Changes in Gene Expression in the Rat Hippocampus after Focal Cerebral Ischemia

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Objective: The rat middle cerebral artery thread-occlusion model has been widely used to investigate the pathophysiological mechanisms of stroke and to develop therapeutic treatment. This study was conducted to analyze energy metabolism, apoptotic signal pathways, and genetic changes in the hippocampus of the ischemic rat brain.

Methods: Focal transient cerebral ischemia was induced by obstructing the middle cerebral artery for two hours. After 24 hours, the induction of ischemia was confirmed by the measurement of infarct size using 2,3,5-triphenyltetrazolium chloride staining. A cDNA microarray assay was performed after isolating the hippocampus, and was used to examine changes in genetic expression patterns.

Results: According to the cDNA microarray analysis, a total of 1,882 and 2,237 genes showed more than a 2-fold increase and more than a 2-fold decrease, respectively. When the genes were classified according to signal pathways, genes related to oxidative phosphorylation were found most frequently. There are several apoptotic genes that are known to be expressed during ischemic brain damage, including Akt2 and Tnfrsf1a. In this study, the expression of these genes was observed to increase by more than 2-fold. As energy metabolism related genes grew, ischemic brain damage was affected, and the expression of important genes related to apoptosis was increased/decreased.

Conclusion: Our analysis revealed a significant change in the expression of energy metabolism related genes (Atp6v0d1, Atp5g2, etc.) in the hippocampus of the ischemic rat brain. Based on this data, we feel these genes have the potential to be target genes used for the development of therapeutic agents for ischemic stroke.

Key Words: Apoptosis · Energy metabolism · Focal cerebral ischemia · Gene expression · Hippocampus · Oxidative phosphorylation.
mentally controlled room at a temperature of 23±2°C, relatively humidity of 55±5%, and a 12-hr light/dark cycle. Food and water were available ad libitum. Experimental procedures were carried out according to the animal care guidelines of the National Institute for Health Guide and the Korean Academic of Medical Sciences.

Ischemic animal model
Male SD rats weighing 300±10 g were used. Focal cerebral ischemia was produced by a modification of the monofilament method as described by Longa et al. Briefly, rats were anesthetized with 5% isoflurane in 25% O₂/75% N₂O for induction, and then maintained throughout the operation with 1.5-2% isoflurane delivered via nasal mask. Rectal temperature was maintained at 37-38°C throughout the surgical procedure with a heating plate. A cervical parasagittal incision was made at the left common carotid artery (CCA) region. The distal left external carotid artery (ECA) was ligated, transected, and rotated 180°. The proximal CCA and distal internal carotid artery (ICA) were clamped transiently with aneurysm clips. After a longitudinal incision of the ECA, a 25-mm nylon monofilament coated with silicon (0.3 mm in diameter) was inserted into the ECA and advanced into the lumen of the ICA. The clamp on the distal ICA was released, and the filament was advanced 20 mm from the CCA bifurcation until the origin of the MCA was blocked. The filament was then tied at the ECA stump and proximal ICA, and the clamp on the CCA was released. After 3 hours of occlusion, the proximal CCA was clamped transiently with an aneurysm clip. The filament was withdrawn from the ICA, the ECA stump was tied to prevent bleeding, and the clamp on the CCA was then released.

Regional cerebral blood flow
The rat was mounted in the prone position on a dual small animal stereotaxic instrument (David Kopf Instruments, Los Angeles, CA, USA). After a cranial midline incision, a 1-mm burr hole was made with a microdrill at both sides, 2-mm-posterior and 5-mm-lateral to the bregma. The rat was then placed in the supine position. A laser Doppler probe was placed on the burr hole under the rat skull, almost contacting the dura mater of the brain surface avoiding the large vessels. The parietal cortical perfusion in the territory of MCA was measured. The laser Doppler probe was connected to a BLF21D laser Doppler flowmeter (Transonic systems Inc., Ithaca, NY, USA), and the values were obtained from 10 min before the ischemic event until 15 min after reperfusion. The changes in rCBF are expressed as the percentage of the baseline values. The signals were digitalized and sent to a computer for recording, storage and analysis.

