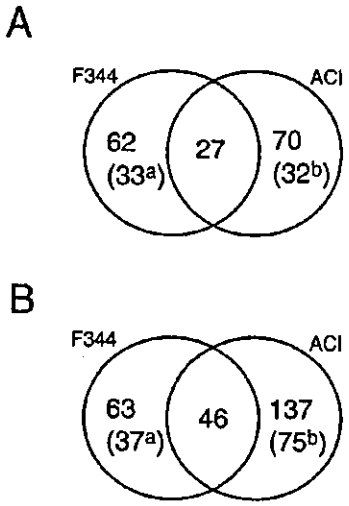

Fig. 1. Numbers of genes over- or underexpressed in colon cancers. Numbers of genes (A) overexpressed or (B) underexpressed in colon cancers of F344 or ACI rats are indicated in Venn diagrams. These genes showed significant differences ($P < 0.05$, Mann–Whitney U-test) between colon cancer tissues and normal colon tissues of ≥3-fold. The numbers in parentheses indicate the numbers of genes that also showed ≥2-fold differences in ACI (a) and F344 (b), respectively.

repeated twice, all of which gave similar results, and representative data are shown.

Results

Gene expression profiles in colon cancers of two rat strains

Of 8749 genes or ESTs on the RG U34A array, 89 and 97 were overexpressed ≥3-fold in colon cancers of F344 and ACI rats, respectively, and 109 and 183 were underexpressed by ≤3-fold, as shown in the Venn diagrams (Figure 1A and B; GeneChip data are available at http://www.ncc.go.jp/jp/nccri/divisions/02bioc/02bioc.html). As illustrated in Figure 1(A), 27 were overexpressed ≥3-fold in common in both F344 and ACI lesions. Although 62 genes were shown to be preferentially overexpressed in F344-derived colon cancers, 33 were also overexpressed ≥2-fold, in both strains (Figure 1A). Similarly, 32 of 70 genes overexpressed ≥3-fold in ACI rats were also overexpressed in the F344 strain by ≥2-fold. Collectively, of 159 genes which showed ≥3-fold expression in cancer tissues in either of the rat strains (Figure 1A), 92 (57.8%) showed ≥2-fold expression in colon cancers in both strains. Similarly, 158 of 246 (64.2%) genes demonstrated ≤2-fold expression in colon cancers in both strains (Figure 1B). We have recently reported that a considerable number of genes are differentially expressed in normal parts of colon epithelial cells between F344 and ACI rats after PhIP treatment (18) and the repertoire of differentially expressed genes may partly account for the different susceptibilities of the two rat strains. In contrast, differences in cancer tissues were relatively small compared with those in normal tissues. Permutation analysis was unable to detect apparent differences in the number of differentially expressed genes between cancer tissues of F344 and ACI rats, although significant differences were present in normal colon epithelium (data not shown). Hierarchical clustering analysis using the entire list of over- and underexpressed genes in cancers could not elucidate any cluster(s) of genes specific for either strain (data not shown).

Genes overexpressed in colon cancers

As described above, 27 genes were overexpressed ≥3-fold in common in both F344 and ACI rats (Figure 1A). Despite our efforts to elucidate meaningful signal pathways in those 27 genes using the bioinformatics software package GenMapp (http://www.genmapp.org/), none could be identified. This could be due, at least in part, to insufficient coverage of genes in signal pathway databases for rats. Manual classification, however, was able to elucidate some interesting tendencies. Genes involved in inflammation, such as those encoding *interleukin 1β*, *small inducible cytokine subfamily A20* precursor, and proteases, such as *matrilysin* (*Mmp7*) and *macrophage metalloelastase* (*Mme*) were highly overexpressed in cancer tissues (Table II). A cell cycle regulator, *cyclin D2*, and the cancer-related gene *retrotransposon virus-like 30s sequence* (*VL30*), which is known to be overexpressed in rodent hepatocellular tumors and lymphomas (19,20), were also highly expressed. Interestingly, a subset of genes encoding defensin and defensin-like proteins, which belong to the small cationic antimicrobial cytotoxic peptides (21–23), were overexpressed ≥10-fold. Differential expression of some of the representative genes was confirmed by semi-quantitative RT–PCR (Figure 2A).

Genes underexpressed in colon cancers

Forty-six genes were underexpressed ≤3-fold in common in colon cancers of both the F344 and ACI strains (Figure 1B). Genes encoding metabolic enzymes, such as alanine aminotransferase, minoxidil sulfotransferase and carbonic anhydrase IV, and signal transduction molecules were among the list (Table III). A considerable number of transcripts related to the structural proteins, i.e. skeletal and smooth muscle-related proteins, matrix-composing proteins and mucin-like proteins, were underexpressed in colon cancers. Down-regulation of mucin genes in colon cancers may reflect the drastic decrease in or complete loss of goblet cells in cancer tissues. Representative results of RT–PCR analyses are depicted in Figure 2A.

Expression of oncogenes and tumor suppressor genes

Expression of tumor-related genes, including those considered to be involved in colon carcinogenesis, was also evaluated utilizing the Chip data. Signals for the *Apc*, *bcl2*, c-*jun*, *erbB3*, *VHL* and *WT1* genes were below detectable levels. The *p53* and c-*fos* genes were expressed at comparable levels in both colon cancers and normal parts of colon tissues (data not shown). Only the c-*myc* gene was expressed at a significantly higher level in cancer tissues than in normal counterparts in both rat strains, with 4.0- and 2.5-fold differences in F344 and ACI rats, respectively.

Comparison of gene expression profiles with human colon cancers

Some of the genes in the list have already been reported to be either over- or underexpressed in human colon cancers (24,25). Average fold changes between colon cancers and normal counterparts were calculated using combined data from both the F344 and ACI strains and genes with ≥5-fold differences are listed in Table IV and compared with human cases, referring to the literature (24–31). The *defensin α5* and *defensin α6* genes were previously reported

Table II. Genes overexpressed in tumors of both F344 and ACI rats[a]

Gene name	Average signal intensity				Fold change (T/N)[b]	
	F344		ACI		F344	ACI
	Normal	Tumor	Normal	Tumor		
HLA and immune function genes						
Anti-acetylcholine receptor antibody gene, rearranged Ig Gamma-2a chain, VDJC region	246.73	3738.53	200.00	3929.67	15.15	19.65
Cytokines, inflammatory mediators, antimicrobial						
(EST) AI639089/similar to mouse defensin NP1 (α1)	1765.02	35820.01	200.00	55038.35	20.29	275.19
Defensin NP3 (α3) gene	898.73	14754.13	919.32	12107.13	16.42	13.17
Interleukin 1-β mRNA	200.00	1225.78	200.00	1658.88	6.13	8.29
Small inducible cytokine subfamily A20	573.80	2328.28	582.04	3176.26	4.06	5.46
Mob-1	214.46	758.60	200.00	979.33	3.54	4.90
Detoxification enzymes						
Glutathione *S*-transferase M5 (Gst-M5)	334.82	2013.20	259.33	1366.90	6.01	5.27
Protease and protease inhibitors						
Matrilysin (Mmp-7) mRNA	200.00	5823.69	200.00	15258.13	29.12	76.29
Macrophage metalloelastase (Mme)	200.00	2047.38	200.00	1990.87	10.24	9.95
Maspin	677.18	1954.74	637.72	2957.50	2.89	4.64
Ion transporters, carrier proteins						
Cation transporter Oct1A	1180.79	6642.65	756.38	6553.23	5.63	8.66
Intracellular calcium-binding protein Mrp14	200.00	1004.26	200.00	2011.03	5.02	10.06
Signal transduction molecules, transcription factor						
Mash-2 mRNA expressed in neuronal precursor cells	200.00	2867.48	303.83	3381.59	14.34	11.13
Platelet phospholipase A2	6078.53	54470.52	7630.13	99549.62	8.96	13.05
Receptor-linked protein tyrosine phosphatase	281.53	2171.51	200.00	2747.78	7.71	13.74
Inhibitor of DNA binding 3 (Idb3)	1585.27	7556.29	1819.98	9419.78	4.77	5.18
Hypertension-regulated vascular factor-1 (Ruk)	1956.67	7039.99	961.72	4728.72	3.60	4.92
Cell cycle regulators						
Cyclin D2	200.00	1281.43	200.00	1218.13	6.41	6.09
Similar to cyclin D2 (Vin1)	5132.35	19215.31	3399.26	18358.46	3.74	5.40
Cancer-related genes (function unknown)						
VL30 element	1055.79	10942.00	1234.52	6470.70	10.36	5.24
c-Ha-*ras* protooncogene mechanism sequence	4157.40	32175.09	2926.38	26356.43	7.74	9.01
Structural proteins						
Type I keratin (Mhr a-1)	200.00	3584.60	200.00	1440.44	17.92	7.20
β-Tubulin T β15	2176.01	8522.65	3252.25	11450.90	3.92	3.52
Serum protein						
α2-Macroglobulin	903.14	5880.35	1023.80	6303.21	6.51	6.16
Function unknown						
(EST) AA859937	572.42	5572.50	251.35	5924.12	9.73	23.57
(EST) AA799396	955.18	4061.69	1094.52	5774.63	4.25	5.28

[a]Genes with ≥3-fold difference compared with those in normal counterpart tissues are listed.
[b]Fold changes were calculated by dividing the signal intensity of colon cancer tissue by that of normal colon tissue.

to be up-regulated in human colon cancers [SAGE data (25)]. In the present study, *defensin NP3 (α3)* and *defensin NP1 (α1)-like molecule* were revealed to be overexpressed, although they have not been reported to be overexpressed in human cases. The matrix proteases *Mmp-7* and *Mme* [DNA chip data (24)] and *Mash2*, *Mrp14* and *cyclin D2* [SAGE data (25)] were also reported to be highly expressed in human colon cancers. In the case of underexpressed genes, many of them were also reported to be down-regulated in human cancers, such as *mucin*, *guanylin*, *carbonic anhydrase IV* and several muscle- and structure-related genes (24,32).

Expression of defensin family genes in rat colon cancers

Defensin genes are composed of mainly two families, α and β, categorized by sequence similarities (23,33). Genes in the former group are expressed mainly in neutrophils and some in the intestine, while the latter are ubiquitously expressed. *defensin NP1 (α1)-like molecule* and *defensin NP3 (α3)* was found to be highly expressed in colon cancers of both strains. *In situ* hybridization analysis revealed mRNAs of *defensin NP3 (α3)* and *defensin α5* to be expressed exclusively in epithelial cells of colon cancers and not expressed in matrix cells (Figure 3A). Normal epithelium did not show any positive signals. Overexpression of these genes in colon cancer tissues was confirmed by RT–PCR (Figure 2B). *defensin α5*, which is an intestinal-type defensin, but is not on the GeneChip, was also expressed exclusively in colon cancers. No expression was observed for *defensin NP4 (α4)*, *defensin β1* (Figure 2B) or *defensin β-2* (data not shown) in either cancers or normal counterpart tissues.

