WPv, HAv and SA). We used healthy rats showing no sign of disease and normal increases in body weight during a 7-day quarantine period before injection. Each 5 ml vaccine was intra-peritoneally (*i.p.*) injected into five rats. Five milliliters of saline was intra-peritoneally injected as a control. We checked the body weights of rats for 4 days. For the LTT, peripheral blood was collected from tail vein at 2, 16, 48, 72 and 96 h after virus vaccine injection. Immediately, we counted the number of peripheral blood leukocytes (PBL), mean corpuscular hemoglobin (HGB), red blood cells (RBC), hematocrit (HCT), mean corpuscular volume (MCV) and platelets (PLT), using an automatic haematocytometer, the Celltac MEK-5254 (Nihon Kohden, Tokyo, Japan). To assess the significance of differences, a z-test for ATT data and a Student's *t*-test for LTT data were performed according to the minimum requirements for biological products in Japan [12]. Spearman's rank correlation coefficient *r* was calculated. All statistical analyses were performed by GraphPad Prism (version 4, GraphPad Software, San Diego, CA).

Histology

Animals were anesthetized with diethylether and the brains, thymuses, lungs, livers, spleens, pancreases, small intestines, kidneys, testes and bone marrows were collected. Tissues were fixed with Bouin's solution (Sigma, St. Louis, MO) and 4% (w/v) paraformaldehyde in phosphate-buffered saline (PBS) for at 4 °C for 24 h. After fixation, tissues were dehydrated through a series of graded ethanols and xylene and embedded in paraffin. Tissue samples were cut into 4 μm sections and stained with hematoxylin and eosin (H.E.). Five rats per group, treated with each vaccine, were analyzed on days 1–4 post-treatment.

RNA preparation

Animals treated with PDv, WPv, HAv and SA were anesthetized with diethylether and lung samples were collected. Lung samples were immediately frozen in liquid nitrogen for storage. Thawed tissue was homogenized and mixed with ISOGEN reagent (NIPPON GENE, Tokyo, Japan). Total RNA was prepared from lysates in accordance with the manufacturer's instructions. Poly(A) + RNA was prepared from total RNA using a Poly(A) Purist Kit (Ambion, Austin, TX), according to the manufacturer's instructions.

Microarray preparation and expression profile acquisition

For the microarray analysis, three lung samples from each rat were analyzed on days 1–4 post-treatment. In total 48 lung samples were analyzed in this experiment.

A set of synthetic poly-nucleotides (80-mers) representing 11,464 rat transcripts derived from 10,490 independent genes, and including most of the RefSeq clones deposited in the NCBI database (MicroDiagnostic, Tokyo, Japan), was arrayed on aminosilane-coated glass slides (Type I; Matsunami, Kishiwada, Japan) using a custom-made arrayer [18,19]. Poly(A) + RNA (2 μg) from each sample was labeled with Cyanine 5-dUTP (PerkinElmer, Boston, MA) using SuperScript II (Invitrogen, Carlsbad, CA); a common rat reference RNA (MicroDiagnostic) was labeled with Cyanine 3-dUTP (PerkinElmer, Boston, MA). Labeling, hybridization and washes of microarrays were performed using a Labeling & Hybridization Kit (MicroDiagnostic) according to the manufacturer's instructions. The rat common reference RNA was purchased as a single batch and labeled as an aliquot with Cyanine-3 for hybridization to a single microarray side by side with each sample labeled with Cyanine-5. Hybridization signals were measured using a GenePix 4000A scanner (Axon Instruments, Whipple Road Union City, CA) and then processed into primary expression ratios ([Cyanine 5-intensity obtained from each sample]/[Cyanine 3-intensity obtained from common reference RNA], which are indicated as 'median of ratios' in GenePix Pro 3.0 software (Axon Instruments)). Normalization was performed for the median of ratios (primary expression ratios) by multiplying normalization factors calculated for each feature on a microarray by the GenePix Pro 3.0 software.

Data analysis

Data processing and hierarchical cluster analysis were performed using Excel (Microsoft, Tokyo, Japan) and an MDI gene expression analysis software package (MicroDiagnostic). The primary expression ratios were converted into $\log_2$ values ($\log_2$ Cyanine-5 intensity/Cyanine-3 intensity) (designated log ratios) and compiled into a matrix (designated primary data matrix). To predict the most obvious differences obtained from cluster analysis of the primary data matrix, we extracted 5346 genes with $\log_2$ ratios over 1 or under −1 in at least one sample from the primary data matrix and subjected them to two-dimensional hierarchical cluster analysis for samples and genes. To identify genes demonstrating significant changes in expression, we undertook the following: (i) mean averages of $\log_2$ ratios were calculated for each gene from data sets of day 1 SA- and WPv-treated samples; (ii) standard deviations were calculated for each gene; (iii) the difference in mean averages between day 1 SA- and WPv-treated samples was calculated for each gene and divided by the sum of the corresponding standard deviation values. The difference in the mean averages/the sum of the standard deviations was defined as the signal-to-noise ratio for each gene. We chose the 76 genes exhibiting the highest expression signal-to-noise indices and extracted expression data corresponding to these genes from the primary data matrix for all samples; this data was subsequently subjected to two-dimensional hierarchical cluster analysis for samples and genes.

Quantitative RT-PCR analysis

Changes of gene expression assessed by microarray analysis were confirmed by quantitative real-time reverse transcription-polymerase chain reaction (RT-PCR) for selected 18 genes. PCR primers (Table 2) were designed for 18 genes using the Primer Express software (Applied Biosystems, Foster City, CA). Total RNA was used to synthesize first strand cDNA using a First-strand cDNA Synthesis Kit (Life Science, Inc., St. Petersburg, FL), according

