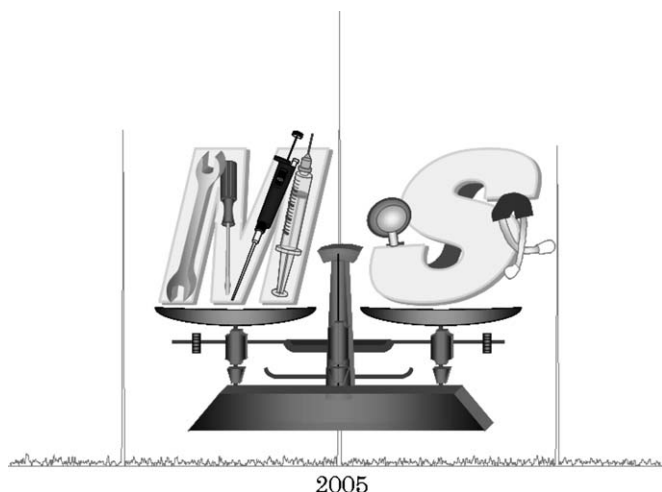


Preface



The 30th Annual Meeting of the Japanese Society for Biomedical Mass Spectrometry (JSBMS) was held on September 8 and 9, 2005, at Senri Life Science Center, Toyonaka, Osaka, Japan.

This year, we introduced several innovations to the program. The fields in which JSBMS is involved are diverse, and efforts are being directed to hereditary or acquired disorders and to the analyses of intrinsic or extrinsic molecules and elements affecting health. This situation may obscure the main point of discussion in the meeting. Therefore, a grand title, “Mass-based Diagnosis: Present and Future”, was given to the 30th meeting, because all JSBMS activities should focus more on the development of diagnostic methods than on detailed descriptions of diseases or conditions.

The first day was devoted to studies of small molecules, including metabolic profiling or metabolomics. In Japan, mass spectrometers in the biomedical field have long been the instrument of choice for research but not for clinical practice. However, tandem MS is replacing conventional chromatography in the neonatal screening program, and mass spectrometers are beginning to be seen in local laboratories. Most of the technical staff who run the instruments have not been educated in MS. Obviously, JSBMS is the best organization capable of facilitating a smooth transition of the screening system. We invited 16 technical experts countrywide to this meeting, and informed them of the current techniques and challenges in a Workshop entitled “Neonatal Screening for Metabolic Diseases: The Present

State and Future” chaired by Professors Yosuke Shigematsu and Nobuo Sakura. Also, the same day, award lectures were given by Professor Tomiko Kuhara, the first laureate of the Matsumoto Isamu Award, and by three Young Scientist Award winners.

The second day was dedicated to studies of large molecules, which are the targets of proteomics, glycomics or lipidomics. Professor Kenzo Hiraoka, the President of the Mass Spectrometry Society of Japan, delivered a plenary lecture on a designated topic, “Mass Spectrometry for the Next Generation”, in which state-of-the-art technologies such as desorption electrospray ionization (DESI), desorption/ionization of silicon (DIOS) and direct analysis in real time (DART) as well as his own innovations, including laser spray ionization, were explained focusing particularly on physical chemistry.

Another tutorial lecture was given over lunch by Professor Toshifusa Toda, who addressed the essence of his own clinical proteomic studies.

Proteomics is a booming research field and a huge number of studies using MS were reported in relevant meetings. However, it is now recognized that proteomic researchers need a deeper knowledge of medicine including clinical details, since the major purpose or target of proteomic and other omic studies is obviously the promotion of health and the conquest of illness. Therefore, JSBMS has a great deal to commit to this field.

There were 34 non-invitational presentations and 159 attendees, both numbers probably being records in the 30-year history of JSBMS.

Chairperson of the 30th Annual Meeting of JSBMS
Yoshinao Wada
Osaka, Japan

Editor-in-Chief of JSBMS
Toshimitsu Niwa
Nagoya, Japan

President of JSBMS
Akira Shimizu
Osaka, Japan

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