Presence of Paneth cells in cancers and preneoplastic lesions of the colon

Since intestinal-type defensins are known to be produced in Paneth cells (23,34), we examined the expression of other marker proteins specific to the Paneth cell lineage. H&E and

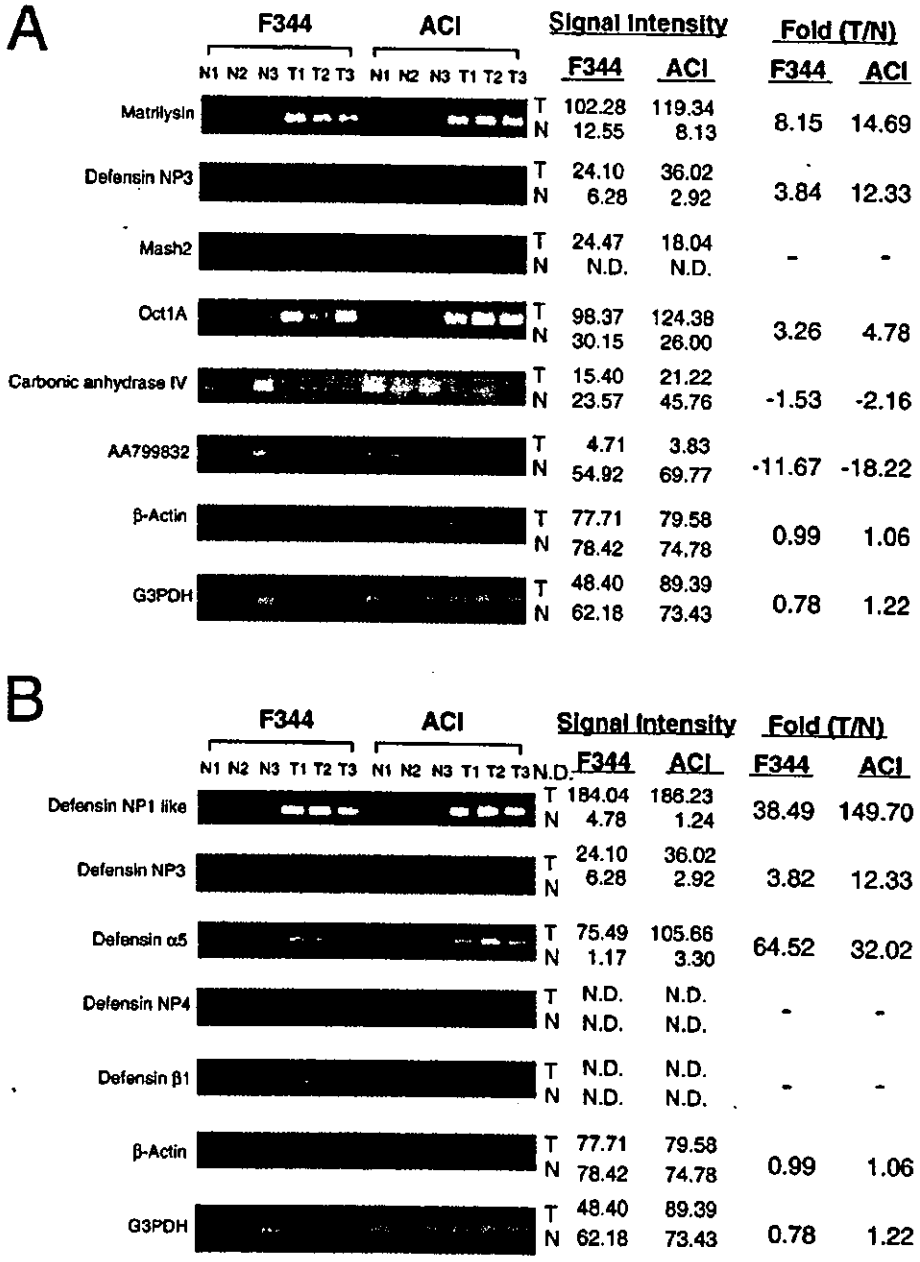

Fig. 2. Semi-quantitative RT-PCR analysis. (A) Among genes over- or underexpressed in colon cancers, expression levels of representative examples were confirmed by semi-quantitative RT-PCR analysis. Each lane indicates the gene expression level of either tumor or normal counterpart tissue from individual animals. The upper four panels illustrate higher expression of *matrilysin*, *defensin NP3*, *Mash2* and *Oct1A*, respectively, in cancer tissues (T_{1-3}) compared with normal epithelium (N_{1-3}). In contrast, *carbonic anhydrase IV* and *phosphoglucomutase 1* were underexpressed in cancers. Expression of *β-actin* and *G3PDH* was analyzed as an internal control. The amounts of PCR products were quantified by NIH image software. The signal values were calculated by subtracting blank values, which are average signal intensities of three different points outside the signal bands. Fold differences were calculated by dividing the average of the value of colon cancer tissues (T) by that of normal colon tissues (N). N.D. indicates a sample with no PCR product visible to the naked eye. (B) Expression levels of several *defensin* genes were analyzed by RT-PCR. *Defensin NP1-like molecule*, *defensin NP3*, *defensin 5* and *defensin NP4* are *α-defensin* family genes and *defensin β1* belongs to the *β-defensin* family gene. Quantification of the amounts of PCR products was carried out as above.

AB-PAS staining revealed the presence of Paneth granules in colon cancer cells and lysozyme expression was also observed in cells with Paneth granules (Figure 3B). Furthermore, Paneth cells were observed in adenomas and, to our surprise, even in preneoplastic lesions. When examined by H&E and AB-PAS staining, three of eight colon cancers and two of three high grade dysplastic ACF observed at 18 or 25 weeks were demonstrated to contain Paneth cells within the lesion (Figure 4A). None of the non-dysplastic ACF demonstrated Paneth cell differentiation (Figure 4B).

Table III. Genes underexpressed in tumors of both F344 and ACI rats[a]

Gene name	Average signal intensity				Fold change (T/N)[b]	
	F344		ACI		F344	ACI
	Normal	Tumor	Normal	Tumor		
Stress proteins and antioxidant						
Heat shock protein 27	8538.00	1967.31	11801.28	2648.38	4.34	4.46
Hsp70.2 mRNA for heat shock protein 70	766.00	200.00	3572.83	210.58	3.83	16.97
Metabolic enzymes						
Alanine aminotransferase mRNA	2078.57	200.00	1557.94	200.00	10.39	7.79
Minoxidil sulfotransferase	2170.13	208.88	1748.53	357.00	10.39	4.90
Carbonic anhydrase IV	2467.84	302.40	2651.28	220.07	8.16	12.05
Inducible carbonyl reductase	1676.98	234.19	1690.85	424.75	7.16	3.98
Skeletal muscle creatine kinase composite	1127.20	237.98	903.73	249.44	4.74	3.62
Mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase	8830.96	2414.46	9434.23	939.58	3.66	10.04
Monoamine oxidase B	680.05	200.00	918.93	200.00	3.40	4.59
Lipoprotein lipase	2259.29	684.09	2316.56	225.35	3.30	10.28
Protease						
Endopeptidase-24.18 α subunit	3327.41	773.59	5676.14	570.71	4.30	9.95
Ion transporters, carrier proteins						
SC1 protein	45395.45	3784.08	24395.65	1981.58	12.00	12.31
Dihydropyridine-sensitive L-type Ca^{2+} channel a-2 subunit	1420.65	229.11	3067.40	200.00	6.20	15.34
Guanylin	26005.42	5019.71	34049.06	6235.18	5.18	5.46
Growth factors and hormones						
Insulin growth factor-binding protein	2446.05	240.24	3255.07	200.00	10.18	16.28
Ebnerin	31568.63	3536.31	5773.52	1388.94	8.93	4.16
Signal transduction molecules, transcription factors						
Neuron-specific protein Pep-19	3125.96	200.00	2721.96	200.00	15.63	13.61
Phospholipase C-β1b	1714.75	244.15	2137.83	323.40	7.02	6.61
D-binding protein	1368.84	200.00	1038.96	200.00	6.84	5.19
Guanylate cyclase 1, soluble, α3	2375.39	384.13	1670.49	519.78	6.18	3.21
Gap-43 gene	1666.24	271.56	982.00	293.22	6.14	3.35
Ssecks 322	6158.29	1093.83	3320.23	522.72	5.63	6.35
N-myc downstream regulated 2	2273.34	486.21	3961.73	710.56	4.68	5.58
Tc10-like rho GTPase	2287.18	582.64	4295.60	511.18	3.93	8.40
BTE-binding protein	2136.52	625.70	3136.92	668.54	3.41	4.69
Structural proteins						
H36-α7 integrin α chain	11056.70	501.93	4844.89	392.89	22.03	12.33
α-Crystallin B chain	4016.12	200.00	3133.37	383.01	20.08	8.18
α b-Crystallin-related protein	4322.27	375.25	3731.25	200.00	11.52	18.66
Mucin-like protein	85858.60	26168.84	85879.95	15703.47	3.28	5.47
Muscle-related proteins						
Skeletal muscle β-tropomyosin and fibroblast tropomyosin 1	15036.62	578.13	8208.40	331.54	26.01	24.76
Myosin regulatory light chain isoform C	32928.30	1592.13	21440.35	576.02	20.68	37.22
γ-Enteric smooth muscle actin isoform	107504.58	5932.44	64435.47	1234.91	18.12	52.18
Calponin	22307.16	1283.39	14767.63	349.48	17.38	42.26
SM22 mRNA	25962.76	1742.56	9714.69	200.00	14.90	48.57
Alternatively spliced smooth muscle myosin heavy chain	21642.04	1629.01	13526.24	591.39	13.29	22.87
Vascular α-actin	28016.47	4213.15	28042.35	2126.16	6.65	13.19
Function unknown						
(EST) AA799832/similar to mouse phosphoglucomutase 5	17333.24	629.26	16572.28	200.00	27.55	82.86
(EST) AA799773/similar to mouse C3H filamin	4300.66	387.96	5571.79	558.87	11.09	9.97
(EST) AA800735/similar to archvillin	3155.42	366.63	3353.20	360.25	8.61	9.31
(EST) AA799580	2256.37	338.94	1619.85	420.47	6.66	3.85
(EST) AA799734	1290.58	200.00	950.38	200.00	6.45	4.75
(EST) AA892888	5611.57	949.04	3961.43	200.00	5.91	19.81
zymogen granule protein (Zg-16p)	14971.90	2743.63	25128.90	1816.38	5.46	13.83
(EST) AA893743/similar to human hox B2	1017.45	200.00	952.02	200.00	5.09	4.76
(EST) AI639501/similar to human brain cell membrane protein 1	4324.68	871.69	4080.30	1027.55	4.96	3.97

[a]Gene with ≥3-fold difference compared with those in normal counterpart tissues are listed.
[b]Fold changes were calculated by dividing the signal intensity of normal colon tissues by that of colon cancer tissues.