Measurement of infarct size
All animals were sacrificed 24 hours after reperfusion. The brains were rapidly dissected and the forebrains were cut into six coronal sections 2 mm thick using a rat brain matrix (ASI Instruments Inc., MI, USA). The sections were stained by incubating them in a solution of 2% 2,3,5-triphenyltetrazolium chloride (TTC) at 37°C for 30 min and then photographed. The photographic images were digitalized and used to determine the volume of each infarct and the volume of each hemisphere for each slice using a computer-assisted image analysis program (Optimas 6.1, Media Cybernetics, Silver Springs, MD, USA). The infarct volume of each slice was calculated by subtracting the normal ipsilateral volume from that of the contralateral hemisphere to reduce errors due to cerebral edema. Infarct volume is presented as the percentage of the infarct volume to the volume of the contralateral hemisphere.

TUNEL staining
To visualize the apoptotic cells, TUNEL staining was performed using an In Situ Cell Death Detection Kit (Roche) according to the manufacturer’s protocol. Briefly, after fixation in ethanol-acetic acid (2:1), the sections were incubated with proteinase K (100 μg/mL) and permeabilized with 0.5% Triton X-100. The sections were then incubated in the TUNEL reaction mixture, and visualized using a Converter-POD with 3,3′-diaminobenzidine.

RNA extraction
Total RNA was extracted using the Mini RNA isolation II™ kit (Zymo Research, USA). In brief, 600 μL of ZR RNA buffer was added to isolated hippocampi. The lysate was transferred to a Zymo-Spin III Column. The column was placed into a 2 mL collection tube, and spun at full speed in a micro-centrifuge for 1 min. The collection tube was emptied and 350 μL of RNA-wash buffer was added to the Zymo-Spin III Column. It was then centrifuged again at full speed for 1 min. The column was transferred to a new 1.5 mL tube, 50μL RNase-free water was added directly to the membrane of the Zymo-Spin III column, and it was then spun briefly to elute RNA. The eluted RNA was immediately stored at -70°C until further use. Quality and quantity were measured using a ND-1000 spectrophotometer (Nanodrop Technology Inc., USA) at absorbances of 260 and 280 nm.

Agilent whole rat genome microarray analysis
The Agilent Whole Rat Genome Oligo Microarray contains 4,000 60-mer oligonucleotide probes representing 41,000 unique genes and transcripts. Amplification and labeling of 500 ng of total RNA was performed according to the manufacturer’s protocol using Cy5 for MCAo RNA and Cy3 for the control RNA (Stratagene UHR). Hybridization was performed for 17 hrs at 65°C and the arrays were then scanned on an Agilent DNA microarray scanner. Images were analyzed and data was extracted using Agilent Feature Extraction Software A.7.5.1. Low normalization was performed for within array normalization between the two channels, and a linear scaling (geometric mean of each channel signal is set to a value of 1,000) was performed for between array normalization. Functional analysis of
the expression of ATPase, H⁺ transporting, V0 subunit D isoform 1 (Atp6v0d1), cytochrome c oxidase subunit IV isoform 1 (Cox4i1), ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (Atp5g2), ATPase, H⁺ transporting, lysosomal V0 subunit a isoform 1 (Atp6v0a1), cytochrome c-1 (Cyc1), NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa (Ndufv1), ATPase, H⁺ transporting, V0 subunit e (Atp6v0e1), ATP synthase, H⁺ transporting, mitochondrial

**RESULTS**

Changes of regional cerebral blood flow and infarct volume by MCAo

In order to confirm the ischemia model, we measured rCBF and infarct volume. MCAo immediately reduced the rCBF value to approximately 50% of the baseline level, indicating focal cerebral ischemia (data not shown). After 2 hours of occlusion, this reduction gradually recovered during reperfusion. The rCBF measurements showed similar patterns in all groups. TTC is a sensitive histochemical indicator of mitochondrial respiratory enzyme function. Brain lesions identified by TTC staining represent tissue whose mitochondrial function and oxidative respiratory enzyme systems have been irreversibly damaged[2]. Fig. 1 shows typical photographs of brain slices. The infarction volumes were assessed 24 hours post-ischemia. The MCAo group showed an average infarct volume of 45.3±0.7% (data not shown).

