

[S-6]

Mechanisms of 5-azacytidine-induced damage and repair process in the fetal brain

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The fetal central nervous system (CNS) is sensitive to diverse environmental factors, such as alcohol, heavy metals, irradiation, mycotoxins, neurotransmitters, and DNA damage, because a large number of processes occur during an extended period of development. Fetal neural damage is an important issue affecting the completion of normal CNS development. As many concepts about the brain development have been recently revealed, it is necessary to compare the mechanism of developmental abnormalities induced by extrinsic factors with the normal brain development.

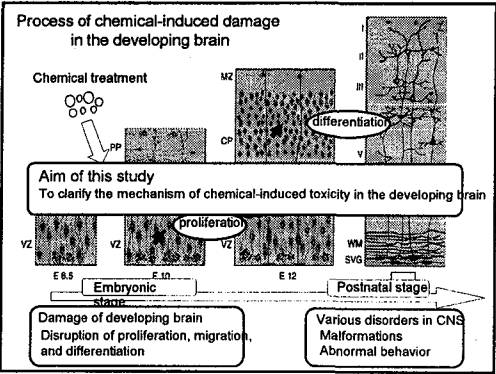
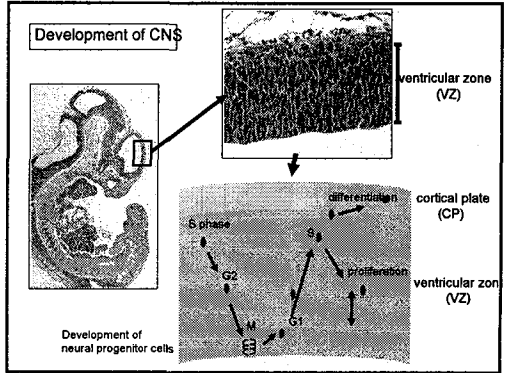
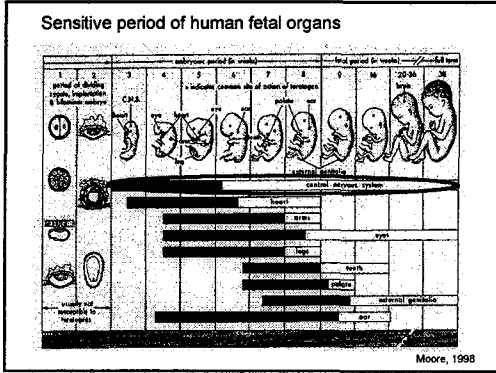
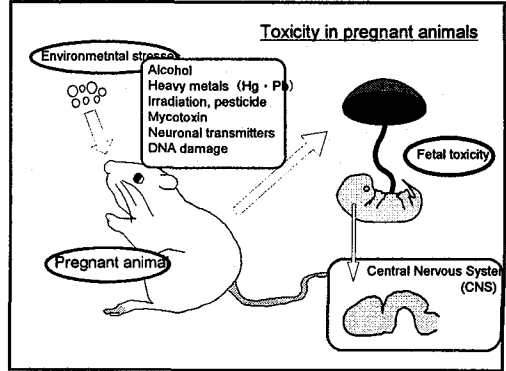
To clarify the mechanism of fetal CNS damage, we used one experimental model in which 5-azacytidine (5AzC), a DNA damaging and demethylating agent, was injected to the dams of rodents to damage the fetal brain. 5AzC induced cell death (apoptosis) and cell cycle arrest in the fetal brain, and it lead to microencephaly in the neonatal brain. We investigated the mechanism of apoptosis and cell cycle arrest in the neural progenitor cells in detail, and demonstrated that various cell cycle regulators were changed in response to DNA damage. p53, the guardian of genome, played a main role in these processes. Further, using DNA microarray analysis, the signal cascades of cell cycle regulation were clearly shown. Our results indicate that neural progenitor cells have the potential to repair the DNA damages via cell cycle arrest and to exclude highly affected cells through the apoptotic process. If the stimulus and subsequent DNA damage are high, brain development proceeds abnormally and results in malformation in the neonatal brain.