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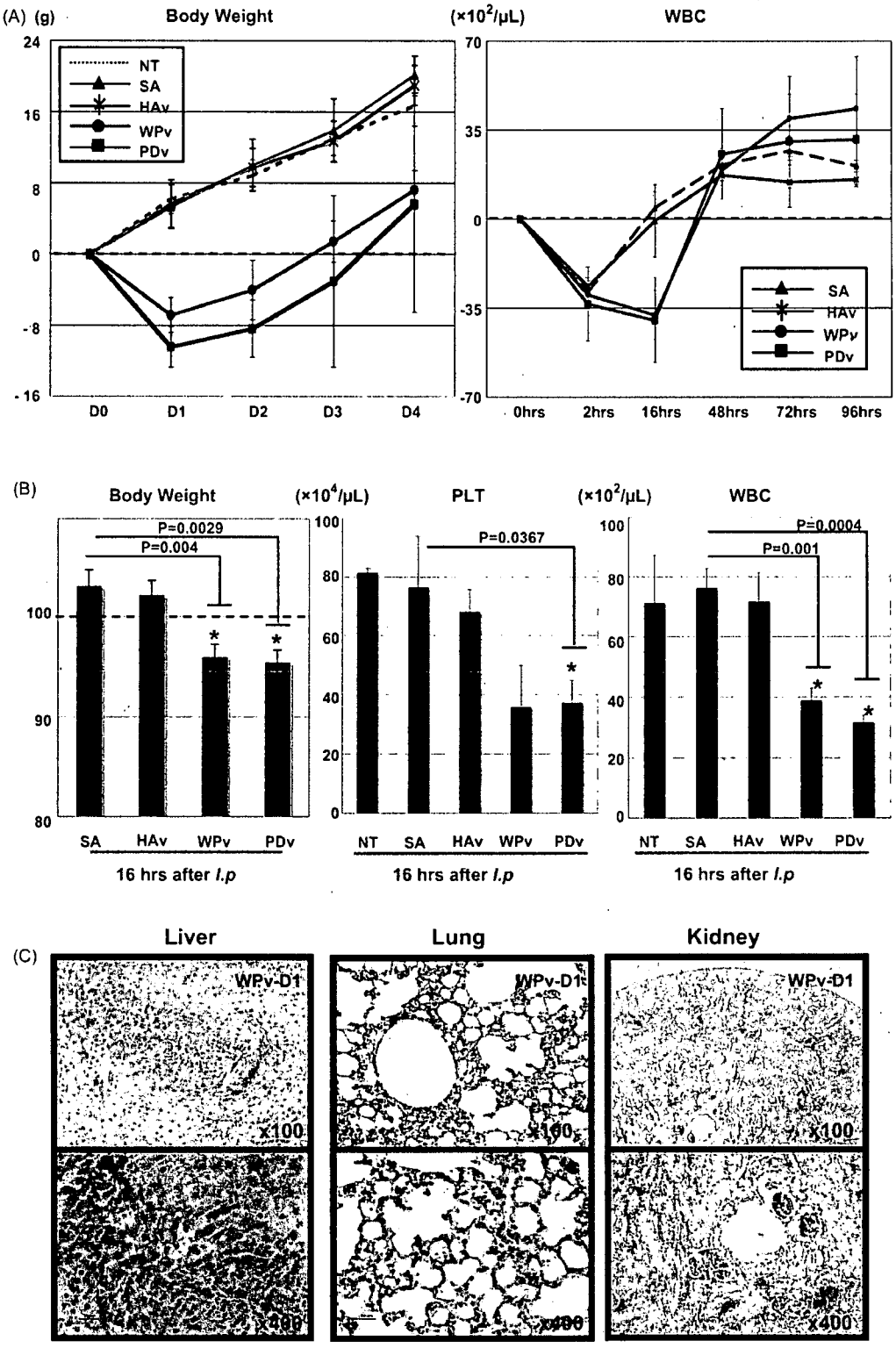

Mizukami et al., Application of Complementary DNA Microarray Technology to Influenza (H5N1) Vaccine Safety Evaluation

Figure 1 Influenza quality was evaluated by conventional National tests. (A) Abnormal toxicity test (left panel) and leukopenic toxicity test (right panel) for influenza vaccine (PDv, WPv, HAv, and SA). Body weight changes were plotted for 4 days (left panel). Changes in body weight are indicated by the mean increase ± S.D. in five animals. The number of WBCs (white blood cells) was plotted for 4 days (right panel). Changes in WBCs are indicated by the mean increase ± S.D. in five animals. (B) The differences

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to the manufacturer's instructions. Expression levels of selected genes were analyzed by quantitative (Q) reverse transcriptase–polymerase chain reaction using a 7500 Fast Real-Time PCR System (Applied Biosystems) with 7500 Fast System SDS Software Version 1.3. cDNA was amplified for Q-PCR using SYBR Green I (Molecular Probes, Inc.) to detect PCR product. One microliters of six-fold diluted cDNA was used in a 20-μl final volume reaction containing 10 μl SYBR Green® PCR Master Mix (Applied Biosystems), 0.2 μM forward primer, and 0.2 μM reverse primer. The 7500 Fast System was programmed to run an initial polymerase activation step at 95 °C for 10 min followed by 40 cycles of denaturation (95 °C for 15 s) and extension (60 °C for 1 min), and product synthesis was monitored at the end of the extension step of each cycle. Each expression values were normalized against rat β-actin. Data presented in the Fig. 4 are the average and standard deviation of two independent quantitative RT-PCR analysis in each sample (SA, HAv, WPv and PDv). Statistical significance was calculated using Student's two-tailed *t*-test (paired two-sample for means) between WPv- and SA-treated rat lung. To determine the correlation between DNA microarray data and quantitative RT-PCR analysis, a Pearson correlation coefficient was calculated.

Results

Abnormal toxicity test for H5N1 influenza vaccine

Animals were treated with 5 ml of pandemic influenza vaccine (PDv; whole-virion H5N1 vaccine adjuvanted with aluminum hydroxide), whole virion-particle vaccine (WPv) without any adjuvant, HA vaccine (HAv) or saline as a control, and the body weight [BW] of each rat was checked at days 1, 2, 3 and 4. Five rats per group were analyzed each day after intraperitoneal (*i.p.*) injection of vaccine or saline. In SA- and HAv-treated animals, no decrease in the body weight (BW) was observed, and there were no significant differences in body weight changes between SA- and HAv-treated animals for 4 days (Fig. 1A). Decrease rate in BW was significantly different between PDv- and WPv-treated animals and SA- and HAv-treated rats, from 16 h to 4 days ($P < 0.05$) after injections (Fig. 1A and B). When we compared the decrease rate in BWs of PDv- and WPv-treated rats, no significant differences were observed between days 1 and 4. The abnormal toxicity test is a test that evaluates vaccine quality based on decreased body weights after *i.p.* injection to the animal in Japan. According to the criteria of the Japanese national regulatory test – Minimum Requirements for Biological Products [12], it can be concluded that vaccine quality in HAv is same as in the SA. However, vaccine quality in WPv and PDv were different from HAv and SA. In addition, within WPv and PDv, there was no significant difference in the vaccine quality.

Leukopenic toxicity test for various influenza vaccines

Animals were treated with 5 ml of PDv, WPv, HAv or SA as a control, and peripheral WBCs (white blood cells) were collected from tail veins at 2, 16, 48, 72 and 96 h after inoculation, and counted. Three rats per group, at each time point after sample *i.p.* injection, were analyzed. A reduction in WBC number was observed in all animals at 2 h after *i.p.* injection of SA, HAv, WPv and PDv. However, the decrease in the number of WBCs continued and a significant decrease in WBC number ($P < 0.05$) was observed in WPv- and PDv-treated animals, compared with SA- and HAv-treated animals, at 16 h after *i.p.* injection (Fig. 1A and B). In addition, a significant decrease ($P < 0.05$) in platelet (PLT) number was observed in WPv- and PDv-treated animals at 16 h after *i.p.* injection. No significant differences of the numbers of RBCs (red blood cells), HGB (mean corpuscular hemoglobin), HCT (hematocrit), or MCV (mean corpuscular volume) were observed among all groups (*data not shown*). According to the criteria of Japanese national regulatory test-Minimum Requirements for Biological Products (12), it can be concluded that vaccine quality in HAv is same as in the SA. However, vaccine quality in WPv and PDv were different from HAv and SA. In addition, within WPv and PDv, there was no significant difference in the vaccine quality.

