Establishing an entire protein assay system of "fission yeast": Trends from genetic information to entire products in genomic analysis

In a jigsaw puzzle, it is a fun to accomplish a beautiful picture eventually by repeated try-and-error matching of the correct-pieces into the right-places. Indeed, human body is made, in a certain sense, from proteins properly delivered and located to the right-places among a huge number of protein-pieces as well. Just like the case when wrong-pieces can not fit in the wrong-places and, thus, a picture-building is not completed, it is very reasonable to imagine that mistakes in delivery and correct localization of human proteins are closely related to severe health disorders. In other words, the entire survey of correct proteins localized in the right places would provide very useful diagnostic information about health conditions.

Before surveying intricate human proteins, Chemical Genetics Laboratory in Discovery Research Institute identified the localization of the entire proteins in "fission yeast", which is a simple and tractable model organism conserving many human-type proteins. "The fission yeast" is a sort of yeasts well-known for the production of breads or alcohols. The group succeeded in isolating 99 percent of all protein coding genes (open reading flames: ORFs) in the fission yeast, which is referring to as ORFeome, and established 90 percent of the localizome catalogue which is the total data base for the localization of the entire intra-cellular proteins.

The obtained localizome catalogue is onlined on June 25, 2006 (click; http://cgl.riken.go.jp) and will provide new tools for drug development and contribute to a better understanding of the action mechanism of drugs in the cell.

The research details are reported in Nature Biotechnology, July (2006) issue.
For more information, please contact:

RIKEN Public Relations Office
Email: koho@riken.jp