Discussion

With the present comprehensive gene expression analysis, conducted using PhIP-induced rat colon cancers in two rat strains, PhIP-induced colon cancers were found to possess somewhat common gene expression profiles in both F344 and ACI rats, despite the significant differences in gene expression between their normal colon epithelium (18). Furthermore, a subset of genes known to be overexpressed in

Table IV. Comparison of overexpressed and underexpressed genes in tumors of rat and human

Gene name	Rat	Human		
	Fold	DNA chip[a]	SAGE[b]	Other data
Overexpressed				
Defensin NP1 (α1)-like protein	53.30	Unchanged		
Matrilysin (Mmp-7) mRNA	41.89	8.00		Overexpressed (26,27)
(EST) AA859937	14.37	[c]		
Defensin NP3 (α3) gene	13.47	Unchanged		
Platelet phospholipase A2	12.02	Unchanged		Overexpressed (28)
Type I keratin (Mhr a-1)	9.86	[c]		
Anti-acetylcholine receptor antibody gene	9.63	[c]		
Mash-2 mRNA expressed in neuronal precursor cells	9.62	[c]	9/0	
c-Ha-*ras* protooncogene mechanism sequence	8.90	[c]		
Intracellular calcium-binding protein Mrp14	8.18	Unchanged	11/0	
Receptor-linked protein tyrosine phosphatase	8.06	[c]		
Macrophage metalloelastase (Mme)	7.45	5.10		
Cation transporter Oct1A	7.43	[c]		
VL30 element	6.75	[c]		
Interleukin 1-β mRNA	6.05	Unchanged		
Cyclin D2	5.60	Unchanged	8/0	Overexpressed (29)
α2-Macroglobulin	5.55	[c]		Overexpressed (30)
Under-expressed				
(EST)AA799832	40.36	2.7		
H36-α7 integrin α chain	15.58	2.8		
Neuron-specific protein Pep-19 mRNA, complete cds	13.61	2.1		
Scl protein	12.18	4.5		Underexpressed (31)
Zg-16p	11.35	[c]		
α b-crystallin-related protein	11.34	[c]		
Dihydropyridine-sesitive L-type calcium channel	10.42	Unchanged		
α-Crystallin B chain	10.19	4.3		
(EST)AF119148/Musmus C3H filamin	9.56	5.8		
Alanine aminotransferase mRNA	9.35	[c]		
Insulin growth factor-binding protein	9.28	1.6		
(EST)AA892888	7.77	[c]		
Carbonic anhydrase IV	7.68	2		
(EST) AA800735/similar to mouse Supervillin	7.16	[c]		
Guanylin	6.04	20	55/0	
Phospholipase C-β1b	5.78	[c]		
Ssecks 322	5.68	[c]		
D-binding protein	5.05	[c]	8/0	

The values indicate tag counts of normal tissues/tumor tissues.
[a]Data from Notterman *et al.* (24). Values indicate fold difference (normal/tumor).
[b]Data from Buckhaults *et al.* (25) and on-line SAGE database to which they submitted their results.
[c]There is no information in Notterman *et al.* (24) about these genes.

human colon cancers was highly expressed in colon cancers of both rat strains. In addition, there are substantial similarities in a list of underexpressed genes between human (24) and rat tumors (present study). The histological features of the rat cancers also showed a high similarity with human cases, as described previously (10,11,13,14). Taking all the data together, the PhIP-induced colon carcinogenesis model in rats thus appears an appropriate and relevant system for investigation of human colon carcinogenesis.

High expression of *cyclin D2* and c-*myc* may result from activation of the Wnt/β-catenin signaling pathway as a consequence of β-catenin accumulation, this being a common feature in rat and human tumors (2,13,35). An mRNA species for a mucin-like protein, homologous to mouse mucin 2, was here shown to be underexpressed in cancer tissues. Mucins are known to be abnormally expressed in neoplastic lesions of the colon of humans (36). Moreover, since *mucin* $2^{-/-}$ mice demonstrated reduced numbers of goblet cells and spontaneously developed adenomas in the small intestine (37), down-regulation of the mucin-like protein mRNA may play an important role in PhIP colon carcinogenesis in rats.

Some of the genes found in the present study, including those encoding helix-loop-helix protein MASH2, organic cation transporter (OCT1A4), calcium-binding protein MRP14 and regulator of ubiquitous kinase (RUK), have not been reported so far to be differentially expressed in human colon cancers. Some of them are intriguing with regard to their biological functions, although there are few reports suggesting their involvement in human colon carcinogenesis. Considering the size (small), the non-invasive nature of rat lesions and the rare occurrence of *p53* or K-*ras* mutations in PhIP-induced colon cancers (38,39), differential expression of these genes in cancer tissues may suggest that their alteration occurs at an early stage of human colon carcinogenesis. Alternatively, of course, this could simply be a rodent-specific phenomenon. Further analysis is warranted in the future to clarify this point.

Snyderwine *et al.* recently reported gene expression profiles in PhIP-induced mammary gland tumors (40). Expression of a few genes overlapped between mammary gland (40) and colon tumors (present study) induced by PhIP, except for the *tubulin β15* gene. In PhIP-induced rat mammary cancer, deregulation of cyclin D1/Cdk4 and phospho-Rb was postulated to play a

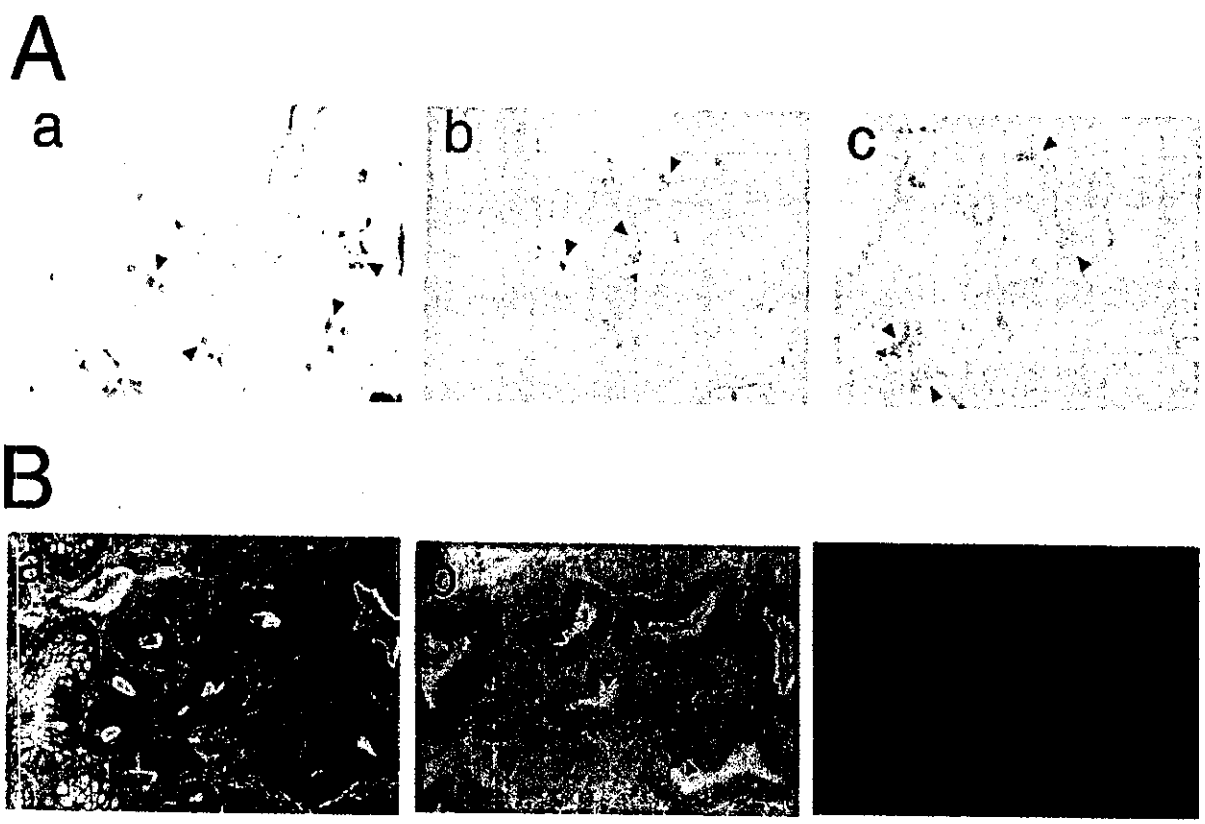

Fig. 3. Histological analysis of colon cancer tissues. (A) Frozen tissue sections were subjected to AB-PAS staining (a) and *in situ* hybridization with a *defensin NP3* (b) or *defensin 5* probe (c). Arrowheads in (b) and (c) indicate cells with *defensin NP3* and *defensin 5* transcripts, respectively. (B) Serial sections of paraffin embedded colon cancer tissues were subjected to H&E staining (a), AB-PAS staining (b) and immunostaining with an anti-lysozyme IgG antibody (c). As arrowheads indicate, Paneth cells can be recognized by the presence of typical pink granules (Paneth granules) by H&E staining. Paneth granules are also clearly visualized by AB-PAS staining (b) and by immunostaining for lysozyme protein (c).

central role (41). The results indicate that the molecular basis underlying PhIP carcinogenesis could differ from organ to organ, although cell proliferation may be accelerated by PhIP in both cases. In fact, β-catenin mutations are frequently observed in rat colon cancers (11–13), but only rarely in mammary tumors (42). Moreover, the mutation spectra found in PhIP-induced tumors also differ with the organ (43).

It is of great interest to note that Paneth cells were observed in colon cancers and even in much earlier lesions, dysplastic ACF. Paneth cells exist mainly in the small intestine and sometimes in colonic tumors, but are rarely found in normal colon epithelium (44,45). Yamada *et al.* have recently reported the presence of Paneth cells in crypts which accumulated β-catenin (BCAC) induced by an alkylating agent, azoxymethane (46,47). Based on their observations and a previous report by Wilson *et al.* (48), Yamada and Mori (49) suggested a dysdifferentiating potential of BCAC and that Paneth cell differentiation could promote intestinal carcinogenesis. Taking the results together, the appearance of Paneth cells in colon cancers does not appear to be carcinogen-specific, but could be a common phenomenon in the development of colon cancers. Although the molecular mechanisms underlying the induction of Paneth cells in colon cancers remain to be clarified, activation of the Wnt/Apc/β-catenin signaling pathway could be one causative event. Inhibition of β-catenin/TCF signaling in colon cancer cell lines indeed results in G_1 arrest or induction of markers which are characteristic of differentiated colon epithelial cells, as described previously (50). Mice deficient for the TCF4 transcription factor completely lack proliferating cells in the fetal small intestinal epithelium (51). The Wnt/APC/β-catenin signaling pathway thus could be essential for maintenance of the differentiated or undifferentiated status of intestinal epithelial cells. Activation of the Wnt/APC/β-catenin pathway may therefore affect the differentiation process and induce dysdifferentiation of colon epithelial cells as a consequence. Activation of this pathway is commonly observed in both PhIP- (10–15) and azoxymethane-induced (35,52,53) colon cancers and also in preneoplastic lesions (15). Gene expression analysis of teratomas, derived from embryonic stem cells with null APC, showed up-regulation of *defensin* α genes compared with teratomas derived from embryonic stem cells with wild-type APC (54). Paneth cells were also observed in APC-deficient teratoma tissues (54). Again, it is highly plausible that activation of the Wnt/APC/β-catein signaling pathway is a genetic causation of Paneth cell differentiation in colon cancer tissues. Although the biological consequences of Paneth cell differentiation (or metaplasia) for colon carcinogenesis remain to be clarified, it is