Histological analysis of influenza vaccine-treated rats

Animals were treated with 5 ml of PDv, WPv, HAv or SA as a control, and various tissues (brain, thymus, lung, liver, spleen, kidney, testis, pancreas, and small intestine) were histologically evaluated. Among these tissues, focal necrosis (FN) of the liver was observed in the livers of both WPv- and SA-treated rats at day 1 after injection (Fig. 1C); after day 2, we could not detect any FN in the liver, indicating that FN was induced by experimental stress. No histopathological changes were observed in any other tissue.

Microarray analysis of vaccine-treated lung

To evaluate the effect of influenza vaccines on gene expression in the lung, we prepared three rats per group; PDv-, WPv-, HAv- and SA-treated groups were sacrificed and lung samples were taken at days 1, 2, 3 and 4. A total of 48 independent lung tissue samples were analyzed. We labeled poly(A) + RNA purified from these samples and

among PDv-, WPv-, HAv- and SA-treated animals 16 h after vaccine injection. Significant differences in body weight changes were observed between SA- and WPv-treated rats ($P < 0.01$), SA and PDv ($P < 0.01$). Increasing and decreasing rate in body weights are indicated as a percentage (%) compared to the body weight before injection; means ± S.D. of five animals are shown. A significant difference in the numbers of platelets (center panel) and WBCs (right panel) was observed between SA- and WPv-treated rats ($P < 0.01$), as well as between SA- and PDv-treated rats ($P < 0.01$). (C) Histological analysis of vaccine-treated rat liver. Lung and kidney at day 1 after injection. Sectioned samples were stained with H.E. and analyzed at low (upper panel) and high (lower panel) magnification. NT, non-treatment; SA, saline; HAv, HA vaccine; WPv, whole particle vaccine and PDv, pandemic vaccine.

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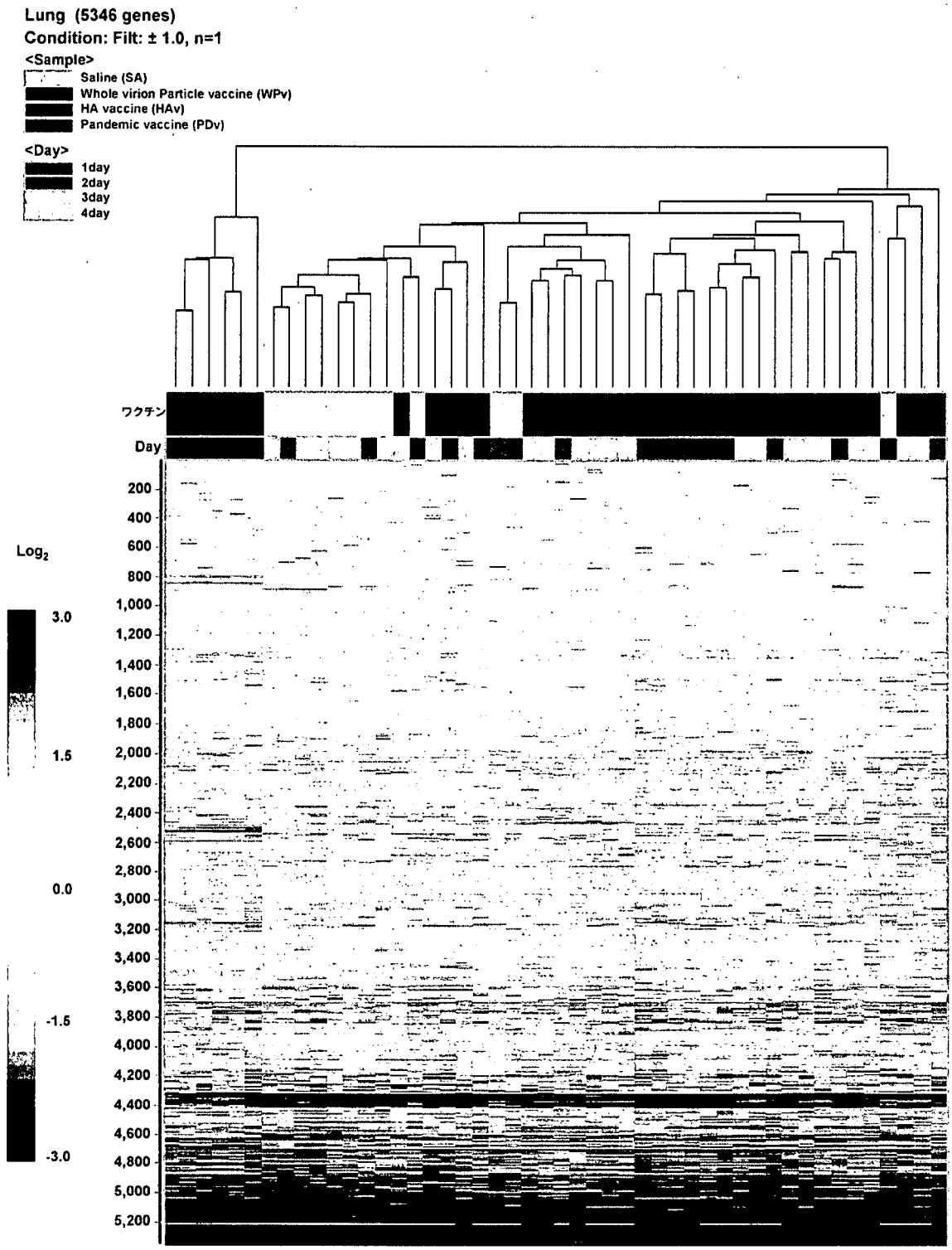

Figure 2 Overall gene expression profiles obtained from SA-, HAv-, WPv- and PDv-treated rat lung. Genes expressed in saline and vaccine-treated lungs are assembled in the order obtained from the results of cluster analysis. The color bar at the left shows the ratio vs the common reference RNA in $\log_2$; red and blue indicate up and down-regulated genes, respectively. A matrix of 5346 genes that were up- or down-regulated in at least one experiment from day 1 to 4 after injection.

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Figure 3 Microarray analysis of gene expression in the SA-, HAv-, WPv- and PDv- treated rat lung. A matrix of 76 genes regulated in at least one experiment from day 1 to 4 after injection. Hierarchical clustering of the 76 selected genes that were preferentially regulated in WPv-treated rat lung compared with SA-treated rat lung at day 1 ($P < 0.005$). ClsA, cluster A; ClsB, cluster B and ClsC, cluster C.

