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• 計畫英文名稱	Microarray and Knowledge-Based on-line Database on the Relationship of Human Diseases and Genes		
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• 英文摘要

Cancer has currently become one of the deadly diseases and ranked second leading cause of death in Taiwan. Hepatocellular carcinoma (HCC) is the first death leading cause in Taiwan. Cancer occurrence is not taken place randomly. The cancer risks include inherited mutations, immune conditions, and external environment. These causal factors may act together or in sequence to initiate or promote carcinogenesis. Along with the development of high throughput biotechnology and the complete of human genome program, human beings are getting to know more about the "molecular-self". We eventually are able to see the differences between cancerous and normal tissues in a comprehensively global view. Over 2,000 papers on cancer gene expression transcriptomes have been published to date. Scientists gradually realized the importance to collect all these precious and important data in some indicated databanks. However, due to the great size of each dataset, and the demanding usage for the gene expression tools, it is not an easy or a convenient way for a traditional wet laboratory to have the raw data retrieved and not to mention to have an advanced analysis in details. Therefore, there is a critical need for a disease-driven analysis on the relationship of genesto-HCC, where pre-analyzed and annotated gene lists, calculated from a comprehensive collection of gene expression data on the build of each cancer type, are to be presented. During the course of the work, we found the data format produced from a diverse range of approaches is rather confusing and is hard to cross-compare. To facilitate our work to carry forward, we have built a database-interrogation platform as a conversion window for all the high throughput data, especially gene expression data from microarray, SAGE and 2D. This platform is named under what it meant, Database Interrogation Platform for Gene Expression (abbreviated as DIPLEX). The first version of this tool has been released and the manuscript is under preparation.

With the unification for gene identifier, the raw data will be processed and to analyze individually. Differentially expressed genes in HCC and normal liver resulted from microarray, SAGE and 2D are also compared and shown in the project.