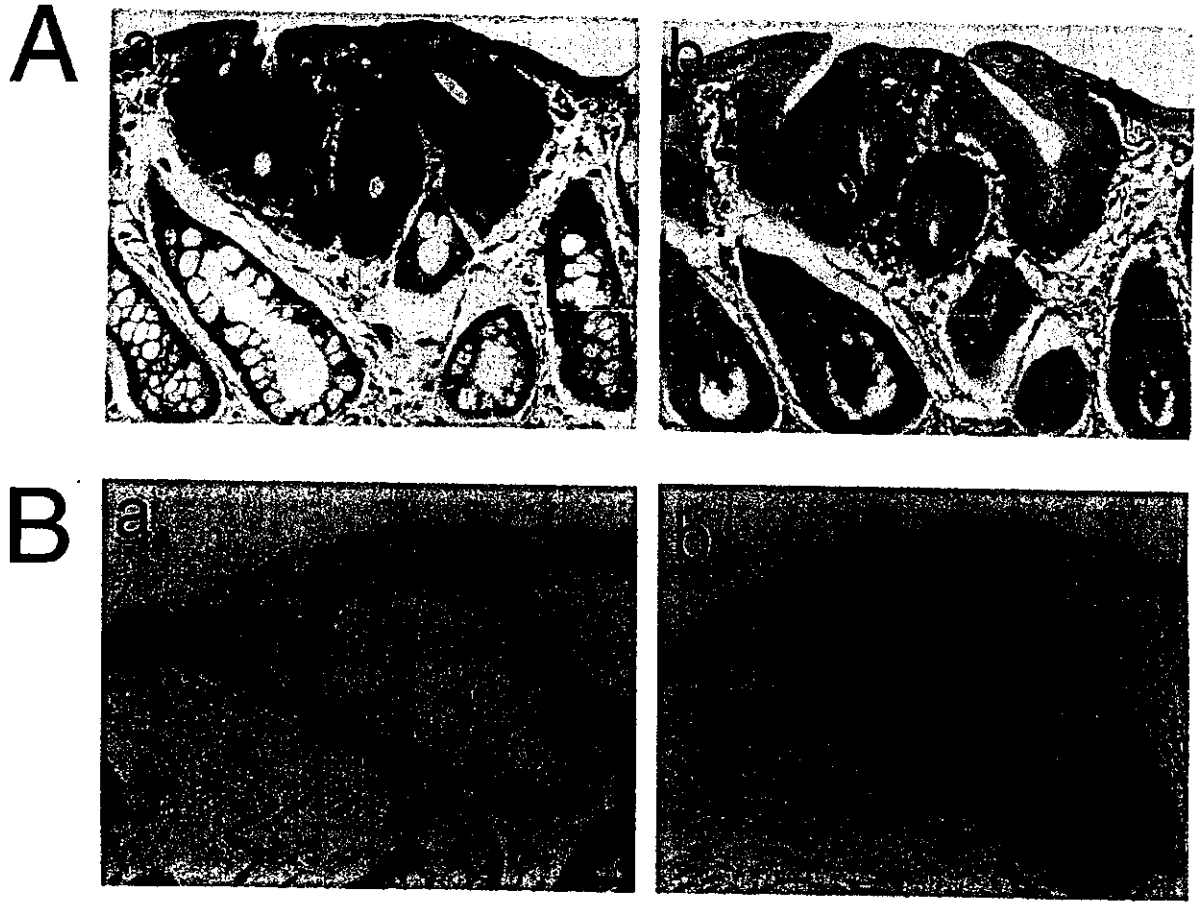

Fig. 4. Histological analysis of ACF. Serial sections of paraffin embedded high grade dysplastic (A) and non-dysplastic ACF (B) observed at experimental week 18. AB-PAS-positive Paneth granules are clearly evident in the high grade dysplastic ACF, but not in the non-dysplastic lesion. Another high grade dysplastic ACF collected at week 25 also gave similar results (data not shown). (a) H&E staining; (b) AB-PAS staining.

possible that the appearance of Paneth cells reflects aberrant differentiation of colonic stem cells. Whatever the case, defensin could be utilized as a potential serological marker for early detection of colon cancers because of its nature as a secreted molecule.

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ORIGINAL ARTICLE

Comprehensive expression analysis of a rat depression model

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ABSTRACT

Herein we report on a large-scale analysis of gene expression in the 'learned helplessness' (LH) rat model of human depression, using DNA microarrays. We compared gene expression in the frontal cortex (FC) and hippocampus (HPC) of untreated controls, and LH rats treated with saline (LH-S), imipramine or fluoxetine. A total of 34 and 48 transcripts were differentially expressed in the FC and HPC, respectively, between control and LH-S groups. Unexpectedly, only genes for NADH dehydrogenase and zinc transporter were altered in both the FC and HPC, suggesting limited overlap in the molecular processes from specific areas of the brain. Principal component analysis revealed that sets of upregulated metabolic enzyme genes in the FC and downregulated genes for signal transduction in the HPC can distinguish clearly between depressed and control animals, as well as explain the responsiveness to antidepressants. This comprehensive data could help to unravel the complex genetic predispositions involved in human depression. *The Pharmacogenomics Journal* (2004) **4**, 114–126. doi:10.1038/sj.tpj.6500234

Keywords: learned helplessness; DNA microarray; frontal cortex; hippocampus; antidepressant

INTRODUCTION

Depression is a complex psychiatric disease with specific symptoms that include depressed mood, loss of interest, diminished appetite, sleep disturbances and psychomotor retardation. Depression is common, with lifetime prevalence estimated to be up to 20%,[1] and the condition exacts high personal and social costs on sufferers. The illness is also a major cause of suicide. Epidemiological studies suggest a genetic component to affective disorder,[1,2] and efforts to identify susceptibility genes by linkage and other genetic analyses are being conducted.[3] However, the precise etiologies remain elusive, as does the development of new therapies against depression, particularly for cases that are refractory to conventional therapy. In the case of complex trait diseases, isolating genetic mechanisms using human disease material is often difficult because of sample heterogeneity and other confounding factors. Analysis of suitable animal models under strictly controlled conditions would therefore be beneficial.

To investigate the molecular basis of depression, we have applied DNA microarray technology to analyze gene expressions in learned helplessness (LH) rats, an animal model of depression. After pretreatment with repeated inescapable shocks, animals with LH display decreased ability to escape adverse situations. This behavioral model was originally described in dogs,[4] and later analogous behavior was induced in rats.[5] LH animals display behavioral phenotypes resembling human depressive symptoms, and LH can be ameliorated

using antidepressant drugs.[6,7] LH therefore fulfills the parameters of construct validity, face validity and predictive validity,[8] confirming the suitability of the model for studying the neurobiology of depressive illness and the actions of antidepressants.[9–11] It is also important to note that the 'depressive state' in LH animals lasts for over 3 weeks,[12] making this model particularly useful for studying the chronic changes in brain physiology that accompany depression. We examined the frontal cortex (FC) and hippocampus (HPC) of LH rats, because positron emission tomography scanning and functional magnetic resonance imaging studies have recently indicated a potential abnormality in the frontal cortex of both familial bipolar and unipolar depressives.[13] In addition, recent evidence has suggested that neurogenesis in the HPC may be disturbed in depressive patients.[14–16]

In this study, we have analyzed brain transcripts altered during LH and followed their responsiveness to a classical tricyclic antidepressant (TCA), imipramine, and a new generation selective serotonin reuptake inhibitor (SSRI), fluoxetine. In addition, we performed principal component analysis (PCA) to extract essential gene sets from complex expression data sets that can best explain the different pathophysiological conditions. This was achieved by considering genes as variables in PCA. When genes are variables, the analysis creates a set of principal gene components indicating the features of genes that best explain the experimental responses. Using these comprehensive pharmaco-behavioral genetic approaches, we have attempted to generate data that would eventually allow for the formulation of hypotheses to help understand the molecular and genetic pathophysiology of depression. This in turn could lead to the development of novel antidepressants with greater efficacy.

RESULTS AND DISCUSSION

Effectiveness of Antidepressants in Learned Helplessness

The LH model is difficult to generate, requiring meticulous refinement of multiple experimental parameters. In our experimental setting, after inescapable shock pretreatment, animals were subjected to 15 avoidance trials at 30 s intervals. In each trial, a current was applied via the floor grid during the first 3 s. If an animal moved to a neighboring compartment within this period (escape response), the shock was terminated. Failures in escape response were counted as a measure of LH. We defined animals as being in a state of LH when escape failures were demonstrated in more than half of the trials in the session. Using this system, we reproducibly induced LH in rats with a success rate of ~40%. LH rats were subsequently treated with repeated injections of saline (LH-S), fluoxetine (LH-F) or imipramine (LH-I), then re-evaluated for escape responses in the test session. Figure 1 shows a schematic of these procedures. During the escapable shock of the test session, all animals in the LH-S group ($n=10$) showed more than eight escape failures, and the mean failure was significantly higher than that of control rats (those that were not given inescapable shock, $n=15$) (Figure 2). Antidepressant administration significantly reduced the number of escape failures for both LH-F ($P<0.05$) and LH-I ($P<0.01$). Imipramine recovered all

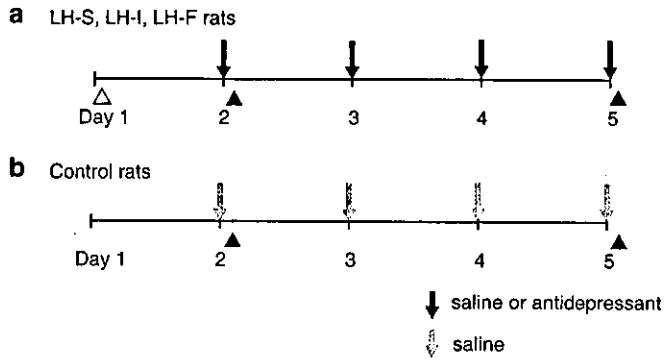

Figure 1 Schematic representation of behavioral procedures. (a) To induce the LH state, animals were given inescapable shock (△) on day 1. On day 2, they received escapable shock (▲), and were selected as 'LH rats' if they showed greater than 50% failure in escape responses. LH animals were then administered saline (LH-S) or antidepressants (LH-F, LH-I) for 4 consecutive days. These animals received escapable shock (▲) again on day 5 to determine whether they were still in the LH state. (b) Control rats were not given inescapable shock on day 1, but treated in the same way thereafter as the LH rats.