MCAo-induced apoptosis in the hippocampus

A TUNEL assay was performed to investigate whether cell death due to brain ischemia following MCAo was caused by apoptosis. As shown in Fig. 2, TUNEL-positive cells stained dark brown. The TUNEL assay showed that DNA strand breaks did occur, indicating the induction of apoptosis by MCAo in the hippocampal region of rats.

Analysis of microarray data

The expression of ischemia-related genes was determined by comparing MCAo-induced expression to the expression in a sham-operation group. A cDNA microarray that contained duplicate cDNA probes from 44K rat clones was used. To normalize the intensity ratio of each gene expression pattern, the global M method was used. First, the primary data were normalized by the total spots of intensity between the two groups, and then normalized by the intensity ratio of reference genes, such as house-keeping genes in both groups. Finally, the expression ratio of the MCAo group to the sham group was converted to the log2 ratio of each gene, which was represented by the scatter plot (Fig. 3).

After normalizing the data, a cut-off value of global M was set at 2 or -2. More than 44,000 genes on the arrays were analyzed after 2 hours of occlusion and 24 hours of reperfusion from three stroke and three control mice. A total of 1,882 genes were upregulated and 2337 were downregulated in the hippocampi of rats after MCAo. These genes were then divided into categories according to signaling pathways (http://www.genome.jp/kegg/pathway.html).

Of the genes whose expression changed, the majority were oxidative phosphorylation related genes. As shown in Table 1, the expression of ATPase, H⁺ transporting, V0 subunit D isoform 1 (Atp6v0d1), cytochrome c oxidase subunit IV isoform 1 (Cox4i1), ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (Atp5g2), ATPase, H⁺ transporting, lysosomal V0 subunit a isoform 1 (Atp6v0a1), cytochrome c-1 (Cyc1), NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa (Ndufv1), ATPase, H⁺ transporting, V0 subunit e (Atp6v0e1), ATP synthase, H⁺ transporting, mitochondrial
F0 complex, subunit c, isoform 3 (Atp5g3), ATPase, H+ transporting, V0 subunit C (Atp6v0c), and NADH dehydrogenase (ubiquinone) flavoprotein 2 (Ndufv2) increased more than 2-fold following brain ischemia due to MCAo. On the other hand, the expression of NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (Ndufa1), cytochrome c oxidase subunit VIIb (Cox7b), NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (Ndufb2), NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (Ndufa7), cytochrome C oxidase subunit Vb (Cox5b), ubiquinol-cytochrome C reductase core protein II (Uqcr2), and Cytochrome c oxidase subunit VIII-H (heart/muscle) (Cox8h) decreased by more than 2-fold following brain ischemia due to MCAo (Table 2).

In addition, we looked at the changes in apoptosis-related gene expression in ischemic stroke. Table 3 shows the apoptosis-related genes that increased by more than 2-fold following brain ischemia due to MCAo. The expression of murine thymoma viral (v-akt), oncogene homolog 2 (Akt2), phosphatidylinositol 3-kinase, regulatory subunit, polypeptide (Pik3r2), tumor necrosis factor receptor superfamily, member 1a (Tnfrsf1a), protein phosphatase 2 catalytic subunit, beta isoform (Ppp3cb), apoptosis stimulating of p53 protein 1 (Ppp1r13b), inhibitor of kappa B kinase beta (Ikbkb), and protein kinase, cAMP-dependent, regulatory, type 2, alpha (Prkar2a) increased more than 2-fold. On the other hand, the expression of type II cAMP-dependent protein kinase regulatory subunit (Prkar2b), ataxia telangiectasia mutated homolog (Atm), nuclear factor kappa B (Nfkb1), and conserved helix-loop-helix ubiquitous kinase (Chuk) decreased by more than 2-fold (Table 4).

**DISCUSSION**

In the present study, gene expression profiles of the hippocampus after 2 hours of MCAo followed by 24 hours of reperfusion were examined using Agilent DNA microarray techniques. Ischemic damage by MCAo was confirmed using TTC staining. The expression ratio between two groups was converted to log2 ratio.