Although the mechanisms of fetal brain injury and features of brain malformation after birth have been well studied, the process between those stages is largely unknown. We hypothesized that the fetal CNS has the ability to repair itself post-injuring, and investigated the repair process after 5AzC-induced damage. We found that the damages were repaired by 60 h after the treatment and developmental processes continued. During the repair process, amoeboid microglial cells infiltrated in the brain tissue, some of which ingested apoptotic cells. The expressions of genes categorized to glial cells,

inflammation, extracellular matrix, glycolysis, and neurogenesis were upregulated in the DNA microarray analysis. We show here that the developing brain has a capacity to repair the damage induced by the extrinsic stresses, including changing the expression of numerous genes and the induction of microglia to aid the repair process.

Mechanisms of 5-Azacytidine-induced damage and Repair Process in the Fetal Brain

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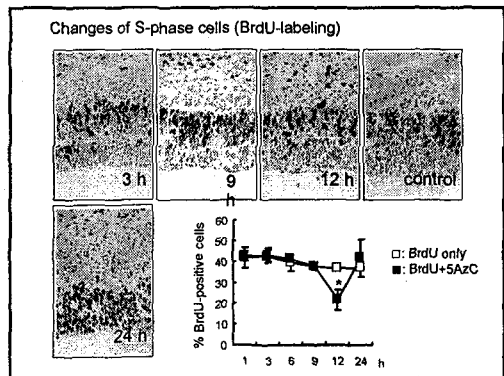
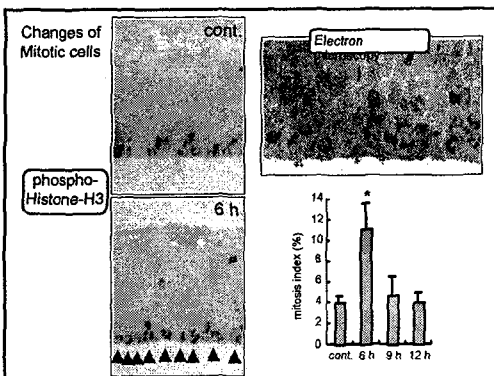
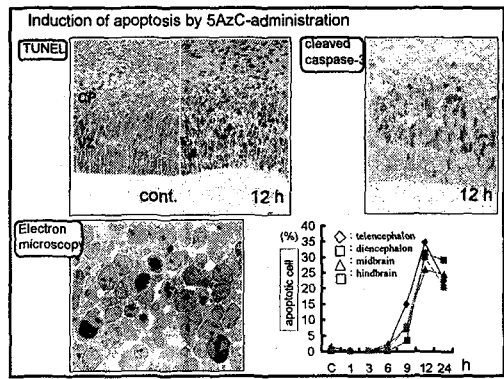
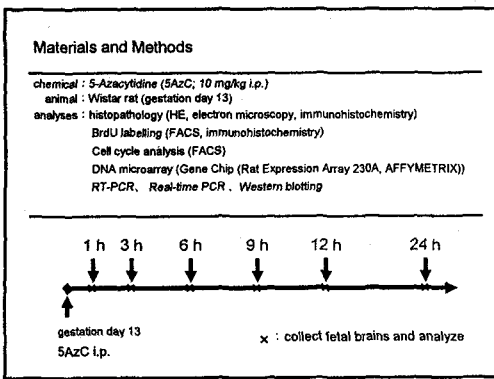
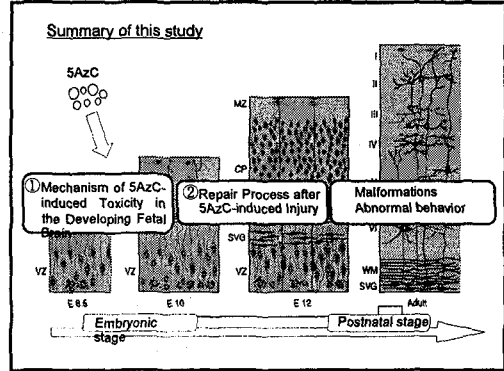
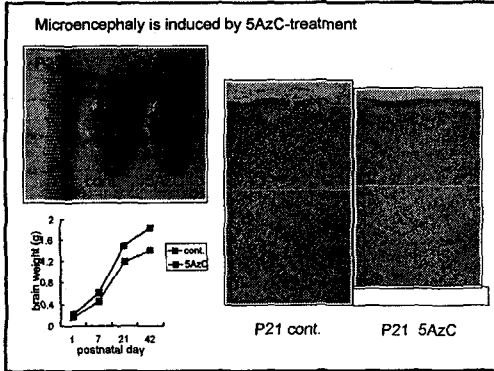