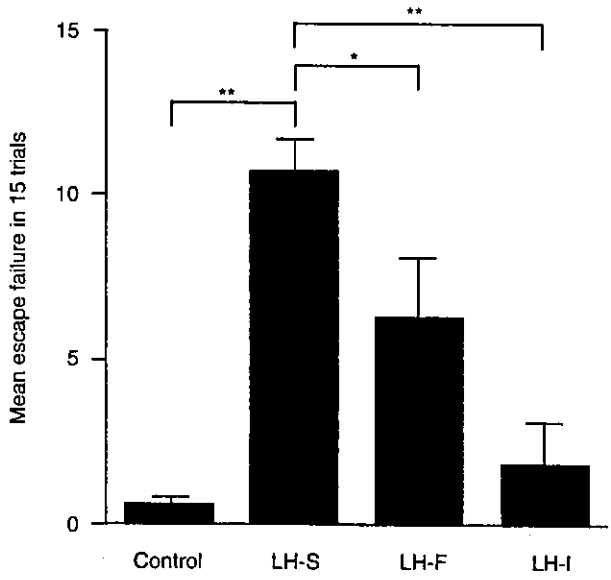

Figure 2 Mean number of escape failures (±SE) during the 15 avoidance trials. Controls ($n=15$) were not given inescapable shocks. Rats exposed to prior inescapable shocks were treated with saline (LH-S) ($n=10$), fluoxetine (LH-F) ($n=7$) or imipramine (LH-I) ($n=9$) once a day for consecutive days (days 2–5). Escape failure refers to the failure of animals to move into the safe compartment during electric footshock (0.5 mA, 3 s duration). The mean numbers of escape failures among groups were evaluated by ANOVA, $F(3,37)=23.69$. $^{*}P<0.01$ and $^{**}P<0.001$ by *post hoc* Tukey–Kramer test.

rats from the LH state ($n=9$), and fluoxetine reinstated five out of seven. These results confirm the persistency of LH in our animals and the effectiveness of antidepressants in this model.[5,17–20] Fluoxetine produced a weaker response compared to imipramine in alleviating the LH phenotype (Figure 2). We also tested larger doses of each drug, 10 mg/kg i.p. of fluoxetine and 50 mg/kg i.p. of imipramine, but did not observe any significant change in the number of escape failures (10 mg/kg of fluoxetine, 5.0 ± 1.0 ($n=3$); 50 mg/kg of imipramine, 2.0 ± 1.3 ($n=3$)) between the two doses. In addition, Anthony *et al*[21] showed that 5 mg/kg of fluoxetine, the same dose as used in the present study, was enough to elicit monoaminergic perturbation such as a reduced 5-hydroxytryptamine receptor 1B expression in the dorsal raphe of rats. Bristow *et al*[22] also demonstrated the validity and efficacy of 5 mg/kg of fluoxetine in ameliorating depressive behavior in rats. We attempted to minimize the nonspecific effects of the drugs by using the lowest possible dose that maintained antidepressive efficacy.

The present results may reflect the different clinical potencies of the individual agents. TCAs such as imipramine inhibit the reuptake of both serotonin and norepinephrine at nerve terminals by acting on monoamine transporters. In contrast, SSRIs including fluoxetine specifically block the reuptake of serotonin.[2] These differences in pharmacological profiles underlie the distinct antidepressive competences exerted by TCA and SSRI. Although human patients require over 2 weeks of medication before antidepressive effects are observed, we administered the drugs for 4 days in our rodent experiments, in keeping with the protocols of Geoffroy *et al*[6] (5-day treatment) and Tordera *et al*[23] (4-day treatment), and could replicate distinct behavioral responses to therapy.

We also measured weight gain during the 5 days of experiments. Weight increase in the LH-S group was significantly lower than that in controls (LH-S, 18.8 ± 4.4 g; control, 31.7 ± 2.2 g; $P<0.05$).

General Profiles of Gene Expressions Associated with LH and Antidepressant Treatments

We selected six animals each from the control (rats showing no escape failure in the escapable shock session) and LH-S groups, and five each from the LH-F and LH-I groups (these showed $\leqslant 7$ failures in the 15 trials), to perform microarray analyses. Patterns of gene expression in the two brain regions from the four rat groups were examined using the Affymetrix GeneChip U34A, which represents 8799 probe sets and codes over 8000 transcripts including known genes (>5000) and expressed sequence tags (ESTs). Transcript expression from extracted RNA displayed good linearity in both FC and HPC samples (Figure 3). Our stringent criteria identified 34 and 48 transcripts as differentially expressed between control ($n=6$) and LH-S ($n=6$) groups in the FC and HPC, respectively (henceforth referred to as 'LH-associated transcripts') (Figures 3a and b). However, none of these transcripts survived after the Benjamin and Hochbery False Discovery Rate analysis. This observation may confirm the statements of Mirnics *et al*[24] that true gene-expression changes in psychiatric traits are small and

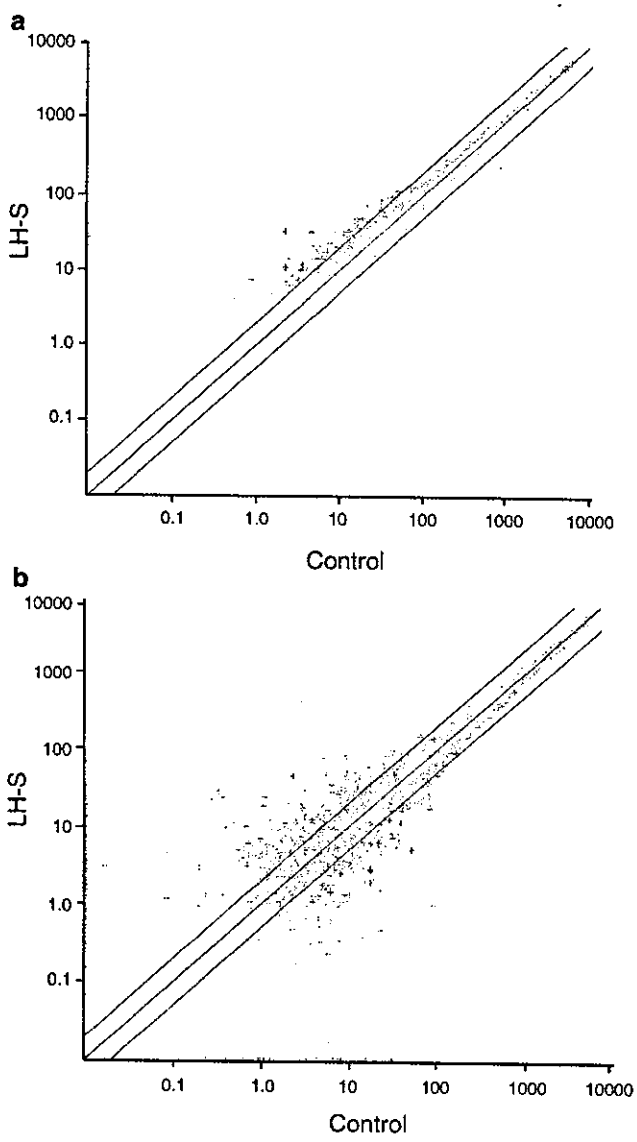

Figure 3 Scatter plot of log-intensity values for the over 8000 genes assayed with the RG-U34A chip in the frontal cortex (a) and hippocampus (b). Each point represents the log value from an average of six control or six LH-S animals.

psychiatric diseases may result from cumulative subtle changes.

Among LH-associated transcripts, five transcripts and one gene showed significant recovery to control levels from the LH state under both imipramine ($n=5$) and fluoxetine ($n=5$) administration in the FC and HPC, respectively (white portions in Figures 4a and b). Transcripts in the pink and yellow areas of Figure 4 represented expression levels that returned to normal after administration of imipramine and fluoxetine, respectively. Interestingly, no LH-associated transcripts demonstrated significant deviation from control levels after drug treatment. That is, none of the LH-associated genes were further decreased or excessively

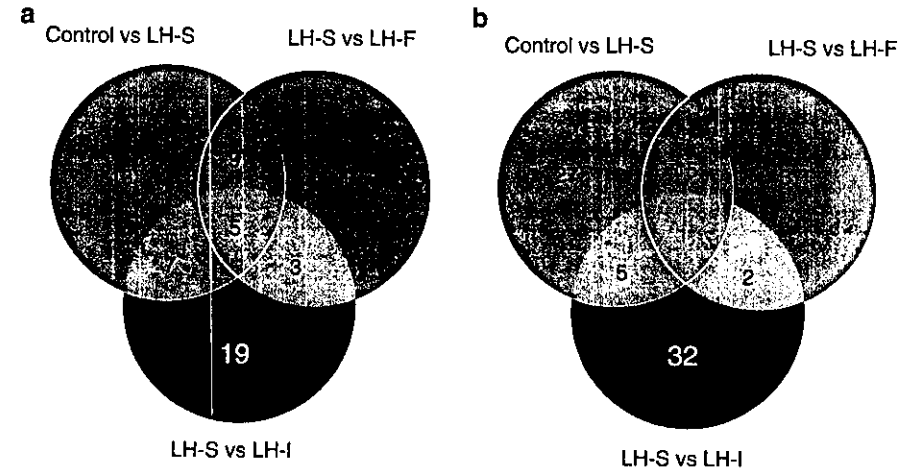

Figure 4 Venn-diagram selection of LH- and antidepressant-associated transcripts in the frontal cortex (a) and hippocampus (b). Comparisons were made between control ($n=6$) and LH-S rats ($n=6$), between LH-S and LH-F rats ($n=5$), and between LH-S and LH-I rats ($n=5$). The LH-I and LH-F rats were those that showed more than 50% success in escape behavior after drug treatments. The number in each compartment denotes the number of differentially expressed transcripts between two groups (see Materials and Methods for a definition of our criteria).

increased after initiating therapy. Approximately 38% of LH-associated transcripts in the FC and 56% in the HPC could not be normalized by either antidepressant (Figure 4; red area). These transcripts could represent the potential targets for novel antidepressants with efficacy against refractory depression. The green, purple and light blue segments in Figure 4 depict the transcripts with expression levels that did not differ between control and LH-S groups, but were significantly altered by fluoxetine, imipramine or both drug treatments, respectively. The information on these transcripts is provided as supplementary Tables S1 and S2. Some of these transcripts may be relevant to the manifestation of adverse reactions by TCA and SSRI. Tables 1 and 2 show the listing of LH-associated transcripts according to putative functions, along with *P*-values between different treatment groups. Data are also provided on the 'average difference' ±SE of each transcript (that corresponds to an absolute value) in supplementary Tables S1 and S2. In all, 17 known genes and one EST showed downregulation (marked in red), whereas 16 transcripts including ESTs were upregulated in the FC (Table 1). In contrast, the majority of known LH-associated genes in the HPC were downregulated (27 of 31) (marked in red in Table 2). Even allowing for ESTs, the number of downregulated transcripts in the HPC significantly exceeds the upregulated transcripts (32 *vs* 16) (Table 2).

We chose four genes from each of Tables 1 and 2, and examined mRNA levels in the same RNA samples used for microarray experiments under 'one-step' quantitative RT-PCR reactions (Table 3). These results showed the same direction of expressional changes seen in the microarray experiments, but less correlation was found with the degree of change between the two methods, as indicated in prior studies.[25,26] Furthermore, since only a limited number of transcripts were confirmed by independent methods and no transcripts were confirmed when Bonferroni's correction was applied to the quantitative RT-PCR results, the present DNA microarray data are broadly unconfirmed.

