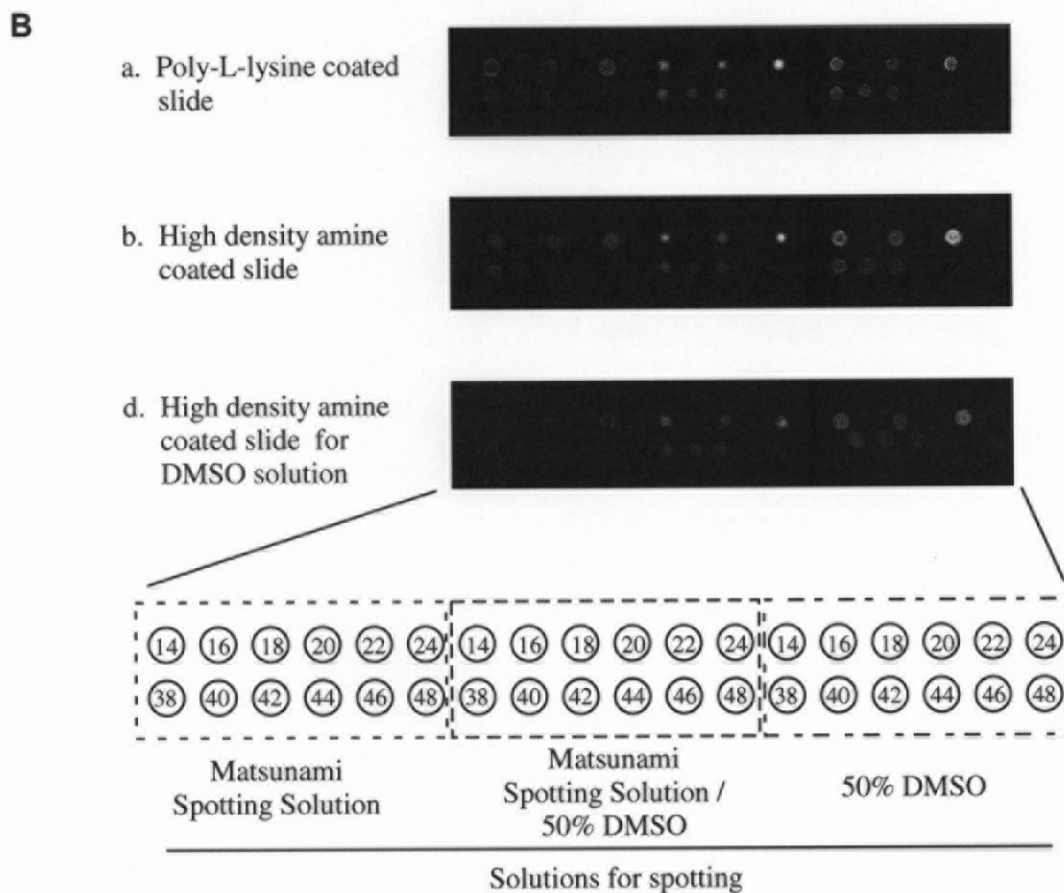
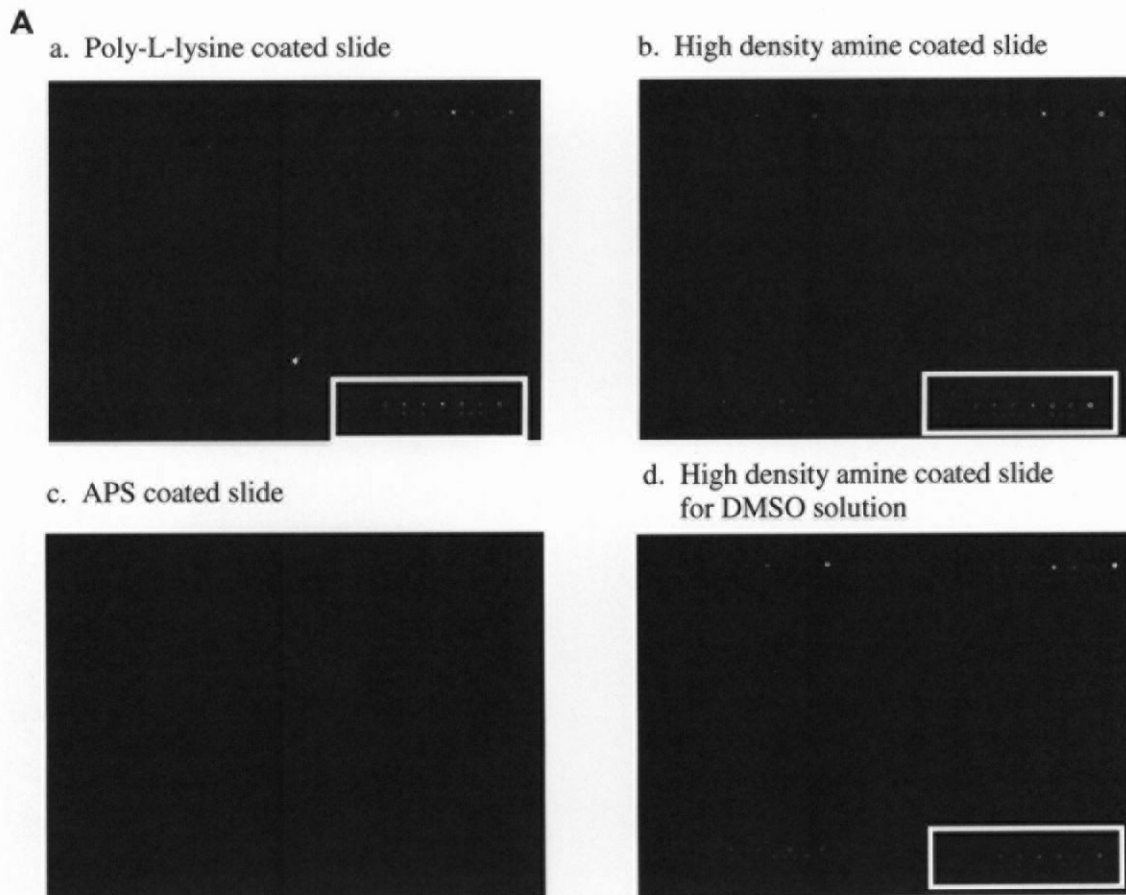


