

Chemical Genetics from Post-Genomic Information

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In the post-genomic era, it is undoubtedly important how efficiently we can identify and validate therapeutic targets from the genome information. Recently, much attention has been drawn to chemical and genetic approach to the target molecules for the active compounds, called "Chemical Genetics". Mutations, which serve as the genetic determinants responsible for particular phenotypes in classical genetics, are replaced by the small-molecule compounds in chemical genetics. Once the specific target molecule of a certain compound is identified, such the compound can be used widely as a convenient, conditional targeting method applicable to any type of cells.

To identify the drug targets systematically, we need to establish a platform for functional proteome study for the detection of both physical and genetic interactions between the drug and the gene product. To this end, we constructed "ORFeome", a global ORF collection, using the recombination-based cloning. The fission yeast *Schizosaccharomyces pombe* shares many traits, notably cell division, with cells of higher eukaryotes, hence the information of the fission yeast proteome will be invaluable for functional and comparative studies of eukaryotic cell processes. In addition, *S. pombe* has the most compact genome at least in the eukaryotes whose genome has been so far sequenced. Nevertheless, it includes many genes related to human diseases. We therefore performed the first proteome-scale analyses in fission yeast, including a global analysis of subcellular localization named localizome, a global analysis of gel mobility in SDS-PAGE named mobilitome, and the chemical genetic screening, using the ORFeome constructed by the recombination-based ORF cloning system. I will discuss the usefulness of these omic databases for chemical genomics.