LH-associated Transcripts in the FC

When classified according to function, genes defined as receptors or ion channel/transporters were all downregulated in LH animals (Table 1). Among them, the serotonin receptor type 2A (*Htr2a*) gene showed a 1.6-fold decrease, and recovery with both fluoxetine and imipramine. Evidence from other animal models for depression[27,28] and clinical observations[29] have also suggested a pathological role for *HTR2A* in the depressive state. The change in inositol-1,4,5-triphosphate receptor type 1 (*Itpr1*) level was small, but statistically significant. Both types of antidepressant normalized the reduced expression of *Itpr1*. The observed decrease in both *Htr2a* and *Itpr1* and their restitution to original levels by antidepressants is in keeping with a proposed theory of dysregulated monoamine-mediated calcium signaling in depression.[30,31] Other members of the receptor and ion channel/transporter gene families that showed restoration with fluoxetine or imipramine included a voltage-gated potassium channel and zinc transporter (Table 1). Conversely, three genes from the signal transduction family were all upregulated in LH-S rats compared to controls (Table 1). Of interest is prostaglandin D synthase, an enzyme that produces prostaglandin D_2, a potent endogenous sleep-promoting substance.[32] This enzyme has recently been implicated in the regulation of nonrapid eye movement (NREM).[33] Sleep disturbance is a typical symptom of human depression. Examination of sleep parameters in LH rats, particularly the NREM period, would therefore be of interest. Protein kinase C epsilon (PKCε), which is a member of nPKC, showed a small but significant increase in LH-S compared with controls.

Table 1 LH-associated transcripts in the frontal cortex

Functional Groups	*Fold change*[a]	*P-value*[b]			*Accession no.*
		Cont vs LH-S	*LH-S vs LH-F*	*LH-S vs LH-I*	
Receptor					
Inositol-1,4,5-triphosphate receptor type I	−1.1	0.0032	0.0078	0.0078	J05510
Serotonin receptor 2A	−1.6	0.0479	0.0352	0.0358	M64867
Ion channel/Transporter					
Voltage-gated potassium channel	−1.1	0.0289	0.0078		X62840
Dri 27/ZnT4 (zinc transporter)	- 1.3	0.0289		0.0026	Y16774
Cl-/HCO3- exchanger (B3RP2)	−1.4	0.0484			J05166
Signal transduction					
Prostaglandin D2 synthetase	1.3	0.0484	0.0006	0.0181	J04488
PKC epsilon	1.2	0.0158	0.0181		M18331
Neurexophilin 4	2.0	0.0156			AF042714
Neural growth/ structure					
Tau	−1.1	0.0479	0.0358		X79321
Jagged2 precursor	1.3	0.0158		0.0358	U70050
Similar to cdc37	1.6	0.0484			D26564
MAP2	−1.4	0.0158			S74265
H36-alpha7 integrin alpha chain	−1.5	0.0289			X65036
Neu differentiation factor	−1.6	0.0484			M92430
LIMK-1	−9.5	0.0436			D31873
Metabolic enzymes					
Thioradoxin reductase 1	−1.2	0.0011	0.0181		AA891286
F1-ATPase epsilon subunit	1.1	0.0011		0.0026	AI171844
Mitochondrial fumarase	−1.1	0.0110		0.0181	J04473
Lipoprotein lipase	1.5	0.0484			L03294
24-kDa subunit of mitochondrial NADH dehydrogenase	1.4	0.0484			M22756
Bleomycin hydrolase	1.4	0.0158			D87336
Stress response					
Rapamycin and FKBP12 target-1 protein (rRAFT1)	1.1	0.0158	0.0358		U11681
Neuronal death protein	2.3	0.0484			D83697
Poly(ADP-ribose) polymerase	1.6	0.0077			U94340
Others					
Taipoxin-associated calcium binding protein-49 precursor	−1.2	0.0032	0.0119		U15734
Cytosolic resiniferatoxin binding protein RBP-26	−1.3	0.0289	0.0358		X67877
RNA binding protein (transformer-2-like)	−1.2	0.0110	0.0181		D49708
C15	−1.2	0.0002		0.0006	X82445
resection-induced TPI (rs11)	1.4	0.0011			AF007890
Anti-proliferative factor (BTG1)	−1.4	0.0484			L26268
Unknown					
EST	−1.5	0.0158	0.0474	0.0026	AA892280
EST	1.2	0.0484	0.0026		AI230632
EST	1.4	0.0484		0.0078	AA894234
EST	1.2	0.0484		0.0181	AF069782

[a]The fold change was calculated between mean values of control (n = 6) and LH-S rats (n = 6). Positive values indicate an increase, and negative a decrease in gene expression in the LH.
[b]Statistical comparison was made by Mann-Whitney test (two-tailed). Only significant *P*-values (< 0.05) are denoted.

Activation of serotonin 2 receptors reportedly diminished γ-amino butyric acid type A receptor current through PKC in prefrontal cortical neurons.[34] Expression changes in the *Htr2a* and PKCε genes in LH may indicate a functional link between the two systems in the depressive state. The precise role of neurexophilin 4 in the intercellular signaling system remains unclear,[35,36] but the gene may underlie a depression/stress-related physiological pathway that cannot be corrected using TCAs or SSRIs (Table 1).

Of the LH-associated genes identified from the FC, LIMK-1 (LIM domain kinase 1: *Limk1*) displayed the most dramatic decrease, a 9.5-fold reduction compared with control levels (Table 1). Transcriptional levels were not completely normalized by imipramine or fluoxetine treatment. This

Table 2 LH-associated transcripts in the hippocampus

Functional Groups	*Fold change*[a]	*P-value*[b]			*Accession No.*
		Cont vs *LH-S*	*LH-S* vs *LH-F*	*LH-S* vs *LH-I*	
Receptor					
HGL-SL1 olfactory receptor pseudogene	−2.0	0.0005	0.0358		AF091574
olfactory receptor-like protein (SCR D-9)	−1.4	0.0050			AF034899
heparin-binding fibroblast growth factor receptor 2	−2.4	0.0373			L19112
HFV-FD1 olfactory receptor	−2.5	0.0019			AF091575
Ion channel/Transporter					
Dri 27/ZnT4 protein (zinc transporter)	1.2	0.0464	0.0181		Y16774
Chloride channel RCL1	−1.1	0.0373	0.0181		D13985
High-Affinity L-proline transporter	−1.3	0.0050		0.0078	M88111
Plasma membrane CA2+-ATPase isoform 3	−1.4	0.0018			M96626
Signal transduction					
Paranodin	1.2	0.0213	0.0078		AF000114
Arl5 (ADP-ribosylation factor-like 5)	1.4	0.0213			AA956958
Grb14	−1.4	0.0213			AF076619
Neurotransmission					
Synuclein SYN1	−1.2	0.0213	0.0358		S73007
Alpha-soluble NSF attachment protein	−1.1	0.0213		0.0078	X89968
Rab13	−1.9	0.0005		0.0358	M83678
Rab3b	−1.6	0.0213			AA799389
GTP-binding protein (ral B)	−2.0	0.0110			L19699
Neural growth/ structure					
Tuba1 (Alpha-tubulin)	1.2	0.0213	0.0006		AA892548
Zinc-finger protein AT-BP2	−1.4	0.0213			X54250
CRP2 (cysteine-rich protein 2)	−1.4	0.0373			D17512
Nfyb CCAAT binding transcription factor of CBF-B/NFY-B	−1.4	0.0373			AA817843
Decorin	2.2	0.0213			AI639233
Metabolic enzymes					
NADH-cytochrome b-5 reductase	−1.1	0.0110	0.0358	0.0181	AI229440
Siat5 (Sialyltransferase 5)	−1.7	0.0050	0.0078		X76988
24-kDa mitochondrial NADH dehydrogenase precursor	−1.4	0.0373			M22756
2-oxoglutarate carrier	−1.4	0.0110			U84727
Soluble cytochrome b5	−1.5	0.0110			AF007107
Stress response					
Ischemia responsive 94 kDa protein (irp94)	−1.4	0.0050			AF077354
MHC class I antigen	−1.5	0.0373			AF074609
Others					
RNA splicing-related protein	−1.4	0.0373			AI044739
Aes Amino-terminal enhancer of split	−1.4	0.0153			AA875427
Proteasome RN3 subunit	−1.5	0.0110			L17127
Unknown					
EST	1.5	0.0274	0.0358		AA799488
EST	1.4	0.0373	0.0078		AA858617
EST	1.2	0.0213	0.0026		AA892817
EST	1.2	0.0050	0.0026		AA892238
EST	1.1	0.0213	0.0026		AA799893
EST	1.1	0.0050	0.0006		AA799784
EST	−1.5	0.0213	0.0358		AA799525
EST	1.3	0.0373		0.0078	AA893039
EST	−1.1	0.0373		0.0358	AI007820
EST	−1.3	0.0373		0.0358	AA875348
EST	2.4	0.0213			AA875633
EST	1.9	0.0373			AI229655
EST	1.5	0.0373			AA955477
EST	1.5	0.0213			AA893569
EST	1.4	0.0464			AA800803
EST	−1.6	0.0274			AI639477
EST	−1.6	0.0110			AA892353

[a]The fold change was calculated between mean values of control ($n=6$) and LH-S rats ($n=6$). Positive values indicate an increase, and negative values (in red) a decrease in gene expression in the LH.
[b]Statistical comparsion was made by Mann-Whitney test (two-tailed). Only significant *P*-values (<0.05) are denoted.

