

Gene Structure and Regulation of Gene Expression

In-Gyu Kim

Department of Biochemistry, College of Medicine Seoul National University

The human haploid genome consists of 3.5×10^9 base pairs(bp) of nucleotide which is packaged into 23 chromosomes and is divided into unique sequences which encode the about 10^5 genes and repetitive sequences which account for 20~30% of genomic DNA. The average size of human gene is 11kbp and coding region is usually interrupted by intervening sequence(intron). The expression of genes is regulated during development, differentiation and adaptation to the environment. Processes which used to regulate the gene expression are enhancement-silencing, tissue specific expression, regulation by hormone, gene amplification, gene rearrangement and post-transcriptional modification. In the regulation of genes transcription, chromatin structure repress promiscuous gene expression by increasing its dependence on the function of activator proteins that regulate transcription. Interactions between transcriptional factors and chromatin structures are influenced by core histones, acetylation of histones, histone 1, HMG proteins, nucleosome positioning, DNA replication, cooperative nucleosome binding by transcriptional factors and higher order domains of chromatin structure. The transcriptional factors share common type of motifs that are responsible for binding to chromatin. These include steroid receptor, zinc finger motif, helix-turn-helix(homeodomain), helix-loop-helix(HLH) and leucine zipper. The activity of inducible transcriptional factors are also regulated by phosphorylation, ligand binding, release by inhibitor and change of partner. For initiation and regulation of RNA synthesis, three kinds of DNA elements are required. Promoters of each gene consist of different combination of TATA box, CAAT box, GC box and other element. Upstream elements are specific short sequences which interact with enhancer and increase the efficiency of initiation. Responsible elements is upstream sequences that identify groups of promoters or enhancers subject to coordinate control. The elucidation of these interactions that regulate the gene expression may lead to understand the many important biological phenomena.