Systematic isolation of deletion mutants to analyze neural development in the nematode *Caenorhabditis elegans*.

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RNA-mediated interference (RNAi) and deletion mutagenesis are major technologies for the targeted disruption of gene function in *C. elegans*. We have developed an efficient method to isolate deletion mutants for the following reasons. 1. Genetically homogeneous mutant strains are applicable to genetic and biochemical studies. 2. It is possible to isolate null alleles for each member of gene families, and furthermore utilize multiple mutants to elucidate gene redundancy. 3. Transgenic rescue studies using deletion mutants make it possible to reveal protein structure-function relationships by domain-analyses. 4. Deletion mutants are useful to analyze gene function whose expression is limited to nervous system where RNAi is inefficient. We have already generated a mutant bank which consists about 350,000 genomes as described (Gengyo-Ando & Mitani, 2000). By piolt experiments, we have found that the bank covers a large part of *C. elegans* genome.

In multicellular organisms, transcription factors play key roles in genetic regulation during all through the developmental stages and tissues. In *C. elegans*, more than 500 transcription factor genes are present in genomes, although perhaps only one order less genes have been studied genetically. It is interesting to see what kind of phenotypes the mutants of other genes would show. How do those genes act in development to activate or repress other genes? Toward understanding gene cascades in neural development, we are intensively isolating deletion mutants of transcription factors. To analyze phenotypes of each mutant we are also constructing marker plasmids expressing GFP or RFP in specific neurons for double staining. By using these tools, systematic expression and functional analysis of transcription factors on the whole-genome scale are in progress.