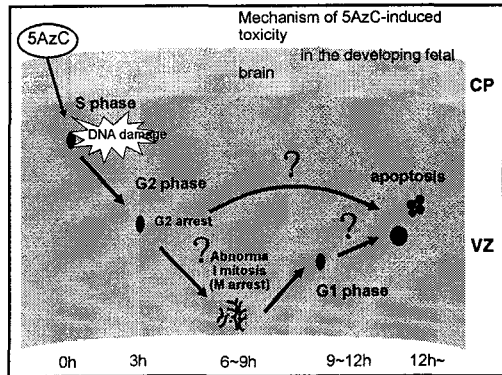
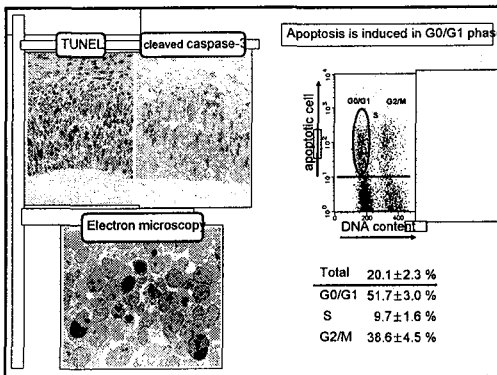
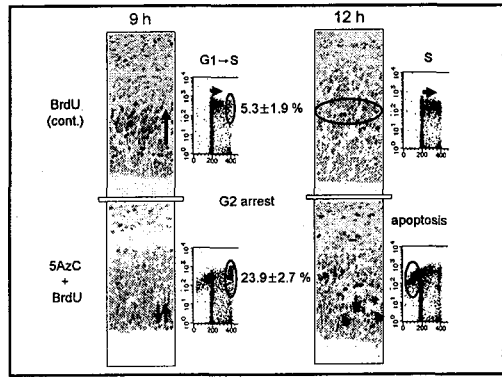
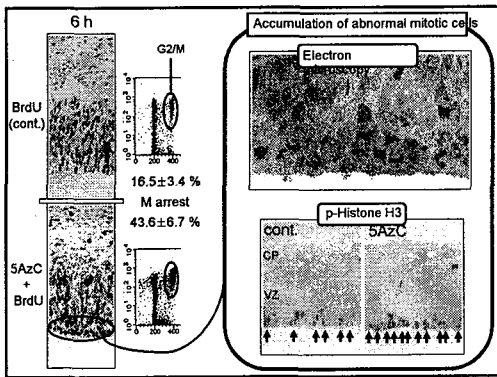
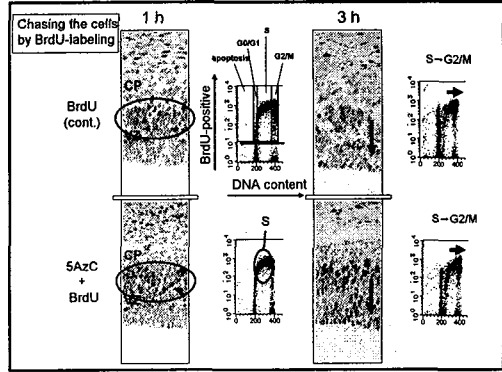
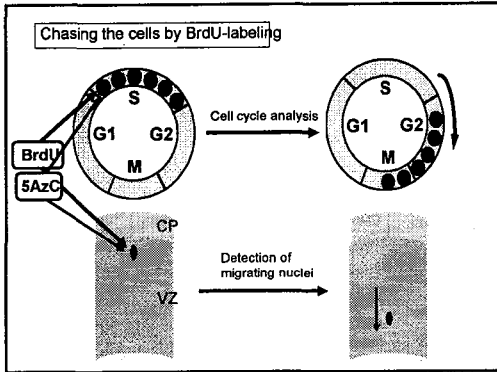
DNA damage affects brain development