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Q8 **Table 1** Genes that were up- and down-regulated by influenza vaccine ($P < 0.005$)

Official gene name	Symbol	ID	PDv-D1 mean ± S.D.	WPv-D1 mean ± S.D.	HAv-D1 mean ± S.D.	SA-D1 mean ± S.D.
IFN-inducible gene						
Myxovirus (influenza virus) resistance 1	Mx1	X52711	6.163 ± 0.276	5.514 ± 0.19	2.198 ± 0.272	0.935 ± 0.117
Interferon regulatory factor 7	Irf7	XM_215121	5.39 ± 0.67	5.51 ± 0.39	2.06 ± 0.87	0.32 ± 0.08
Myxovirus (influenza virus) resistance 2	Mx2	NM_017028	4.08 ± 0.13	3.83 ± 0.06	1.14 ± 0.41	−0.01 ± 0.19
Interferon gamma inducible protein	Ifi47	NM_172019	2.66 ± 0.05	2.32 ± 0.01	0.31 ± 0.12	−0.06 ± 0.12
FLN29 gene product	Fln29	AF329825	2.66 ± 0.15	2.26 ± 0.12	1.03 ± 0.23	0.61 ± 0.05
Similar to interferon inducible protein	Similar	XM_220360	1.84 ± 0.23	1.74 ± 0.06	0.61 ± 0.15	0.45 ± 0.05
Interferon-related developmental regulator 1	Ifrd 1	NM_019242	1.20 ± 0.18	0.94 ± 0.10	0.19 ± 0.14	−0.26 ± 0.12
Chemokine and cytokine function						
Lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp	AF065438	4.50 ± 0.21	4.52 ± 0.19	2.66 ± 0.48	1.28 ± 0.09
Tissue inhibitor of metallopeptidase 1	Timp1	NM_053819	2.75 ± 0.12	2.66 ± 0.22	0.78 ± 0.39	−0.09 ± 0.25
Chemokine (C-X-C motif) ligand 9	Cxcl9	NM_145672	2.54 ± 0.52	2.88 ± 0.13	0.78 ± 0.18	0.35 ± 0.15
Lectin, galactose binding, soluble 9	Lgals9	NM_012977	2.01 ± 0.24	1.85 ± 0.06	0.07 ± 0.18	−0.65 ± 0.20
Colony stimulating factor 1 (macrophage)	Csf1	NM_023981	1.94 ± 0.07	1.81 ± 0.24	0.84 ± 0.13	0.59 ± 0.16
Granulin	Grn	NM_017113	1.84 ± 0.08	1.67 ± 0.07	0.57 ± 0.14	0.43 ± 0.13
Chemokine (C-X-C motif) ligand 11	Cxcl11	XM_223236	1.70 ± 0.37	1.60 ± 0.14	1.32 ± 0.09	0.21 ± 0.07
EGF-containing fibulin-like extracellular matrix protein 1	Efemp1	D89730	0.28 ± 0.18	−0.05 ± 0.18	0.98 ± 0.18	1.15 ± 0.15
Immune response						
Similar to lymphocyte antigen 6 complex,	Similar	XM_216946	4.83 ± 0.19	4.58 ± 0.11	2.96 ± 0.23	2.25 ± 0.23
Ly6-C antigen	Ly6c	NM_020103	3.75 ± 0.11	3.33 ± 0.26	1.89 ± 0.41	1.44 ± 0.08
Similar to histocompatibility 2, complem	Similar	XM_215326	3.67 ± 0.20	3.51 ± 0.05	1.68 ± 0.44	0.74 ± 0.06
RT 1 class Ib locus Aw2	RT1-Aw2	NM_012645	2.93 ± 0.00	2.60 ± 0.06	1.29 ± 0.23	0.74 ± 0.05
Beta-2 microglobulin	β2m	NM_012512	2.90 ± 0.12	2.86 ± 0.11	1.52 ± 0.12	0.86 ± 0.09
MHC class Ia protein (RT1.Al) gene, comp	RT1-A1	AF025309	2.79 ± 0.07	2.74 ± 0.10	1.49 ± 0.19	0.85 ± 0.06
Lymphocyte antigen 6 complex, locus B	Ly6b	NM_139257	2.70 ± 0.20	1.97 ± 0.10	0.80 ± 0.18	0.44 ± 0.18
Transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	Tap2	NM_032056	2.69 ± 0.29	2.51 ± 0.20	1.44 ± 0.06	1.40 ± 0.22

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Table 1 (*Continued*)

Official gene name	Symbol	ID	PDv-D1 mean ± S.D.	WPv-D1 mean ± S.D.	HAv-D1 mean ± S.D.	SA-D1 mean ± S.D.
Complement component 2	C2	NM_172222	2.07 ± 0.10	2.00 ± 0.21	0.93 ± 0.09	0.31 ± 0.09
Proteosome (prosome, macropain) subunit, beta type 9	Psmb9	NM_012708	2.07 ± 0.13	1.73 ± 0.01	0.48 ± 0.05	0.21 ± 0.07
TAP binding protein	Tapbp	NM_033098	1.95 ± 0.13	1.63 ± 0.13	0.12 ± 0.11	−0.10 ± 0.10
RT1 class Ib gene, H2-TL-like, grc region (N3)	RT1-N3	L23128	1.62 ± 0.03	1.45 ± 0.20	0.14 ± 0.16	−0.14 ± 0.22
Proteasome (prosome, macropain) 28 subunit, alpha	Psme 1	NM_017264	1.20 ± 0.10	0.79 ± 0.01	0.06 ± 0.11	−0.63 ± 0.09
Cathepsin S	Ctss	NM_017320	0.99 ± 0.12	0.59 ± 0.17	0.03 ± 0.08	−0.42 ± 0.06
Complement component 1, s subcomponent	C1s	D88250	0.83 ± 0.07	0.82 ± 0.08	−0.93 ± 0.16	−1.90 ± 0.09
Proteasome (prosome, macropain) 28 subunit, beta	Psme2	NM_017257	0.26 ± 0.03	0.02 ± 0.15	−0.78 ± 0.23	−1.41 ± 0.22
Elastin	Eln	J04035	0.01 ± 0.21	0.08 ± 0.26	1.95 ± 0.11	1.83 ± 0.25
Fibrinogen, gamma polypeptide	Fgg	NM_012559	−2.70 ± 0.26	−2.78 ± 0.22	−3.68 ± 0.32	−3.80 ± 0.21
Transcription acitivity						
Z-DNA binding protein 1	Zbp1	AJ302054	2.73 ± 0.46	2.12 ± 0.19	1.02 ± 0.07	0.32 ± 0.15
CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	NM_013154	2.58 ± 0.41	2.20 ± 0.08	1.38 ± 0.15	0.70 ± 0.22
Similar to H1 histone family, member 2;	Similar	XM_225325	1.67 ± 0.19	1.31 ± 0.06	0.21 ± 0.03	0.08 ± 0.18
Activating transcription factor 5	Atf5	NM_172336	0.95 ± 0.06	0.99 ± 0.06	0.76 ± 0.29	−0.74 ± 0.03
AHNAK nucleoprotein (desmoyokin)	Ahnak	AF454371	0.58 ± 0.21	0.36 ± 0.18	0.85 ± 0.11	1.36 ± 0.17
Nuclear protein 1	Nupr1	AF014503	−0.74 ± 0.11	−1.09 ± 0.04	−2.78 ± 0.28	−2.83 ± 0.07
histone cluster 1, H2bl	Hist1h2bl	NM_022647	−0.95 ± 0.07	−0.93 ± 0.13	−1.77 ± 0.06	−1.98 ± 0.13
Apoptosis						
Caspase 1 (Casp1), mRNA.	Casp1	NM_012762	0.92 ± 0.13	0.91 ± 0.07	0.12 ± 0.05	−0.34 ± 0.17
Heat shock protein 27 (Hsp27) mRNA, comp	Hsp27	M86389	0.90 ± 0.14	0.84 ± 0.15	0.08 ± 0.05	−0.20 ± 0.14
Mitochondrial cytochrome oxidase subunits, I, II, III genes, 9		J01435	−3.51 ± 0.27	−3.63 ± 0.10	−1.89 ± 0.16	−2.08 ± 0.12
Protein modification						
Serine (or cysteine) peptidase inhibitor, clade G, member 1	Serping1	NM_199093	2.20 ± 0.12	2.14 ± 0.03	0.66 ± 0.16	0.08 ± 0.13
Cellular signaling						
DNA-damage inducible transcript 3	Ddit3	NM_024134	2.07 ± 0.20	1.97 ± 0.21	0.38 ± 0.22	0.30 ± 0.24
HRAS like suppressor 3	Hrasls3	NM_017060	0.98 ± 0.18	0.46 ± 0.11	−0.84 ± 0.22	−1.23 ± 0.18

