

**F109 Cloning and Characterization of Transcription Factors
Which Interact with LIM-Homeodomain (LH2) Protein
Using Yeast Two-Hybrid System**

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Based on our preliminary results, it was suggested that the LIM domain of the LH-2 protein interact with another transcription factor in yeast, thereby activating the target gene. Employing the EMS mutagenesis, a yeast mutant clone was selected in which gene for this transcription factor was disrupted and this clone was used in yeast two-hybrid system to search for protein gene which interact with LIM domain in human brain. Two positive clones were baited out from human cDNA library and are being sequenced. Thus far, these clones seems to be new genes. We are also in the process of isolating a corresponding yeast gene by complementing the mutant strain with wild-type yeast genomic DNA.

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**The Karyotype and mitochondrial DNA analyses of American
bullfrog, *Rana catesbeiana***

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The chromosomal analysis of *Rana catesbeiana* in Korea was performed by Giemsa-staining and N-banding methods, and the mitochondrial DNA of the species was digested with 12 restriction endonucleases. In karyotype analysis, the diploid number of *R. catesbeiana* was $2n=26$, $AN=50$. The chromosomes of *R. catesbeiana* were consisted of 9 pairs of large group and 4 pairs of small group - No. 1, 4, 5, 6, 7, 11 chromosomes were metacentric, No. 2, 3, 9, 12, 13 submetacentric, and No. 8 subtelocentric. The large secondary constriction was located on the interstitial segments of the short arm in No. 7 chromosome, whereas the one pair of NORs on the long arm in NO. 10. In the mtDNA analysis, the genome size of *R. catesbeiana* mtDNA was 17.9 ± 0.23 Kb. The total number of mtDNA fragments was 18, which is lower than other Korean genus *Rana* (5 species).