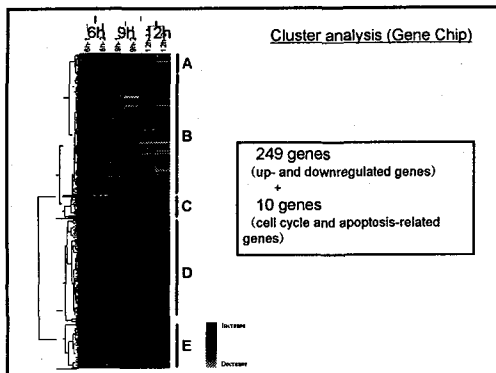
Mutant mice of DNA repair genes	Phenotype	Developmental phenotype
<i>Xpc-HHR23E</i>	Normal	Normal
<i>Xpa</i>	Normal	Normal
<i>Tp53</i>	Normal	Normal
<i>hMSH2</i>	Normal	Normal
<i>hMLH1</i>	Normal	Normal
<i>hMRE11A</i>	Normal	Normal
<i>hNBS1</i>	Normal	Normal
<i>hATR</i>	Normal	Normal
<i>hChk2</i>	Normal	Normal
<i>hChk1</i>	Normal	Normal
<i>hTcl1</i>	Normal	Normal
<i>hRad51</i>	Normal	Normal
<i>hBRCA1</i>	Normal	Normal
<i>hBRCA2</i>	Normal	Normal
<i>hFANCD1</i>	Normal	Normal
<i>hFANCD2</i>	Normal	Normal
<i>hFANCG</i>	Normal	Normal
<i>hFANCI</i>	Normal	Normal
<i>hFANCD3</i>	Normal	Normal
<i>hFANCD4</i>	Normal	Normal
<i>hFANCD5</i>	Normal	Normal
<i>hFANCD6</i>	Normal	Normal
<i>hFANCD7</i>	Normal	Normal
<i>hFANCD8</i>	Normal	Normal
<i>hFANCD9</i>	Normal	Normal
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<i>hFANCD13</i>	Normal	Normal
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<i>hFANCD97</i>	Normal	Normal
<i>hFANCD98</i>	Normal	Normal
<i>hFANCD99</i>	Normal	Normal
<i>hFANCD100</i>	Normal	Normal

DNA damaging chemicals and stimuli
 Irradiation, Ethylnitrosourea (ENU), Hydroxyurea (HU), Etoposide, Cyclophosphamide (CP), Arabinofuranosylcytosine (AraC), 5-Azacytidine (5AzC)