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Table 1 (*Continued*)

Official gene name	Symbol	ID	PDv-D1 mean ± S.D.	WPv-D1 mean ± S.D.	HAv-D1 mean ± S.D.	SA-D1 mean ± S.D.
Similar to signal transducer and activate	Similar	XM_222301	0.80 ± 0.28	0.94 ± 0.23	−0.15 ± 0.08	−0.28 ± 0.12
Retinoicacid receptor, beta Metabolism	Rarb	AJ002942	−2.73 ± 0.09	−2.81 ± 0.21	−1.86 ± 0.16	−1.61 ± 0.22
2′,5′-Oligoadenylate synthetase 1, 40/46 kDa	Oas1	Z18877	4.27 ± 0.41	4.14 ± 0.30	1.96 ± 0.60	1.38 ± 0.43
Similar to 2-5 oligoadenylate synthetase	Similar	XM_222230	1.75 ± 0.35	1.70 ± 0.24	0.43 ± 0.39	0.07 ± 0.08
6-Phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	Pfkfb3	NM_057135	1.72 ± 0.36	1.62 ± 0.16	0.99 ± 0.16	0.47 ± 0.19
Carbonic anhydrase 4	Ca4	NM_019174	−0.85 ± 0.33	−0.84 ± 0.12	0.66 ± 0.15	0.66 ± 0.15
Monoglyceride lipase	Mgll	NM_138502	−0.90 ± 0.03	−1.16 ± 0.23	−0.43 ± 0.05	−0.08 ± 0.22
GTP cyclohydrolase I feedback regulator	Gchfr	U85512	−1.24 ± 0.09	−1.65 ± 0.11	−1.22 ± 0.21	−0.49 ± 0.22
Cytochrome b mRNA, complete cds; mitocho Others	cytb	AF295545	−2.55 ± 0.19	−2.65 ± 0.11	−1.17 ± 0.06	−1.30 ± 0.14
EST351314 gene index, normalized rat, no	EST	AW920010	2.96 ± 0.48	2.42 ± 0.18	2.02 ± 0.48	1.41 ± 0.23
Nerve growth factor receptor (TNFR superfamily, member 16)	Ngfr	NM_012610	2.62 ± 0.30	1.85 ± 0.31	−0.25 ± 0.43	−0.59 ± 0.17
Cdig2 protein	Cdig2	NM_153624	2.62 ± 0.11	2.08 ± 0.09	0.70 ± 0.17	0.46 ± 0.06
Xanthine dehydrogenase	Xdh	NM_017154	2.02 ± 0.11	1.95 ± 0.16	0.77 ± 0.04	0.47 ± 0.28
EST108196 PC-12 cells, untreated cDNA cl	EST	AA685798	1.92 ± 0.11	1.69 ± 0.07	0.54 ± 0.07	0.30 ± 0.10
Similar to torsin family 3, member A; AT	Similar	XM_222769	1.76 ± 0.08	1.48 ± 0.35	0.02 ± 0.38	−0.14 ± 0.20
Glypican 3	Gpc3	NM_012774	1.61 ± 0.08	1.46 ± 0.23	2.62 ± 0.57	2.71 ± 0.13
Similar to RIKEN cDNA 2310008M14 [Mus mu	Similar	XM_217259	1.58 ± 0.02	1.55 ± 0.14	0.58 ± 0.20	0.13 ± 0.04
Similar to peanut-like 2 homolog; peanut	Similar	XM_213413	1.38 ± 0.15	1.33 ± 0.07	2.20 ± 0.18	2.33 ± 0.09
Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member	Slc3a2	NM_019283	1.21 ± 0.13	0.75 ± 0.07	−0.14 ± 0.28	−0.38 ± 0.6
UI-R-A1-em-f-05-0-UI.s1 UI-R-A1 cDNA clo	EST	AA925529	1.15 ± 0.13	0.82 ± 0.07	−0.06 ± 0.15	−0.54 ± 0.14
Superoxide dismutase 2, mitochondrial	Sod2	NM_017051	0.86 ± 0.09	0.60 ± 0.11	−0.77 ± 0.35	−1.04 ± 0.04

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Table 1 (*Continued*)

Official gene name	Symbol	ID	PDv-D1 mean ± S.D.	WPv-D1 mean ± S.D.	HAv-D1 mean ± S.D.	SA-D1 mean ± S.D.
Clusterin	Clu	NM_012679	0.78 ± 0.09	0.74 ± 0.09	−0.21 ± 0.16	−0.37 ± 0.16
DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	NM_022934	0.72 ± 0.16	0.66 ± 0.12	−0.26 ± 0.09	−0.42 ± 0.10
Similar to growth hormone inducible tran	Similar	XM_214285	0.49 ± 0.08	0.26 ± 0.17	−0.47 ± 0.25	−0.80 ± 0.09
Solute carrier family 28	Slc28a2	NM_031664	0.16 ± 0.16	0.01 ± 0.09	−0.71 ± 0.26	−1.15 ± 0.19
Sodium channel, voltage-gated, type VII, alpha	Scn7a	Y09164	−0.39 ± 0.25	−0.48 ± 0.14	0.09 ± 0.41	0.54 ± 0.03
EST224035 Normalized spleen, Bento Soare	EST	AI180292	−2.20 ± 0.34	−1.64 ± 0.20	−4.02 ± 0.30	−2.94 ± 0.25
smooth muscle alpha-actin	Acta2	M22757	−2.77 ± 0.24	−2.34 ± 0.09	−1.18 ± 0.25	−1.17 ± 0.05
Solute carrier family 3, member 1	Slc3a1	NM_017216	−3.10 ± 0.66	−3.56 ± 0.21	−2.92 ± 0.65	−2.40 ± 0.23
S100 calcium binding protein G	S100g	NM_012521	−3.93 ± 0.29	−3.72 ± 0.22	−2.17 ± 0.15	−2.10 ± 0.18

