

Opening the door to the post-genomic era with combinatory use of the microarray technology, bioinformatics, and genetics

KIM Heenam*

The Institute for Genomic Research, 9712 Medical Center Drive, Rockville,

MD 20850 USA.

Conducting genomic studies and dealing with the resulting large data sets require high-throughput means such as the DNA microarray technology and bioinformatics tools. DNA microarrays can provide gene expression data that can be used to validate computational annotation, identify new functions, and unveil interactions of the genes. Besides the gene expression studies, microarrays constructed based on an organism can also be used for comparison studies among the same or closely related species. With the combinatory use of the microarray technology, bioinformatics and genetics, a number of questions can be effectively answered. For example, we bioinformatically predicted and prioritized virulence-regulatory genes in *Burkholderia mallei*, a human pathogen weaponized by the former Soviet Union. These genes are going to be mutagenized and evaluated with microarrays. In another example, we constructed and used *Arabidopsis* whole genome microarrays to validate and facilitate genome annotation. In addition, by examining the distribution of expression along the chromosomes, we identified regions of repressed transcription that may represent previously undescribed heterochromatic regions.