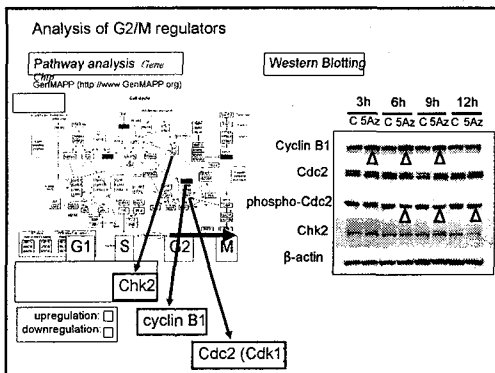
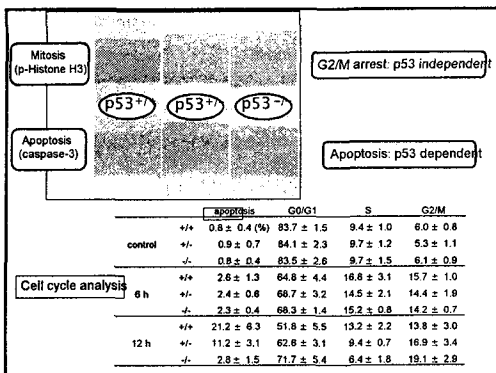
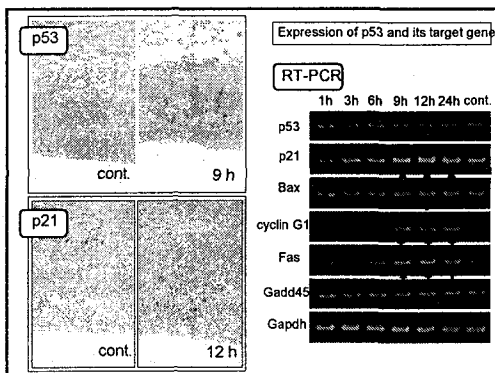
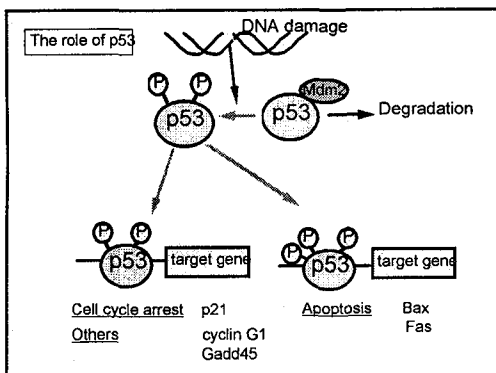
Vinson & Hales (2002)