Cyanine 5-labeled lung RNA and Cyanine 3-labeled rat common reference RNA were competitively hybridized to a DNA microarray. Hybridization signals were processed into primary expression ratio ([Cyanine5- intensity obtained from each sample]/[Cyanine5-intensity obtained from each sample], and normalized (primary expression ratio). The primary expression ratios were converted into $\log_2$ values ($\log_2$ Cyanine5-intensity/$\log_2$ Cyanine5-intensity). $\log_2$ values for each sample were averaged and S.D. values were calculated. SA, Saline; HAv, HA vaccine; WPv, whole particle vaccine, PDv, pandemic vaccine.

from a rat common reference RNA with Cyanine-5 and Cyanine-3, respectively. Next, we hybridized labeled RNAs to microarrays representing 11,464 transcripts derived from 10,490 independent genes, including most of the RefSeq clones deposited in the NCBI database. Hybridization signals were processed into expression ratios as $\log_2$ values (designated $\log_2$ ratios). To predict the most obvious differences obtained from cluster analysis of the primary data matrix, we extracted 5346 genes with $\log_2$ ratios over 1 or under −1 in at least one sample from the primary data matrix. When we performed a cluster analysis for 5346 transcripts, two large clusters were obtained, and whole-virion vaccines (1 day after PDv- and WPv-treated) showed different clusters from the others (HAv and SA) (Fig. 2). To evaluate the differences in gene expression between those induced by whole-virion vaccines and those induced by others (HAv and SA), we extracted 76 genes essential for class separation ($P < 0.005$). When we performed a cluster analysis of these 76 genes, three large clusters were obtained. These 76 genes can distinguish whole-virion vaccines (PDv- and WPv-treated samples (day 1 and day 2)) from the others (HAv and SA) (Fig. 3). The three clusters formed by these 76 genes include: cluster A, whole virion-treated lung at day 1; cluster B, whole virion-treated lung at day 2; and cluster C, sub-virion and SA-treated rat lung at day 1. These 76 genes are listed in Table 1 . Among these 76 genes, we found that the genes up-regulated by influenza infection included interferon-stimulated genes (ISGs), such as *Mx1* (myxovirus (influenza virus) resistance 1), *Ifi47* (interferon gamma inducible protein 47), *Ifrd1* (interferon-related developmental regulator 1), *FLN29* (FLN29 gene product) and *Cxcl9* (chemokine (C-X-C motif) ligand 9), as shown in Table 1. In addition, genes up-regulated by the immune response and antigen presentation, including *Ctss* (cathepsin S), *Psme1* (proteasome (prosome, macropain) 28 subunit, alpha), *Psme2* (proteasome (prosome, macropain) 28 subunit, beta), *Tap2* (transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)), *Tapbp* (TAP binding protein) *RT1-Aw2* (RT1 class Ib, locus Aw2), *RT1-N3* (RT1 class Ib gene, H2-TL-like, grc region (N3)) and *β2m* (β2 microglobulin), were also strongly induced in whole-virion-treated rat lung.

To confirm and validate our DNA microarray analysis, we selected subset of 18 genes (Table 2), and performed quantitative RT-PCR analysis. Data presented in the Fig. 4 are the average, standard deviation and correlation between two independent quantitative RT-PCR and DNA microarray analysis in each sample (SA, HAv, WPv and PDv). As a result of comparison between two detection methods, Pearson's correlation coefficient indicates a statistically significant correlation between DNA microarray and quantitative RT-PCR analysis among our selected 18 genes. This correlation demonstrates excellent concordance between two methods. In addition, significant difference between WPv and SA was also observed in quantitative RT-PCR analysis ($P < 0.05$ [Student *t*-test]), similar to DNA microarray analysis.

These data suggest that vaccine quality in WPv and PDv were different from HAv. In addition, within WPv and PDv, there was no significant difference in the vaccine quality using DNA microarray analysis. Thus, it can be concluded that cDNA microarray technology is an informative, rapid and highly sensitive method with which to evaluate the quality of influenza vaccines. Using DNA microarray system,

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Table 2

Number	Gene name	Forward	Reverse
NM_012512	β2m	TTGAGCTACTGAAGAATGGAAAGAAGA	GGTGGGTGTGAATTCAGTGTGA
NM_172222	C2	TTGTGCCTAGGGACTTCCACAT	GGCAAAAAGTCGAGGACACCAT
NM_145672	Cxcl9	TTTGCCCCAAGCCCTAACTG	TGGGTCTAGGCAGGTTTGATCTC
AF329825	FLN29	CCGGAGGAACTGCTCATTGA	GAAGAGCTGCCAGTATTGAGTGAAC
XM_215121	Irf7	TGCAGCGTGAGGGTGTGTC	TCATCGTAGAGACTATTGGTGCTAGACA
AF065438	Lgals3bp	TCTACCTCACCAACTCCACTGACA	CAGGCTGCTGGAGGTTCCT
NM_172019	Ifi47	CCTAGCCAACCAGGAAATGAATT	GGGAGTTTGGTGGAAGGACAA
NM_019242	Ifrd1	GCAGTACCACTTGCAGACAAATGAAT	AAGTGTTGCAGCATCGAGCATC
L23128	RT1-N3	AGTGGCTTCTTGTCTGGCATTTT	AATGAGGTGTGTGAGAGGATGGAG
NM_017028	Mx2	AAGGAACATAGTGACACCAGTGAGAAG	GGACAGGGCCAGCTTAACCA
NM_012708	Psmb9	CTCTGGCCATGAACCGAGAT	CAGCTCGTCTCCCAGGATGA
NM_017264	Psme1	ATCTATTGAGCCCCCTCTCTCGTT	GGGTGCAGTCTAGAGTTCCTAGTCA
AF025309	RT1-A1	CACTGCCTGTGTTCCCTTCCA	CAAGGAGTGACAGGATGCAGATGT
NM_012645	RT1 -Aw2	TGCCTGAGCCCCTTTCCC	CCACAGCTCCAAGAACAACAGAA
XM_223236	CxcH 1	CTGAAGGCTCATAAAGGACAAAGGT	CACATGTTCTGGCGCCTTAA
NM_033098	Tapbp	GACCGTTCCCAAAGACGAAAAG	TGGAGTCGTTTGGACCAGAGAT
NM_053819	Timp1	CCTGTTCAGCCATCCCTTGC	GCCCCTCAGAGCCCATGA
AJ302054	Zbp1	TTAGTAGTAGCCCCCCAGAGTCAA	ACCTACGGTGGATGGTCATCTT
NM_031144	P-actin	ACCGTGAAAAGATGACCCAGATC	GACCAGAGGCATACAGGGACAAC

consistent with the results of the ATT and LTT, there was no difference in global gene expression in the lung between PDv and WPv.