### Table 1. List of oxidative phosphorylation related genes up-regulated by MCAo

<table>
<thead>
<tr>
<th>Genbank</th>
<th>Gene symbol</th>
<th>Description</th>
<th>Normalized</th>
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</thead>
<tbody>
<tr>
<td>NM_001011927</td>
<td>Atp6v0d1</td>
<td>ATPase, H+ transporting, V0 subunit D isoform 1</td>
<td>3.0534</td>
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<tr>
<td>NM_017202</td>
<td>Cox4i1</td>
<td>Cytochrome c oxidase subunit IV isoform 1</td>
<td>2.8869</td>
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<tr>
<td>NM_133556</td>
<td>Atp5g2</td>
<td>ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1</td>
<td>2.7510</td>
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<tr>
<td>NM_031604</td>
<td>Atp6v0a1</td>
<td>ATPase, H+ transporting, lysosomal V0 subunit a isoform 1</td>
<td>2.6920</td>
</tr>
<tr>
<td>XM_216944</td>
<td>Cyc1</td>
<td>Cytochrome c-1</td>
<td>2.5239</td>
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<tr>
<td>NM_001006972</td>
<td>Ndufv1</td>
<td>NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa</td>
<td>2.4245</td>
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<tr>
<td>NM_053578</td>
<td>Atp6v0e1</td>
<td>ATPase, H+ transporting, V0 subunit e</td>
<td>2.4015</td>
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<tr>
<td>NM_053756</td>
<td>Atp5g3</td>
<td>ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c, isoform 3</td>
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<tr>
<td>NM_130823</td>
<td>Atp6v0c</td>
<td>ATPase, H+ transporting, V0 subunit C</td>
<td>2.1215</td>
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<tr>
<td>NM_031064</td>
<td>Ndufv2</td>
<td>NADH dehydrogenase (ubiquinone) flavoprotein 2</td>
<td>2.0527</td>
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</table>

**MCAo**: middle cerebral artery thread-occlusion

### Table 2. List of oxidative phosphorylation related genes down-regulated by MCAo

<table>
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<tr>
<th>Genbank</th>
<th>Gene symbol</th>
<th>Product</th>
<th>Normalized</th>
</tr>
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<tr>
<td>XM_343760</td>
<td>Ndufa1</td>
<td>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1</td>
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<tr>
<td>NM_182819</td>
<td>Cox7b</td>
<td>Cytochrome c oxidase subunit VIIb</td>
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<tr>
<td>XM_342664</td>
<td>Ndufb2</td>
<td>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2</td>
<td>0.4199</td>
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<tr>
<td>XM_216859</td>
<td>Ndufa7</td>
<td>NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7</td>
<td>0.4027</td>
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<tr>
<td>NM_053586</td>
<td>Cox8b</td>
<td>Cytochrome c oxidase subunit Vb</td>
<td>0.3818</td>
</tr>
<tr>
<td>NM_001006970</td>
<td>Uqcr2</td>
<td>Ubiquinol-cytochrome c reductase core protein II</td>
<td>0.3694</td>
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<tr>
<td>NM_012786</td>
<td>Cox8h</td>
<td>Cytochrome c oxidase subunit VIII-H (heart/muscle)</td>
<td>0.1382</td>
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</table>

**MCAo**: middle cerebral artery thread-occlusion

![Scattered plot of the normalization results by global M method in comparison of sham group versus MCAo group. The primary data were normalized by the total the intensity ratio of reference genes such as housekeeping genes in control and treatment groups. The expression ratio between two groups was converted to log2 ratio.](image)
staining and the TUNEL assay. Within the large-scale temporal gene expression profile of the rat hippocampus that was obtained, we found that 1,882 genes were upregulated and 2,337 genes were downregulated. Among the very large number of genes whose expression changed, we focused on the genes related to oxidative phosphorylation and apoptosis.