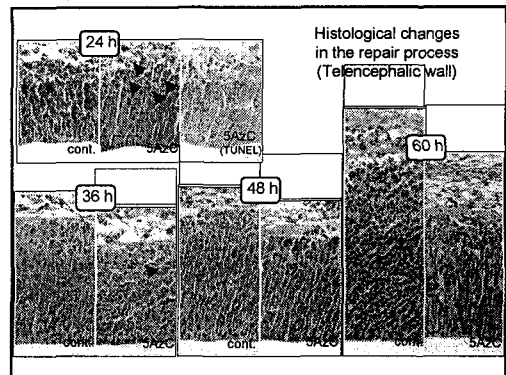
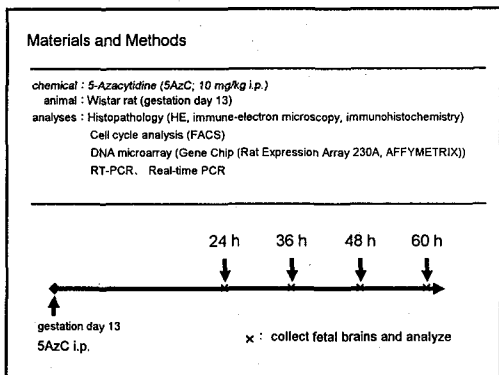
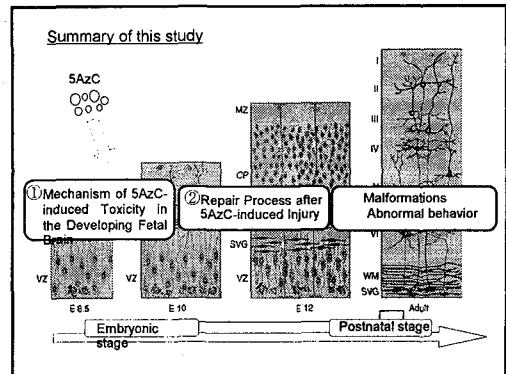
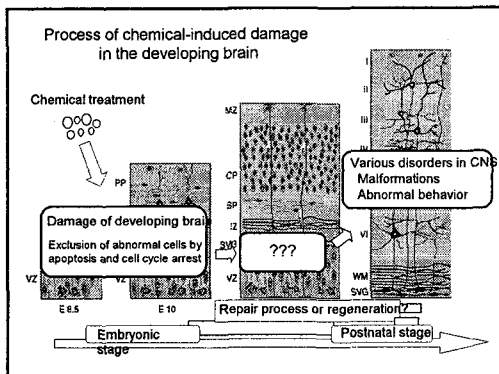
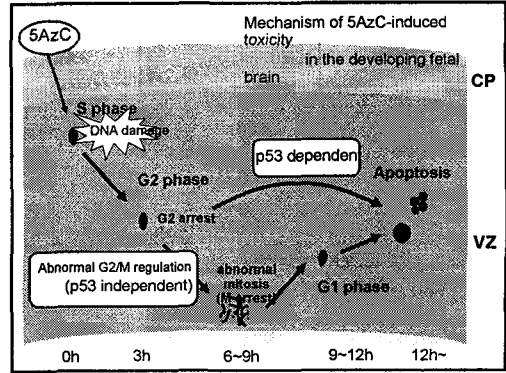
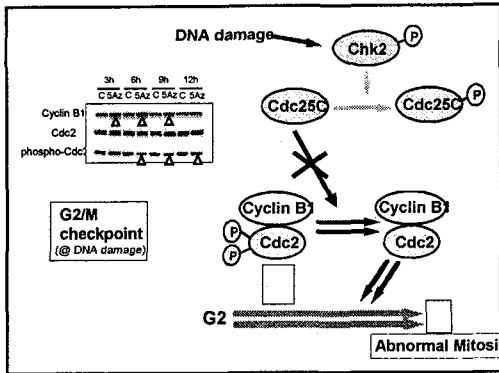