Fig. 2-2. Spot quality assessment of cDNA microarray using various spotting solutions and slide glasses. **A**, an image of the cDNA clones spotted. **B**, an example of spots in white boxes in **A** at higher magnification and spot placement diagram. cDNAs from the OLNHI-1 cell line cultured at 33°C were labeled with Cy5. See Supplementary Fig. 2-1 for the spot placement diagram.

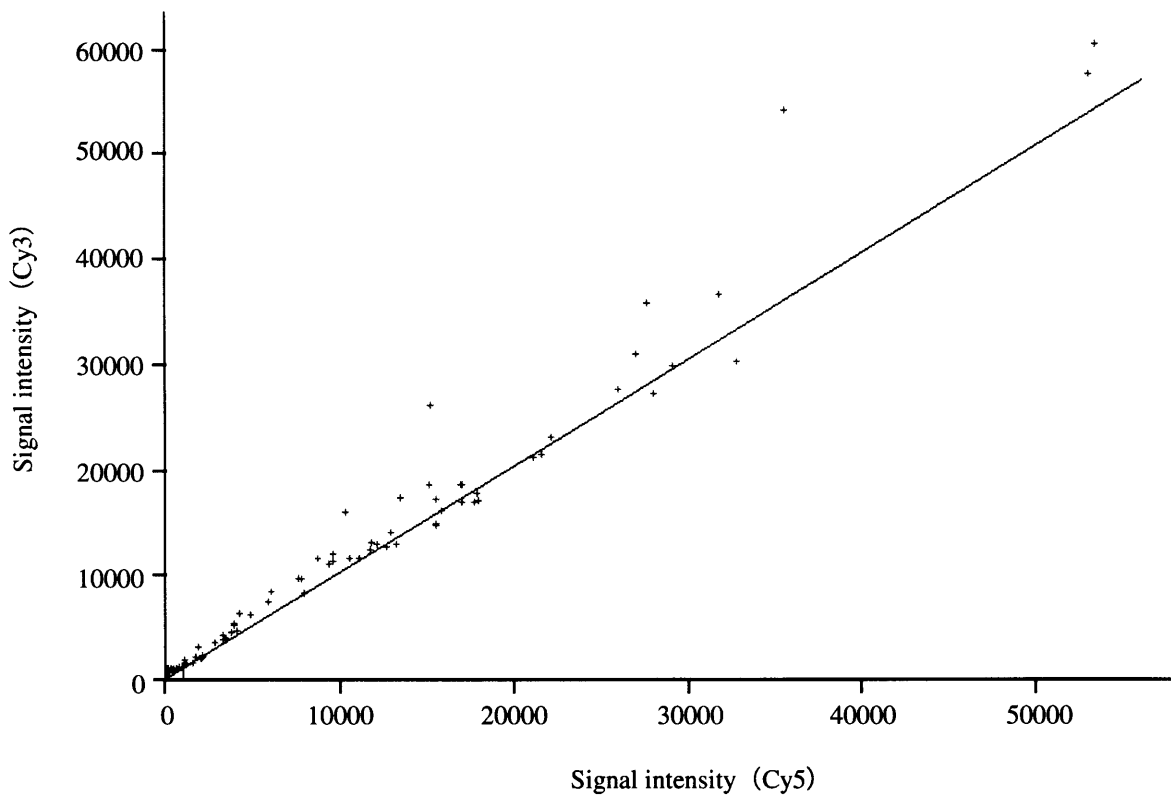


Fig. 2-3. Comparison of the signal intensity between Cy3 and Cy5 probes for microarray using a high density amine coated slide for DMSO solution. cDNAs from the OLHNI-1 cell line cultured at 33°C were labeled with Cy3 and Cy5. The solid line represents a 1:1 ratio of the signal levels of Cy3 and Cy5.