The brain is almost exclusively dependent on a continuous flow of glucose and oxygen for energy production through oxidative phosphorylation because it lacks stores of energy. Damage from oxygen deprivation occurs in minutes. The first consequence of CBF reduction is the depletion of substrates, particularly oxygen and glucose. This causes an accumulation of lactate via anaerobic glycolysis. Acidosis may enhance free radical formation, interfering with intracellular protein synthesis and worsening ischemic brain injury. However, the mechanisms of the deleterious effects of acidosis are still unknown. Energy failure leads to the perturbation of the Na⁺/K⁺-ATPase and Ca²⁺/H⁺-ATPase pumps. In addition, the flow of the Na⁺-Ca²⁺ transporter is reversed. Subsequent ion dyshomeostasis (elevation of intracellular Na⁺, Ca²⁺, and Cl⁻ and elevation of extracellular K⁺) causes cytotoxic edema and leads to events triggered by excess intracellular Ca²⁺. In relation to oxidative phosphorylation, we found that 10 genes were upregulated while 7 were downregulated. Specifically, genes encoding ATPase, including Atp6v0d1, Atp6v0a1, Atp6v0e1, and Atp6v0c, were upregulated, whereas genes encoding NADH dehydrogenase, including Ndufa1, Ndufb2, and Ndufa7, were downregulated after transient focal cerebral ischemia in the rat hippocampus.

In the pathophysiology of acute ischemic stroke, cell death is in part due to the apoptotic process. Mitochondria, important source of ROS, is impaired by free radical-mediated disruption of the inner mitochondrial membrane and the oxidation of proteins that mediate electron transport, H⁺ extrusion, and ATP production. The mitochondrial membrane becomes leaky, in part due to the formation of a mitochondrial permeability transition pore, which promotes mitochondrial swelling, the cessation of ATP production, and an oxygen free-radical burst. As a result, cytochrome C is released from the mitochondria and this provides a trigger for apoptosis. Knowing this, we decided to also investigate changes in the expression of apoptosis related genes. Among the apoptosis related genes, we found that 7, including Akt2 and Tnfrsf1a, were upregulated, while 4, including Nlk1b1, were downregulated after transient focal cerebral ischemia in the rat hippocampus.

Following ischemia, caspase activation occurs in response to pro-apoptotic signals such as the downregulation of Bcl-2 and the upregulation of Bax/Bid and the Death receptor family. It has been shown that caspases 1, 3, 8, and 9 are involved in cerebral ischemia. However, in this study, the expression of these critical genes, including caspase, Bcl-2, and Bax, remained stable after ischemia. As the time of ischemic time was too short, these down-streaming genes of apoptosis were not demonstrated in this study.

Recently, some studies have reported gene expression profiles in the rat hippocampus after MCAo. Sun et al. found modulation of signal transducers and activators of transcription (STAT) factor pathways in the rat hippocampus after middle cerebral artery occlusion. The study suggested that the expression of STAT2, 5a, 5b, 6 and the suppressor of cytokine signaling 4 was increased by ischemia. They suggested that this may be a compensatory response by the brain and may play a protective role for damaged brain tissue. Mitsios et al. demonstrated a significant difference in the number of genes affected and the time-course of expression between the human and rat brain. The total number of deregulated genes in the rat was 335 versus 126 in the human. Of the 393 overlapping genes between the two array sets, 184 changed only in the rat, 36 in the human, and 41 were deregulated in both. Interestingly, the degree of change
was much higher in the human. The expression of novel genes, including p21-activated kinase 1 (PAK1), matrix metalloproteinase 11 (MMP11), and integrase interactor 1, was further analyzed using RT-PCR, Western blotting, and immunohistochemistry. Strong neuronal staining was seen for PAK1 and MMP11. To the best of our knowledge, there has not been a previous study that analyzed the expression of genes involved with oxidative phosphorylation in the rat hippocampus after transient focal cerebral ischemia.

As the rat genome contains approximately 30,000 genes\(^{20}\), the present analysis of 44,000 genes covers the entire genome. The successful identification of many novel ischemia-related genes suggests that performing a similar study using microarrays with a complete set of genes would be even more valuable. While this study focused only on those genes whose expression levels changed by more than 2.3-fold in terms of their hybridization signals, there might have been other genes whose expression was severely altered at the single cell level but were excluded by the criteria of the current study. Therefore, many other genes could be considered as candidate genes based on their physiological relevance in the post-ischemic brain.

**CONCLUSION**

Our analysis revealed a significant change in the expression of energy metabolism related genes (Atp6v0d1, Atp5g2, etc.) in the hippocampus of the ischemic rat brain. Based on this data, we believe that these genes have the potential to be target genes used for the development of therapeutic agents for ischemic stroke.

**References**