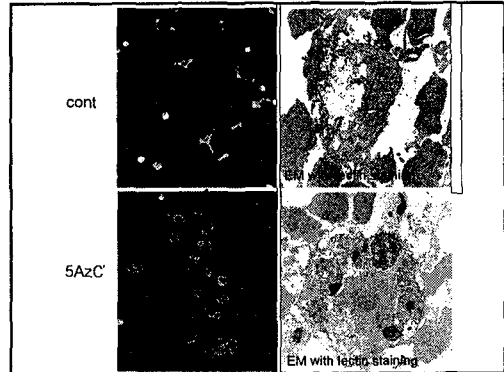
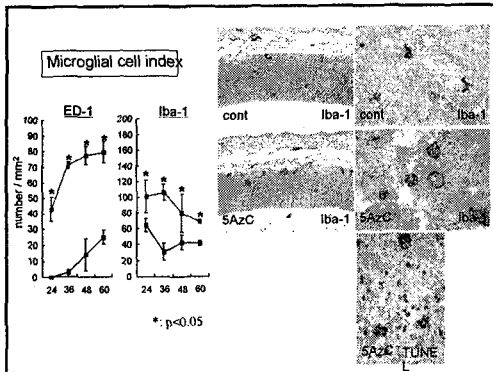
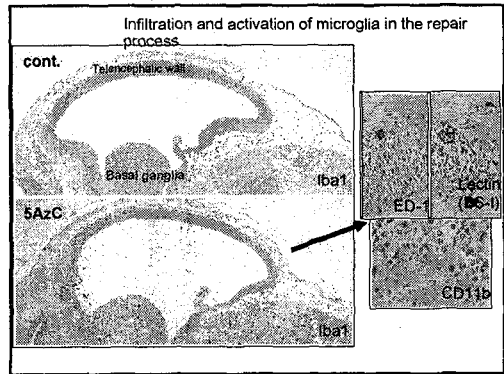
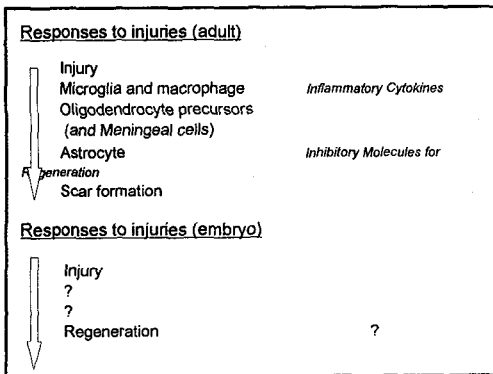
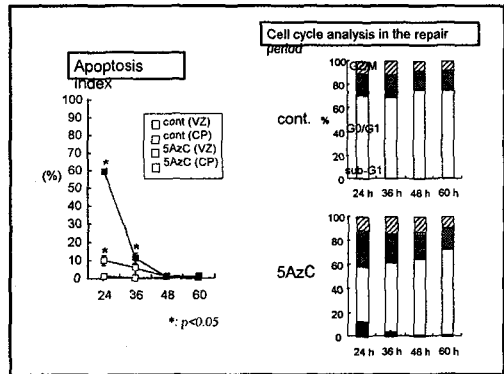
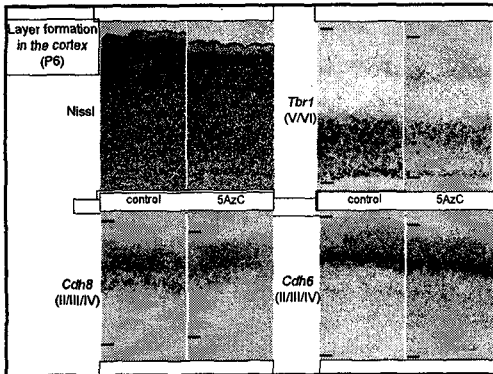