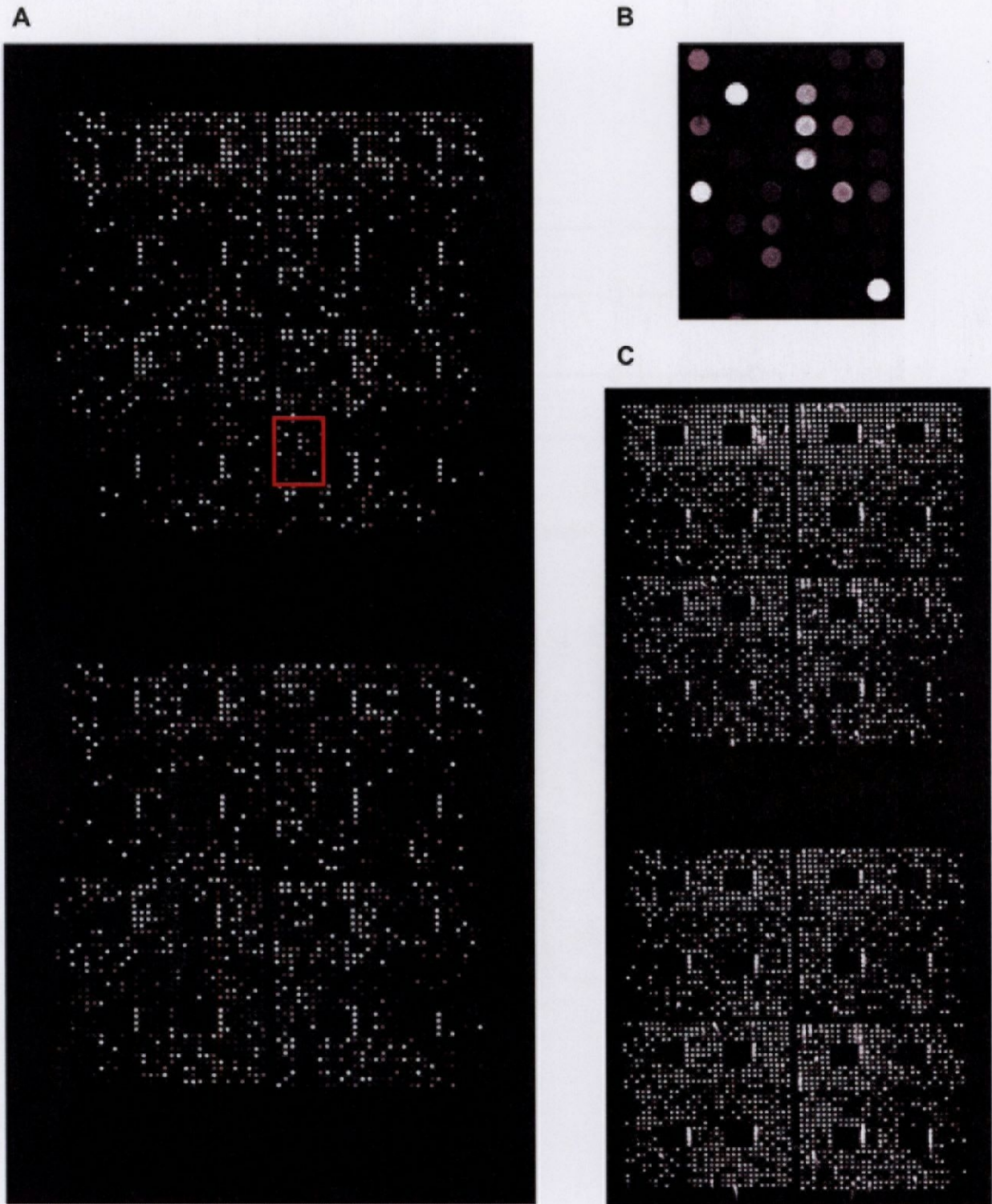


Fig. 2-4. Spot quality assessment of cDNA microarray containing 7,680 spots. **A**, an image of the 7,680 cDNA clones spotted using 50% DMSO on a high density amine coated slide for DMSO solution. cDNAs from the OLHNI-e1 cell line cultured at 25°C were labeled with Cy5. **B**, an example of spots in a red box in **A** at higher magnification. **C**, the image of **A** modified by controlling contrast to clarify positive and negative spots (see Supplementary Fig. 2-2. for spot placement diagram of the cDNA microarray containing 7,680 spots).