Table 3 Gene expression levels evaluated by quantitative RT-PCR and comparisons with the results from microarray analysis

	Frontal cortex				*Hippocampus*			
	LIMK-1	*HTR2A*	*PGDS*	*IP3R*	*SNAP*	*SYN1*	*bFGFR2*	*Ca^{2+}-ATPase*
Control	1.00±0.42	1.00±0.57	1.00±0.19	1.00±0.48	1.00±0.36	1.00±0.44	1.00±0.21	1.00±0.31
LH-S	0.49±0.07	0.36±0.06	1.64±0.25[a]	0.97±0.20	0.61±0.14	0.54±0.17	0.88±0.23	0.80±0.37
LH-F	0.50±0.06	0.57±0.26	1.10±0.20	0.52±0.15	0.86±0.14	0.65±0.23	0.65±0.11	0.80±0.14
LH-I	0.44±0.08	0.53±0.08[b]	0.81±0.33	0.72±0.23	1.45±0.51	0.30±0.07	0.52±0.16	0.70±0.29
Fold change evaluated by RT-PCT (Cont *vs* LH-S)	−2.0	−2.8	1.6	−1.0	−1.6	−1.9	−1.1	−1.3
Fold change evaluated by microarray (Cont *vs* LH-S)	−9.5	−1.6	1.3	−1.1	−1.1	−1.2	−2.4	−1.4

The expression level of each gene is normalized to that of the GAPDH gene (mean±SE, $n=6$, each in control and LH-S, $n=5$, each in LH-F and LH-I). The gene abbreviations are: LIMK-1, LIM domain kinase 1; HTR2A, 5-hydroxytryptamine (serotonin) receptor 2A; PGDS, prostaglandin D synthetase; IP3R, inositol-1,4,5-triphosphate receptor type 1; SNAP, synaptosomal-associated protein; SYN1, synuclein 1; bFGFR2, heparin-binding fibroblast growth factor receptor 2; Ca^{2+}-ATPase, plasma membrane Ca^{2+}-ATPase isoform 3.
[a]$P<0.05$ (control *vs* LH-S).
[b]$P<0.05$ (LH-S *vs* LH-I) by Mann–Whitney test (two-tailed).

partial recovery might be due to the low level of normal transcription and the large variation of expression values (supplementary Table S3). We therefore performed real-time RT-PCR to confirm the expression profile of *Limk1*, and detected a two-fold decrease in LH compared to control animals. This reduction was not recovered by antidepressant treatments (Table 3). *Limk1* is expressed in both fetal and adult nervous systems, and shows ubiquitous expression in the brain with the strongest expression in adult cerebral cortex.[37] Recently, *Limk1*-knockout mice were reported to show abnormalities in spine morphology and enhanced long-term potentiation, accompanied by alterations in fear response and spatial learning.[38] A test of depression-related behavioral parameters in these mice would be intriguing. Additional reports that depressive patients frequently manifest subcortical hyperintensity near frontal white matter ('myelin pallor' on histological examination)[39] suggest that LIMK1 may be involved in an as yet undetermined intercellular signaling pathway disrupted in depression, as LIMK1 is known to phosphorylate myelin basic proteins.[40]

Our criteria for selecting 'altered' transcripts in LH compared to control animals may have been conservative and inadvertently excluded many potential candidates. Decreased levels of brain-derived neurotrophic factor (BDNF) recoverable by antidepressant treatment have been reported in patients with depression.[41,42] Although we could not detect any significant difference in expression between control and LH-S animals, we found that expression of BDNF in the FC was increased in LH-I animals compared with LH-S and control animals (supplementary Table S3).

LH-associated Transcripts Specific to the HPC and Common to Both the FC and HPC

In contrast to the FC, most LH-associated genes in the HPC showed decreased expressions on the induction of LH (Table 2). Genes coding for receptors were downregulated in both regions, although there was no overlap between the two groups of receptors. This category included three olfactory receptor-like genes, *HGL-SL1* olfactory pseudogene, olfactory receptor-like protein (*SCRD-9*) and *HFV-FD1* olfactory receptor. Although these are thought to encode G protein-coupled receptors with seven transmembrane domains, the biological functions are unclear. Heparin-binding fibroblast growth factor receptor 2 (*Fgfr2*) genes were also downregulated in LH-S, but were unaffected by antidepressants (Table 2). We also found a reduction in the *N*-methyl-D-aspartate receptor 2A (NMDAR 2A) subunit gene in three of six LH-S animals. Fgfr2 reduces NMDAR 2A subunit mRNA levels via a receptor-mediated mechanism.[43] Chronic administration of antidepressants decreases the expression of NMDA receptor subunit genes and radioligand binding to the receptor.[42] This discrepancy warrants further investigation, to determine the role of this growth factor and the NMDA receptor genes in depression. All the LH-associated genes defined as involved in neurotransmission were also downregulated in this study (Table 2). The hippocampus is well known as a region of the brain that is highly susceptible to stress.[44,45] Recent studies have demonstrated that repeated stress causes shortening and debranching of dendrites in the CA3 region of the HPC and suppresses neurogenesis of granule neurons in the dentate gyrus.[45,46] In addition, chronic antidepressant treatment increases cell populations and neurogenesis in the rat hippocampus.[15] The extensive suppression of gene expression observed in our LH model may be related to phenotypic changes in the hippocampus produced by stress.

An unexpected finding was the scarcity of common transcripts between the two areas of brain. Of the LH-associated genes, only those coding for the 24-kDa mitochondrial NADH dehydrogenase and Dri27/ZnT4 (zinc transporter) were common to both the FC and HPC (Tables 1 and 2). However, the direction of change differed between the two regions. This selectivity was also seen in genes that were not affected by LH, but displayed a response to

Table 4 List of genes contributing to the first component in principal component analysis

Brain region[a]	*Eigenvalue*	*Gene name*[b]	Function[c]	*Fold change*	*Accession no*	Locus[d]
Frontal cortex	0.2197	Rapamycin and FKBP12 target-1 protein (rRAFT)	Stress response	1.1	U11681	5q36
	0.2194	F1-ATPase epsilon subunit	Metabolic enzyme	1.1	AI171844	20q13.3
	0.1965	Jagged2 precursor		1.3	U70050	14q32
	0.1929	24-kDa subunit of mitochondrial NADH dehydrog	Metabolic enzyme	1.4	M22756	18p11.31-p11.2
	0.1876	Bleomycin hydrolase	Metabolic enzyme	1.4	D87336	17q11.2
	0.1820	EST	Unknown	1.4	AA894234	—
	0.1760	Poly(ADP-ribose) polymerase	Stress response	1.6	U94340	1q41-q42
	0.1617	EST	Unknown	1.2	AI230632	—
	0.1531	Resection-induced TPI (rs11)	Others	1.4	AF007890	12p13
	0.1525	EST	Unknown	1.2	AF069782	—
Hippocampus	0.2114	HGL-SL1 olfactory receptor pseudogene		−2.0	AF091574	—
	0.2092	Proteasome RN3 subunit	Others	−1.5	L17127	1q21
	0.2019	24-kDa mitochondrial NADH dehydrogenase prec	Metabolic enzyme	−1.4	M22756	18p11.31-p11.2*
	0.1997	HFV-FD1 olfactory receptor		−2.5	AF091575	—
	0.1983	Soluble cytochrome b5	Metabolic enzyme	−1.5	AF007107	18q23*
	0.1865	2-Oxoglutarate carrier	Metabolic enzyme	−1.4	U84727	17p13.3
	0.1845	Grb14	Signal transduction	−1.4	AF076619	2q22-q24
	0.1626	EST	Unknown	−1.6	AA892353	—
	0.1606	GTP-binding protein (ral B)	Signal transduction	−2.0	L19699	2cen-q13
	0.1595	Rab3b	Signal transduction	−1.6	AA799389	1p32-p31*

[a]The 10 largest contributing genes to the first component in each region are listed.

[b]The genes in black indicate those up-regulated in LH animals compared to controls, while genes in red are down-regulated.

[c]The gene functions are color coded according to functional properties.

[d]*indicates that the chromosomal region shows genetic linkage to bipolar disorder.

treatment with fluoxetine, imipramine or both. In this case, from the three subsets (green, light blue and purple areas in Figure 4), five of 105 transcripts were common to both the FC and HPC (supplementary Tables S3 and S4). These findings may highlight region-specific molecular mechanisms involved in the etiology of LH. In human studies, decreased mitochondrial function was demonstrated in the basal ganglia of chronic schizophrenics,[47,48] and inhibition of mitochondrial respiratory complex I activity was reported as a cellular pathology of Parkinson's disease.[49,50] Evidence, including that of decreased ATP in frontal lobes detected in depressive patients,[51] has generated speculation about the role of mitochondrial dysfunction in depression.[52,53] NADH dehydrogenase is located on human chromosome 18 at p11.31–p11.2, a susceptibility region for affective disorder and schizophrenia.[3,54,55] These data suggest a possible link between mitochondrial NADH dehydrogenase and neuropsychiatric illnesses, including depression. The observed alteration in levels of a zinc transporter gene may tie in with recent reports that zinc exerts an antidepressant-like effect in the rodent forced swimming test,[56] and that patients with major depression demonstrate lower serum zinc levels.[57] This may imply perturbed zinc metabolism in depression, but the precise mechanisms are poorly understood.

Given that imipramine was more effective in improving LH behavior than fluoxetine, it may seem contradictory that a larger number of LH-associated transcripts showed a greater response to fluoxetine than to imipramine (Figure 4). Imipramine-responsive transcripts are likely to play a more pivotal role in behavioral recovery.

We also applied parametric statistical analysis (Student's *t*-test) to our array data. The total number of transcripts detected was slightly lower in both the FC and HPC compared to numbers detected by nonparametric tests (3 and 12 fewer in the FC and HPC, respectively). Between the two statistical methods, 10 genes in the FC (32%) and three genes in the HPC (8%) were different (supplementary Tables S7 and S8).

PCA on Altered Transcripts

PCA is a mathematical technique that exploits essential factors to define patterns in data, reducing the effective dimensionality of gene-expression space without significant loss of information.[58] This technique can be applied to both genes and experiments as a means of classification. When genes are variables, the analysis creates a set of principal gene components highlighting features of genes that best explain their experimental responses. We used the LH-associated transcripts from the FC and HPC separately as variables in PCA, to allow for better visualization of the region-specific data sets. Figures 5a and b indicate the eigenvalue distributions on the components in the FC and HPC samples, respectively. The sudden drop in eigenvalues with increasing component number suggests that it is possible to select a small number of components modeling the gene-expression differences among rat groups. We chose a three-component model for both the FC and HPC, which

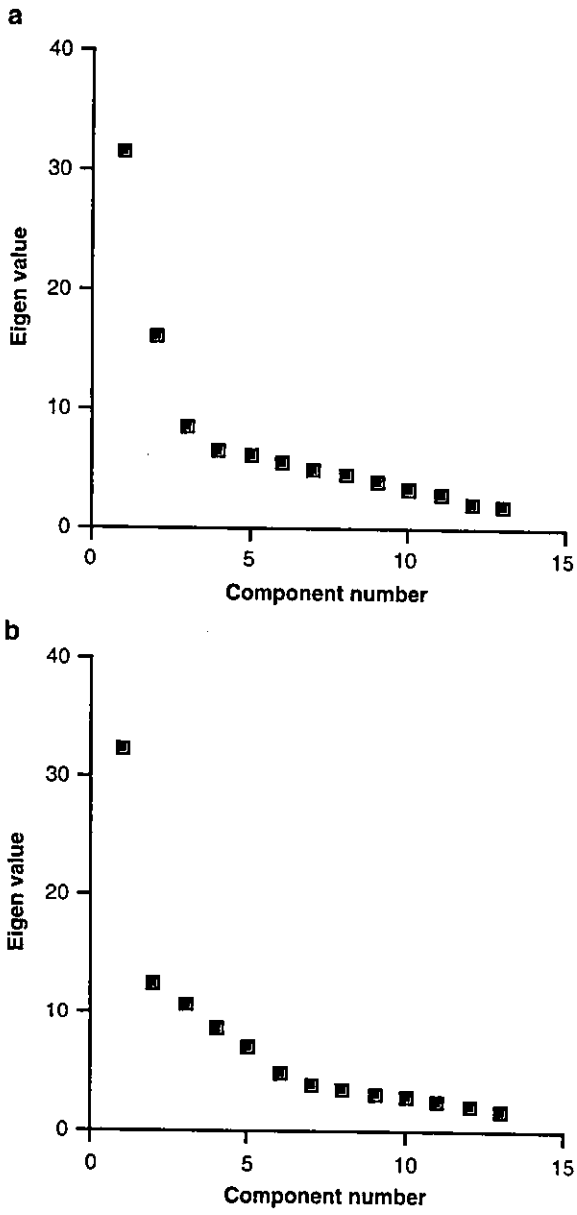

Figure 5 Component number *vs* eigenvalue in the FC (a) and the HPC (b).