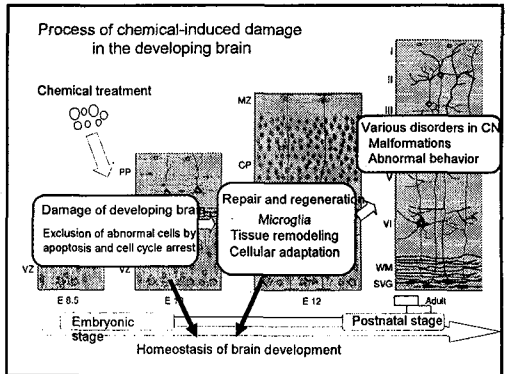
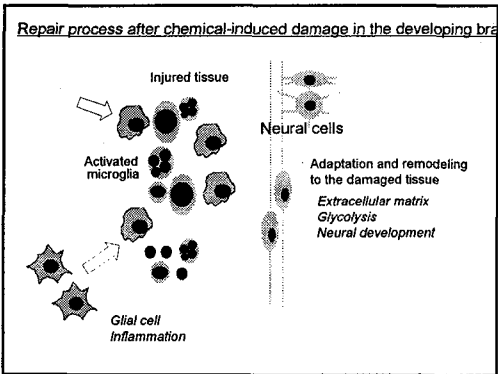
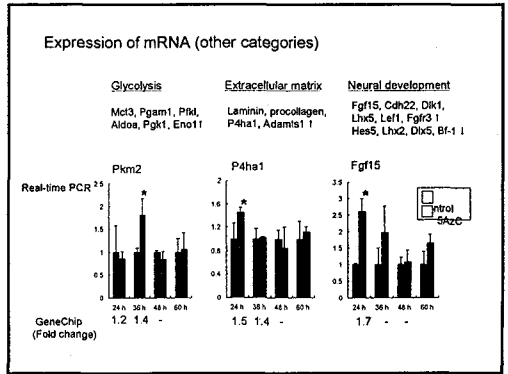
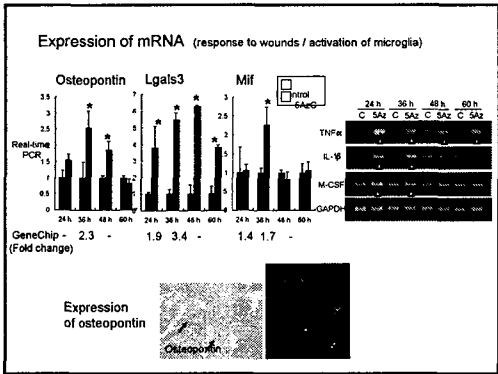
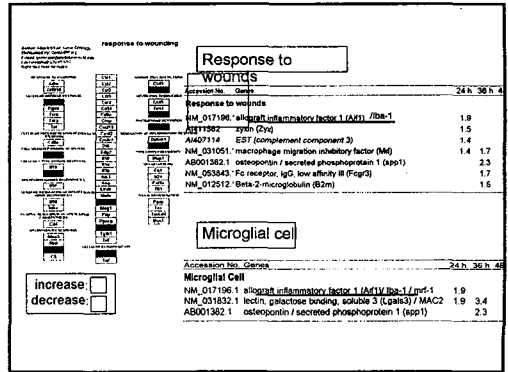
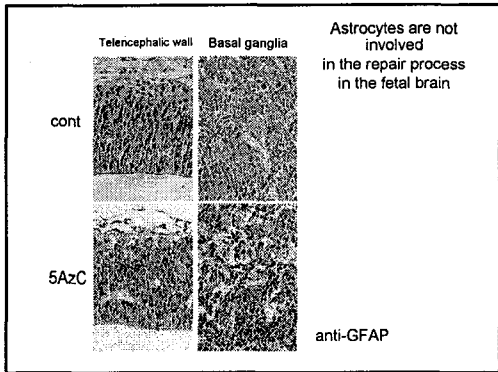


Session No.	Genes	Fold change			Clus
		6h	9h	12h	
all cycle					
_02182.1	topoisomerase (DNA II) alpha (Top2a)		1.3		E
341.1	Cdc20 / p55CDC		1.5		D
589.1	cyclin B (Ccnb1)		1.4		D
_012780.1	lost on transformation 1 (Lott) / pleomorphic adenoma gene-like 1 (Plagl1) / Zac1	-1.2			D
_054008.1	rpc32 protein (Rgc32)		-1.9		A
_022883.1	vasopressin-activated calcium-mobilizing receptor protein (VACM-1) / cullin-5 (Culs5)		-1.6		A
_021882.1	DNA polymerase delta, catalytic subunit (Pold1)		-1.5		A
_017258.1	B-cell translocation gene 1, anti-proliferative (Btg1)		-1.3		A
33-target genes					
_012923.1	cyclin G1 (Ceng1)	1.9	3.0	3.2	D
1174.1	p21 (Waf1 / Cip1)	4.1			E
548539	ESTs, Moderately similar to S15349 mdm2 protein - mouse (M.musculus)	1.8			D
_031821.1	serum-inducible kinase (Snk) / PIK2	1.4			D
_012588.1	insulin-like growth factor-binding protein (igfbp3)	2.3	1.9		D
growth factor					
_022286.1	connective tissue growth factor (Ctgf)		1.4		D
_019198.1	fibroblast growth factor 17 (Fgf17)		1.5		D
_030859.1	midline (Mds)		1.3		D









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