Homo-Protein cDNA bank bridging the gap between human genome and proteome

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In the middle of 1980s, I tried random sequencing of a human cDNA library and found that this approach is an effective way for discovering human novel proteins. This experience led me to propose a project for constructing a Homo-Protein cDNA bank composed of human cDNA clones in the expressible form. The project includes collecting whole human cDNA clones, expressing them, and searching their functions. As the final goal is to obtain proteins, the cDNA clone must be a full-length one. Thus we started to develop technology for synthesizing a full-length cDNA. Fortunately we succeeded to develop two methods for full-length cDNA sysnthesis, a tailing method and chimeric oligo-capping method (Kato et al., Gene 150: 243-250, 1994).

The obtained human full-length cDNA clones were full-sequenced and expressed in vitro and in mammalian culture cells. These analyses gave us information on the amino acid sequence and subcellular localization of the protein encoded by each cDNA clone. The cDNA clones encoding secretory and membrane proteins were supplied for biological assay in pharmaceutical companies as candidates for drug discovery. The remaining ones encoding intracellular proteins were used for searching their binding partner that might be useful to estimate their functions.

The whole human geneome sequence will soon be available. Although many post-genome sequencing projects are proposed from both genome and proteome sides, there is still a large gap between genome and proteome. The Homo-Protein cDNA bank is expected to become a powerful tool for bridging the gap between genome and proteome. In this presentation, I will show our strategy and recent progress of the Homo-Protein cDNA bank project.