권 확보와 기업 생존을 위하여 연구개발 구조 재편 및 사업 구조 전환에 박차를 가하고 있으며, 상업적 가치를 지닌 유전자 및 단백질의 선점을 위하여 천문학적인 자금을 투입하여 과감한 연구개발을 진행하고 있는 상황이다.

SL 102 Comparative Proteome Analysis Using Two-Dimensi onal Electrophoresis

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Proteome research (proteomics) is gaining more and more attention as a core of functional genomics because the ultimate functional molecules in living organisms are proteins. Proteome is originally defined as all proteins expressed by a genome, which is continuously changed in an organism in space and time. In order to analyze this dynamic state of proteomes, protein array or protein map is prerequisite and two-dimensional polyacrylamide gel electrophoresis (2D PAGE) is currently only method to separate thousands of proteins simultaneously. Although 2D-PAGE was introduce more than two decades ago, the reproducibility and resolving power are recently improved mainly by immobilized pH gradient (IPG) in isoelectric focusing (IEF). Using homemade IPG strips with various ranges of pH gradient and mini gels for SDS-PAGE, we demonstrate that the production of reference protein map is rather simple and rapid.

Using two-dimensional electrophoresis and MALDI-TOF mass spectrometry, we performed the comparative analyses of proteomes from cultured cells, patient tissues, model animals, cellular organelles, or molecular complexes. I will introduce some experiences of our proteome studies to illustrate the scope of proteomics technology.

In first case, we found that the expression of peroxiredoxin 1 was increased in malignant lung epithelial cells (A549) in relation to normal ones (BEAS-2B) through the comparative analysis between two cells. This augmented expression of Prx-I was confirmed in tissues from lung cancer patients. In second case, it was found that cellular retinoic acid binding protein II (CRBP-II) was down-regulated with differentiation by the proteome analysis during chondrogenesis. It should be closely related with the effect of retinoic acid on chondrogenesis.

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SL 103 Structural Genomics/ Proteomics as the Next Frontier in Biotechnology and an Example of Obtaining Insights into Biochemical Function from Three-dimensional Structure

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Genome sequencing in the past decade has provided massive genetic information on many microorganisms and a smaller number of eukaryotic organisms. One of the next frontiers in the 21st century biotechnology is structural genomics/proteomics, the protein structure determination at the genome-wide scale. Its ultimate goal is to provide all the

necessary information on three-dimensional structures of proteins. It is expected that structural genomics/proteomics will have a major impact on drug discovery. This is reflected by a tremendous commercial interest in structural genomics/proteomics research. Several biotechnology companies like Structural GenomiX and Syrrx have embarked on high-throughput determination of protein structures. In this talk, I will briefly describe the current status and future prospect of structural genomics/proteomics research worldwide as well as in my laboratory. As an example of structural genomics/proteomics study, I will describe a recent work from my laboratory, which has provided insights into the biochemical function of an evolutionarily conserved protein family.

SL 104 One gene one product or one gene many products in Caenorhabditis elegans

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Entire human genome sequences 3000 Mb have been reported this February. Surprisingly the total gene numbers are 35,000 that are less than we have expected. Total genome sequences (gene numbers) of yeast, the nematode and the fly are 12 Mb (6,000), 97 Mb (19,000) and 120 Mb (13,600) respectively. Gene numbers of animals are not exactly related to the complexity of the gene products. We are studying muscle genes of *Caenorhabditis elegans* and can compare these genes to the fly. The worm has mainly two muscle tissues: pharynx for feeding and body wall muscle for locomotion. Two of each myosin heavy chain gene are expressed in pharynx and body wall of the nematode respectively. In Drosophila one myosin heavy chain gene encodes more than 30 isoforms. In many muscle genes of the worm one gene encodes one isoform. Interestingly one tropomyosin gene encodes two of each pharynx and body wall isoforms. These results means gene number is not essentially to explain the function of the gene products. Comparatively higher number of gene number of the worm means that *C.elegans* contains many basic genes, which are not exactly the same function of mammals.

Results of *C. elegans* researches are not directly of use commercially but have the potential to provide information relevant to vertebrates including humans. Studies of a living animal are much more informative than the biochemical experiments. How medicines or drugs affect multi-cellular organisms in terms of development, growth and life span are useful for designing an experiment on mammals. Single gene functions, metabolic pathways and molecular interactions have already been documented but nowadays many scientists want to know about cross talk between different molecular signals. In that case genetically approaches are much powerful for the purpose. The handling and keeping of the worms are easy and *C. elegant* is a good model for this purpose. Finally I should say that communication, collaboration and archiving are a common sprit in the worm community all over the world.