Discussion

Recently, quality assurance of the vaccines was rigorously controlled according to the good manufacturing practices (GMP), process validation, inspection and tests of the national regulator authority (NRA) in Japan and similar bodies in other countries. Current quality control and safety tests, such as the abnormal toxicity test and the leukopenic toxicity test, are useful to evaluate influenza vaccine safety for 50 years. ATT (also known as the general safety test or inocuity test) is a test for extraneous toxic contaminants in other countries. However, in Japan, the ATT is an established test that can evaluate vaccine quality based on changes in body weight over a period of 7 days after inoculation of final container vaccine compared to the trend data from past quality control test, statistically. These trend data was constructed at least 100 lot of each vaccine, which have already passed by the ATT and for which safety has been determined after post marketing surveillance. Whereas the ATT is a useful and long-performed test, the mechanism of the ATT was not well defined until recently [17]. In addition, inherent toxicity of vaccines and the intra-peritoneal injection root have been raised. For this reason, the relevance of the ATT has been questioned by some regulatory authorities. Currently, the FDA is discussing whether to abolish the requirement for the ATT, and the EMEA (European Agency for the Evaluation of Medicinal Products) has already decided to abolish the ATT for testing vaccines for human use.

In this study, we developed a new quality control method for influenza vaccine using DNA microarrays. We successfully translated the vaccine quality, immunogenicity and reactogenicity of influenza vaccine into gene expression profile data. According to the ATT, decrease in the body weight was only observed in whole virion-treated rats, and these tests did not distinguish PDv from WPv. Giving the same results as the ATT, the LTT showed that whole virion is different from sub-virion influenza vaccine, and there is no difference in vaccine quality between PDv and WPv. In the DNA microarray system, consistent with the results of the ATT and LTT, whole virion-treated rat lung was located in a different cluster from sub-virion- and SA-treated rat lung. Using gene expression profiles, we could not distinguish PDv from WPv. These data suggest that the DNA microarray system is not only equivalent to the ATT and LTT, but is also more informative. More interestingly, intra-peritoneal injection of influenza vaccine induced gene expression related to the immune response in a manner to be described below. These data predict that ATT and LTT are useful to evaluate the immunogenicity and reactogenicity, and intra-peritoneal injection can induce normal immunity. Moreover, using the DNA microarray system, the effect of vaccine treatment could be determined and substituted by gene expression profile changes.

In general, quality of gene expression data obtained from cDNA microarray has varied with platform and procedures used and validation of cDNA microarray should be required for eliminate the effect of dye biases [20]. Our cDNA microarray method have been performed and validated by several different researchers, samples and condition [21–24]. In previous report, we performed two independent experiments of cDNA microarray and they are validated with another method of real-time PCR and *in situ* hybridization [17]. Real-time PCR is often referred to as a gold standard for gene expression measurement and validation of DNA microarray [25]. As a result of our validation, we have shown that there is a strong correlation between cDNA microarray and real-time-PCR analysis. These reports suggest that our cDNA microarray method have high reproducibility, reliability for the vaccine quality control. In this

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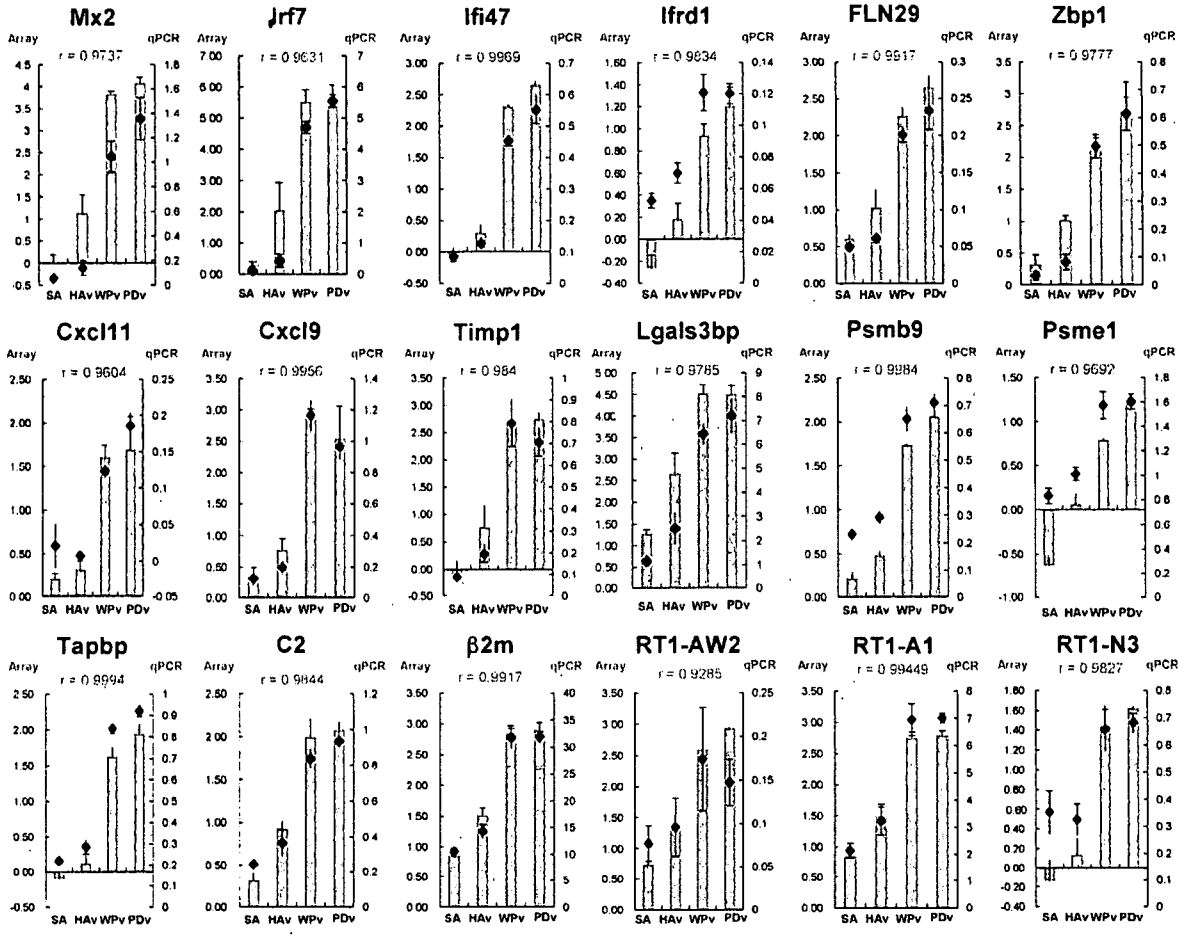

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Figure 4 Comparison of cDNA microarray and quantitative real-time-PCR analysis. Expression of selected 18 genes from DNA microarray analysis (bar) is compared with real-time quantitative PCR data (dot) within the same pareto graph. Bar represented relative $\log_2$ ratios (average ± S.D.) that extracted from the secondary data matrix for each selected genes (left side). Dot represented expression level (average ± S.D.) of selected genes relative to rat β-actin derived from two independent quantitative RT-PCR analysis (right side). A Pearson correlation coefficient was shown within each pareto graphs. Significant correlation between DNA microarray and quantitative PCR analysis was observed in our selected genes.

study, we have designed our experiment in same way of our previous research and also done real-time PCR analysis for 18 genes and yield statistically significant correlation between cDNA microarray and real-time PCR. These data have suggested that our cDNA microarray method for evaluating vaccine quality is reliable and validated.

