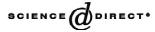


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JOURNAL OF CHROMATOGRAPHY B

Journal of Chromatography B, 792 (2003) 3-4

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Complimentary address to Mr. Koichi Tanaka, the winner of Nobel Prize in chemistry 2002

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Koichi Tanaka, 43, assistant manager of the Life Science Laboratory, Analytical and Measuring Instruments Division, Shimadzu Corp. (Kyoto City's Nakagyo-Ku), has won the 2002 Nobel Prize in Chemistry. The Royal Swedish Academy of Sciences announced on October 9, 2002, that Tanaka won the prize for developing methods of identifying and analyzing the structure of biological macromolecules. Tanaka has developed methods that facilitate analyzing biological macromolecules and introduced a technique that causes the proteins to float freely. Matrix assisted laser desorption ionization developed by Mr. Tanaka and electrospray ionization developed by Dr. J.B. Fenn are now commonly performed ionization methods and are widely available. These soft ionization mass spectrometry methods are now part of the investigative arsenal for life science research. Great discoveries will proceed from using these technologies. To date, the developers of electrophoresis, monoclonal antibody technique and polymerization chain reaction have won the Nobel Prize. These technologies have contributed enormously to life science and medical practice. The influence of soft ionization mass spectrometry to life science may be larger than the formers. As the total genome nucleotide sequence was completed, the sequence information may be applied to protein identification with the aid of the genome database and analysis by soft ionization mass spectrometry. Mass spectrometry will contribute to the diagnosis and treatment of cancer and other serious diseases. This prospect may have been a component in selecting the Nobel Prize winner.

Tanaka's selection is a great pleasure for those of us who use mass spectrometry as a leading research technology. This event will illuminate the future direction of research. It was my great fortune that I was able to meet and talk with Mr. Tanaka, on Oct. 23. 2 weeks after the announcement of the Nobel Prize winner. It was the mid-point of the 18th International Congress of Clinical Chemistry, and the Joint Domestic Meeting, that was the 42nd Annual Meeting of the Japanese Society of Clinical Chemistry, which was being held at the Kyoto International Conference Hall. Mr. Tanaka fortunately accepted our invitation to attend the banquet of the Congress despite his busy schedule between the announcement and award-ceremony in Stockholm. To these domestic and international congresses, we, the members in Osaka Medical College, Department of Clinical Pathology, have presented papers using mass spectrometry every time. While the welcoming ceremony of the banquet progressed for about 20 minutes, I talked with Mr. Tanaka. He told me that the improvement of the accuracy, sensitivity, and miniaturization of the MS machine continue to be important. He wants to be able to use the MS

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equipment for quick clinical checks. He also expects that MS equipment can be miniaturised to the size of a desktop type of personal computer.

We talked about his first presentation of laser desorption time-of-flight mass spectrometry in 1987. He presented this work at the annual meeting of our society, that is, the Japanese Society for Medical Mass Spectrometry, held from October 29-31, 1987 in Osaka and chaired by Professor Ikuya Yano, Osaka City University Bacteriology (at that time). We first listened to his valuable research at that time. He also presented this work at the Japan-China Joint Symposium on Mass Spectrometry, held in Takarazuka (Hyougo Pref, Japan) at almost the same time. The proceedings of our society were published in Japanese. However, the description was more exhaustive than that in the Joint Symposium, which was written in English. The Proceeding of our society Vol. 12 is now a memorable issue for us.

We collaborated with Mr. Tanaka and published a paper in 1994 [1]. To apply mass spectrometry to proteins, most researchers used materials isolated by ion-exchange chromatography, affinity chromatography and so forth, at that time. We intended to develop a simple preparation, and asked Mr. Tanaka

to analyze a mixture of protein and antibody against the protein. He analyzed the mixture by MALDI-TOFMS Kompact Maldi/III (Kratos-Shimidzu), and obtained a clear spectrum, showing the existence of carbohydrate-deficient transferrin. Many laboratories have followed our method for diagnosing variant proteins. i.e., transthyretin variant causing amyloidosis. The MS analysis with immunoprecipitated protein is very convenient and now practically being applied for clinical purpose. Analytical chemists of other companies hesitated to analyze a dirty mixture using sophisticated MS in those days.

I thank Mr. Tanaka for participating in collaborative research in 1994, and for accepting our invitation to attend the Congress Banquet in 2002.

References

 T. Nakanishi, N. Okamoto, K. Tanaka, A. Shimizu, Laser desorption time-of-flight mass spectrometric analysis of transferrin precipitated with antiserum: a unique simple method to identify molecular weight variants, Biol. Mass. Spectrometry 23 (1994) 230–233.