Plenary Lecture 2

Industrial Scale *Drosophila* Genetics as a Functional Analysis Tool of Human Genome

KIM Jaeseob
KAIST and Genexel, Korea

With publication of the human genome sequence in 2001 following a decade-long effort, the challenge is no longer the identification of genes, but understanding their functions, their encoded proteins, and determining the consequences of their modulation. The protein products of genes often function through interactions with each other in coordinated networks, but only a fraction of these networks have been identified and characterized through classical biochemistry, structural analyses, and activity assays. The genetic study of model species facilitates the discovery of genes that interact within homologous disease-associated networks. This provides crucial insight into how the human counterparts of the encoded gene products function in humans and how aberrations in gene function contribute to human disease. We have developed and industrialized the world's most comprehensive *Drosophila* system for functional genomics to understand the genetic and molecular mechanisms underlying various biological phenomena. It is now known that extensive similarities among many important genetic or biochemical pathways exist between humans and *Drosophila melanogaster*. These similarities enable us to utilize the fruit fly to rapidly and systematically identify genes within the fruit fly genome that modulate the activity of human genes, and subsequently identify the corresponding human genes. A low cost, short life cycle time, well-characte rized biology, and ease of genetic manipulation make the fruit fly a superior platform for genomic discovery. The wide flexibility of the fruit fly genetic system makes it possible to scan its genome for genes involved in many diseases such as cancer, dia b etes, neurological disorders, susceptibility to infection, predisposition for obesity, or responses to therapeutic agents. However, to be most effective, the system must represent the entire genome. By developing nearly 100,000 inducible or knock-out fruit fly lines, we employ the most comprehensive system in existence in its coverage of the genome of a living animal.