explained 56% of the total variability seen in the 34 transcripts from the FC and the 48 transcripts from the HPC. The extracted dimensions represent the linear organization of data from independent systems. Each animal was plotted in a three-dimensional subspace (Figures 6a and b). The first components retain the maximal amount of correlated information (ie coordinated activity of genes) restricting the uncorrelated information to higher order components. In the FC, the first component (axis) showed good separation for the four experimental groups (control, LH-S, LH-F and LH-I), placing the antidepressant-treated groups between the control and LH-S groups. Table 4 shows

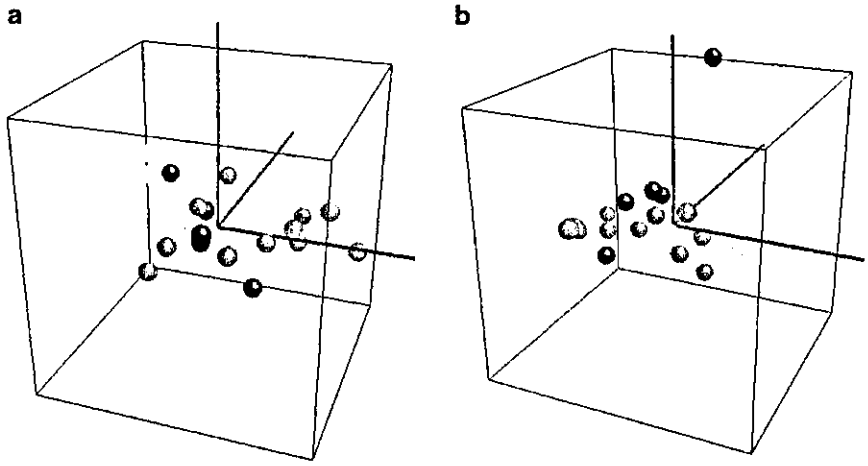

Figure 6 All animals were plotted with respect to the first (blue), second (green) and third (red) principal components. PCA was performed on transcripts listed in Table 1 (frontal cortex) (a) and Table 2 (hippocampus) (b). Yellow-colored dots represent control animals, green LH-S rats, red LH-F and blue LH-I.

transcripts from the FC that were arranged according to the magnitude of correlation with the first component (PC1) (those to the second and third components are shown in supplementary Table S5). They comprised genes for metabolic enzymes and stress responses. All genes listed in PC1 were increased in LH animals compared to controls. Among the genes coding for metabolic enzymes, the F1-ATPase epsilon subunit and 24-kDa subunit of mitochondrial NADH dehydrogenase are both localized to the mitochondria, further suggesting an important role for mitochondrial function in depression.[53] The second and third components in the FC did not further subdivide the experimental groups (supplementary figure S1). However, based on the data including the second component of PCA in the FC (supplementary Table S5), we speculate that genes responsible for neuronal growth and structure including *Limk1* could be key factors in depression/stress-related pathology. In downstream pathways, alterations of these genes may affect recruitment and maintenance of multiple neurotransmitter receptors.[38] In support of this theory, structural abnormalities have recently been reported in the frontal lobe white matter of depressive patients.[59]

According to PC1 in the HPC, LH-S rats were separated from controls, with the drug-treated animals being more closely localized than the LH-S group (Figure 6b). This highlights the limited efficacy of TCA and SSRI antidepressants against dysregulated genes in the HPC, although these drugs reversed the behavioral phenotype of LH rats. The genes contributing to PC1 from the HPC would therefore represent suitable targets for future novel antidepressants. PC1 in the HPC contained genes that were downregulated in LH rats and were clustered as metabolic enzyme and signal transduction (Table 4). The second component in the HPC detected eight genes that correlated with responsiveness to fluoxetine (supplementary Table S6 and Figure S2). One animal was separated from the others along the third component (Figure 6b). The reason for this was not clear. The animal may have suffered from highly aberrant expression of metabolic enzyme- and signal transduction-related genes and other transcripts (Table 4). Finally, the fact that the 24-kDa subunit of mitochondrial NADH dehydrogenase was extracted from both the FC and HPC with high eigenvalues is intriguing, suggesting that this gene may represent an indicator of depressive state. Moreover, the two genes, for soluble cytochrome b5 on 18q23 and Rab3 on 1p32-p31, mapped to reported linkage regions for bipolar disorder.[60]

MATERIALS AND METHODS

Animals and Experimental Design

Male Sprague–Dawley rats, 5–6-week old, weighing 150–180 g, were purchased from SLC (Shizuoka, Japan). They were housed three per cage under standard laboratory conditions, with access to food and water *ad libitum*. After 1 week of handling, the animals were used for experiments. Antidepressants, imipramine and fluoxetine were purchased from SIGMA (St Louis, MO, USA).

On day 1, animals were subjected to IS pretreatment (0.5 mA, 10 s duration, shock interval 1–5 s, 160 trials) in a Plexiglas chamber ($460\,W \times 200\,D \times 180\,H\,mm^3$, Muromachi, Tokyo, Japan). Two rats were processed simultaneously using two chambers. Control rats were placed for 1 h in the same chambers, but no shocks were administered.

On day 2, to evaluate escape and avoidance performance, avoidance training was initiated 24 h after IS pretreatment in the same chamber, which had been converted to a two-way shuttle box by dividing it into two equal-sized compartments using an aluminum partition. The partition included a square gate ($6 \times 6\,cm^2$), through which animals

could move into the adjacent compartment. Animals were subjected to 15 avoidance trials with 30 s intervals. In each trial, 0.5 mA of current was applied via the grid floor during the first 3 s. If an animal crossed the gate and moved to the other compartment within this period (escape response), the shock was terminated. Failures in escape response were counted as a measure of LH. Animals were defined as suffering from LH when they showed eight or more failures during a session. Control rats and a proportion of LH rats (LH-S) were administered saline once a day for three consecutive days, starting on day 2 after the avoidance trial. The remaining LH animals were treated using either imipramine (25 mg/kg, i.p.) (LH-I) or fluoxetine (5 mg/kg, i.p.) (LH-F).

On day 5, 30 min after the final injection, rats were tested for escape ability under escapable shock conditions. Among LH-I and LH-F rats, only those animals that showed a >50% successful escape response (ie <8 failures in the 15 trials; all LH-I rats fulfilled this criterion) were used for gene-expression analysis.

The present protocol was approved by the RIKEN animal committee.

RNA Preparation and Array Hybridization

Animals were killed on day 6, 24 h after the final electroshock procedure. Total RNA was extracted from the FC (defined as the region anterior to the genu of corpus callosum, with the ventral olfactory structures depleted) and HPC using an acid guanidium thiocyanate/phenol chloroform extraction method (ISOGEN, NIPPON Gene, Toyama, Japan). Double-stranded cDNA was synthesized from 10 μg of total RNA using the SuperScript Choice System (Invitrogen, Carlsbad, CA, USA) and a primer containing poly (dT) and a T7 RNA polymerase promoter sequences (Geneset, La Jolla, CA, USA). Biotin-labeled cRNA was synthesized from cDNA using an Enzo BioArray High Yield RNA Transcript Labeling kit (Enzo Diagnostics, Santa Clara, CA, USA). After fragmentation, 15 μg of cRNA was hybridized for 16 h at 45°C to a U34A chip (Affymetrix, Santa Clara, CA, USA) that contained probes for over 8000 transcripts, including all known rat genes (http://www.affymetrix.com/products/netaffx.html). After hybridization, arrays were washed automatically and stained with streptavidin–phycoerythrin using the fluidics system. Chips were scanned using a GeneArray scanner (Affymetrix).

Data Analysis

All samples were scaled to a target intensity of 100. Data analysis was performed using Microarray Suite 4.0 (Affymetrix) and GeneSpring 4.1 (Silicon Genetics, Redwood, CA, USA). Transcripts with an 'average difference' (as described in the GeneChip software) of <20 for each probe set in controls were excluded (5157 genes were selected out of 8799). From the remaining transcripts, those that gave an 'absolute call' of 'P' (present) for at least four samples in six for control and LH-S rats were considered for further analysis (3541 genes were chosen).

Before statistical analysis, each transcript was converted into a logarithmic value and normalized to itself by making a synthetic positive control and dividing all measurements by this control, assuming that the control value was at least 0.01. A synthetic control is the median of the transcript's expression values over all the samples. Two-group comparison was conducted for each transcript by a Mann–Whitney test between: (i) control and LH-S groups, (ii) LH-S and LH-F groups and (iii) LH-S and LH-I groups. The results are illustrated as a Venn diagram (Figure 2), where the overlapping areas representing (i)-, (ii)- and (iii)-type comparisons include transcripts that were selected solely using Mann–Whitney test ($P<0.05$) and Student's t-test ($P<0.05$). Transcripts in non-overlapping areas represent genes whose expressional changes between the two states displayed ⩾1.4-fold difference, in addition to fulfilling the P-value criteria. We also evaluated these selected transcripts by implementing the Benjamin and Hochbery False Discovery Rate program included in the GeneSpring software package. The differential gene expressions revealed by the microarray chips were examined using real-time quantitative reverse transcription (RT)-PCR, with a LightCycler and RNA Amplification kit SYBR Green I (Roche, Basel, Swizerland).

Principal Component Analysis

PCA is a statistical method for determining the coordinate transformation that explains the maximum amount of variance for the data.[25] PCA finds the principal components and each component is mutually orthogonal. To calculate the transformation, data were first normalized with reference to each gene, and then sample mean and sample variance–covariance matrix S were calculated from estimates of the mean and variance–covariance matrix. From this symmetrical matrix S, an orthogonal basis was calculated by determining eigenvalues and eigenvectors according to the equation:

$$|S - \lambda_i E| = 0 \quad (1)$$

where E is an identity matrix and λ_i is the ith eigenvalue. i takes the value (1 to n), and n is the total number of genes.

$$SA_i = \lambda_i A_i \quad (2)$$

where A_i is the ith eigenvector (n-dimension). The first and ith principal components were calculated as follows: $PC1 = \sum A_1 D$, $PCi = \sum A_i D$, where A_1 is the eigenvector with maximum eigenvalue, and D is the n-dimensional data vector. The proportion of the ith component was the ith eigenvalue divided by the total sum of all eigenvalues. Animals were projected into the first three-dimensional component space.[62,63]

CONCLUSION

In an effort to better understand the molecular and genetic bases underlying the pathophysiology of depressive disorder and to improve the rationale for the design of antidepressant drugs, we have performed DNA microarray analysis using an animal model of depression. Using Affymetrix GeneChip arrays, we have screened over 8000 rat genes and