Based on the changes in the expression profiles of 76 genes, we can distinguish whole-virion influenza vaccine (PDv: pandemic influenza vaccine and WPv: whole particle vaccine) from sub-virion vaccine (HAv: HA vaccine) and saline (Fig. 3). Among the 76 genes we extracted, we found that some genes were already reported as the endemic and pandemic influenza virus infection-inducing genes. The most common gene that influenza infection and vaccination induced was *Mx1* (myovirus (influenza virus) resistance 1). *Mx1* is an IFN-stimulated gene (ISG) and is induced by interferon (IFN) in many species. Some Mx GTPases have antiviral activity against a wide range of RNA viruses, including influenza viruses and members of the bunyavirus family [26]. Human influenza (H1N1 A/Texas/36/91) infection in lung [27] and 1918 pandemic influenza virus infection in bronchi [28] both induced MX (homologue of murine *Mx1*) genes, as shown by cDNA microarray analysis in Macaques. In the human middle ear epithelial cells, infection with influenza A/Alaska (6/77) (H3N2) also induced *Mx1* [29]. In our experiment, *Mx1* expression was highly induced in whole-virion influenza vaccine-treated rat lung, but not in sub-virion vaccine-treated rat lung. These data suggest that Mx1 is one of the most promising biomarkers with which to evaluate influenza vaccine quality, and whole-virion vaccines have the same immunogenicity as influenza infection in the lung.

Similar to the influenza infection, other ISGs, *Ifi47* [30], *Ifrd1 FLN29* [31], and the gamma interferon-induced

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monokine *Cxcl9* (chemokine (C-X-C motif) ligand), were up regulated in whole-virion influenza vaccine-treated rat lung (Table 1). *Cxcl9* was induced by influenza infection in primary human umbilical vein endothelial cells (HUVECs) [32]. *Cxcl9*, which is a ligand of *Cxcr3*, stimulated the directional migration of activated CD8+T cells to the lung, and contributed significantly to the accumulation of cytotoxic T lymphocytes (CTL) in the lung [33]. In addition, in the first case of H5N1 influenza infection in January 2003, patients with H5N1 disease had unusually high serum concentrations of *Cxcl9* and *IP-10* [34]. These data strongly suggest that whole-virion influenza vaccine induces proinflamatory cytokines like influenza A (H5N1) infection, and that Cxcl9 is a common molecule related to influenza pathology and toxicity.

Among our extracted 76 genes, antigen modification and presentation-related genes, including *Ctss* (cathepsin S), *Psme1* (proteasome (prosome, macropain) 28 subunit, alpha), *Psme2* (proteasome (prosome, macropain) 28 subunit, beta), *Tap2* (transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)), Tapbp (TAP (transporter associated with antigen processing)-binding protein), RT1-Aw2 (RT1 class Ib, locus Aw2), RT1-N3 (also known as MHC class I) and β2m (beta2-microgloblin), were up-regulated in PDv- and WPv-treated rat lung. Tapbp has an affinity to bind *Tap2*, which is a member of the family of ABC transporters and transports peptides from the cytosol into the endoplasmic reticulum for binding to MHC class I and β2m complex molecules for subsequent viral antigen presentation [35]. RT1-Aw2 and RT1-N3 form a MHC complex and β2m enhances the MHC stability and antigenicity of suboptimal CTL epitopes. These four genes have a major role of antigen presentation to CD8-T cells [36]. These data suggest that whole-virion vaccine more strongly induced CTL than sub-virion vaccine. These evidences support that whole-virion influenza vaccines have high immunogenicity than HA vaccine, and our method can potentially evaluate the effectiveness and efficacy of the vaccine by monitoring the expression of these genes. Further analyses are required whether these genes expression correlated to the antibody response and efficacy of influenza vaccine.

Among our screened genes, *Timp1* is induced by whole-virion influenza vaccine. Timp1 (tissue inhibitor of metallopeptidase 1) is a member of the physiological inhibitors of matrix metalloproteinases (MMPs) and is produced in the respiratory tract on the development of airway inflammation and remodeling in the lung [37]. Recently, it was proposed that an imbalance between serum MMP-9 and TIMP-1 damages the blood–brain barrier and promotes febrile seizures or encephalopathy in cases of influenza virus infection [38]. These data suggest that Timp1 up-regulation could be a possible phenotypic marker of toxicity related to encephalopathy. Acute disseminated encephalomyelitis (ADEM) and Guillain-Barre Syndrome (GBS) are both observed in 10–20 cases per 1 million adults and are most important issue in influenza vaccine safety [39]. In the United States, it was reported that highest number of GBS cases occurred in patients receiving an influenza vaccine followed by hepatitis vaccine [40]. Our data help us to understand the mechanism of adverse event in the vaccine injection. Further analysis will be required to determine whether up-regulation of these genes was observed in a particular lot of influenza vaccine, resulting in encephalopathy.

The most concerning matter is whether safety of aluminum adjuvanted pandemic influenza vaccine can be evaluated or not in this system. Using current quality control tests, such as the ATT, LTT and even more histological analysis, there was no significant difference in vaccine quality between PDv- and WPv-treated rats at any time point (Fig. 1A and C). In the DNA microarray system, there was no difference between PDv- and WPv-treated rats. These data strongly suggest that the vaccine quality of whole-virion vaccine with or without aluminum hydroxide were unchanged in the lung. These data might be helpful to understand the safety of aluminum hydroxide. More interestingly, it has been proposed that strain is a key factor in the influenza vaccine. Comparing H5N1 and H1N1, no difference in vaccine quality was observed using DNA microarray analysis. These data strongly suggest that strain differences do not affect vaccine basal quality and that the type of vaccine, whether whole virion or sub-virion, is a main issue to induce high immunity if the influenza type for vaccine production matched to endemic or pandemic influenza infection.

Thus, it may be concluded that cDNA microarray technology is an informative, rapid and highly sensitive method with which to evaluate endemic and pandemic influenza vaccine quality. These findings suggest that our new method have a potential to shorten the time for the safety tests and can reduce the number of animals used. In addition, our test may contribute to the development of urgently required vaccine. Further analyses are required to confirm these gene expression changes correlate to the vaccine quality. At any rate, in terms of sensitivity and the amount of information available from one animal test, this method may be even better than current safety tests.

We previously reported several pertussis vaccine toxicity-related genes and proposed DNA microarray analysis as a new model for quality control tests [17]. In this study, we again proposed that DNA microarray analysis have a potential for the quality control of pandemic and endemic influenza vaccines.

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