Proteome analysis of experimental animal models with hereditary diseases

Masamichi Oh-Ishi, Yoshio Kodera, and Tadakazu Maeda
Kitasato University School of Science, Department of Physics

While human plasma or human tissues would be major sample resources to be analyzed in this field, proteome analysis of human samples often made complicated results depending on patient's individuality and/or conditions of the patient. Experimental animal models with hereditary diseases would be substitutes of various human diseases. We would like to introduce our proteome analysis strategy with two examples listed below: (i) \textit{rdw} rat with hereditary hypothyroidism and dwarfism, and (ii) OLETF rat with hereditary diabetes. With 2-DE with agarose gels in the first dimension (agarose 2-DE), being capable of analyzing high-molecular-mass proteins (>100 kDa), in combination with LC-MS, and/or detecting method of oxidatively-induced protein carbonyls, we will present a means toward understanding the mechanism of the onset, progression, and complication of these diseases.