

## **Microbial Metabolome Bank ([www. microbank.re.kr](http://www.microbank.re.kr)) : It's importance and Application for Metabolomics**

Kwang-Hee Son, Tae-Kwang Oh, and Choong-Hwan Lee

*Microbial Resources Bank, Korea Research Institute of Bioscience and Biotechnology (KRIBB),  
Taejon, Korea*

Microbial natural products have been studied as tremendous pools of new drug discoveries for past 50 years. The microbiological resources still have huge undiscovered genome entities and their products as well. Only one of over 100 microorganisms was separated, cultured and utilized for the discovery of valuable small molecules.

Although, microbial natural products have known to have several benefits such as uniqueness, exclusiveness and molecular diversity, their development including screening, isolation and production feedback was very difficult. Furthermore, microbial natural product candidates showed low purities with poor information for their structure compare with synthetic chemicals. The microbial natural products had been good drug candidates in activity-guided screening era, but they were not sufficient to fulfill the requirements of HTS system.

Drug discovery process in post genomic era requires two keys. One is target protein and another is small molecule that can bind to the target and can control the biological phenomena as a result. Genomics and Proteomics studies focused on the new target proteins. And large libraries of chemicals and natural products have been small molecule candidates.

Larger and larger libraries of small molecules would be essential for the drug development in the era of genomics and proteomics because the new drug targets would be increased as well. In the searching program of the new drug candidates from the huge mass of molecules, the molecular diversity and novelty will be the first concern for their choice. Microbial natural products and their derivatives have provided lots of the antibiotics and medical agents for clinical therapies. Although, the enormous molecular diversity of microbial secondary metabolites makes it as potent sources of new leads in drug discovery program, the microbial metabolome, the sets of secondary metabolites, should be fractionated and figured out as informative chemical entities.

A searchable library of MS/MS spectra, obtained using a quadrupole ion trap mass spectrometer and electrospray ionization, is presented. The application of wideband excitation and normalized collision energy leads to highly reproducible mass spectra which are searched using the NIST algorithm. These observations serve as a basis for determining a universal set of conditions for building MS/MS libraries. This approach lends itself to the creation of fragmentation libraries using the LC/MS/MS, permitting library

searching of MS/MS data in conjunction with LC/MS analysis. Flow injection and LC/MS/MS applications of this powerful technique in the microbial metabolite and drug screening areas are described. The ability to obtain library searchable spectra is demonstrated for the analysis of several microbial secondary metabolites.

In this report, we'll suggest a new form of microbial metabolome bank as a source of small molecule library. This pre-fractionated microbial metabolome library having 96-well plate format, showed over 80 % of purity by TLC and HPLC. And those analyzed by <sup>1</sup>H-NMR and LC/MS/MS. The hundreds of structure-based metabolomes also having 96-well plate format, analyzed those structures completely. The thousands of the test metabolomes is now open to researchers on the Microbial Genomics and Applications Center, Korea (<http://www.microbank.re.kr/>).

Acknowledgement: This work was supported from Microbial Genomics & Applications Center.

## Microbial Resource Banks

