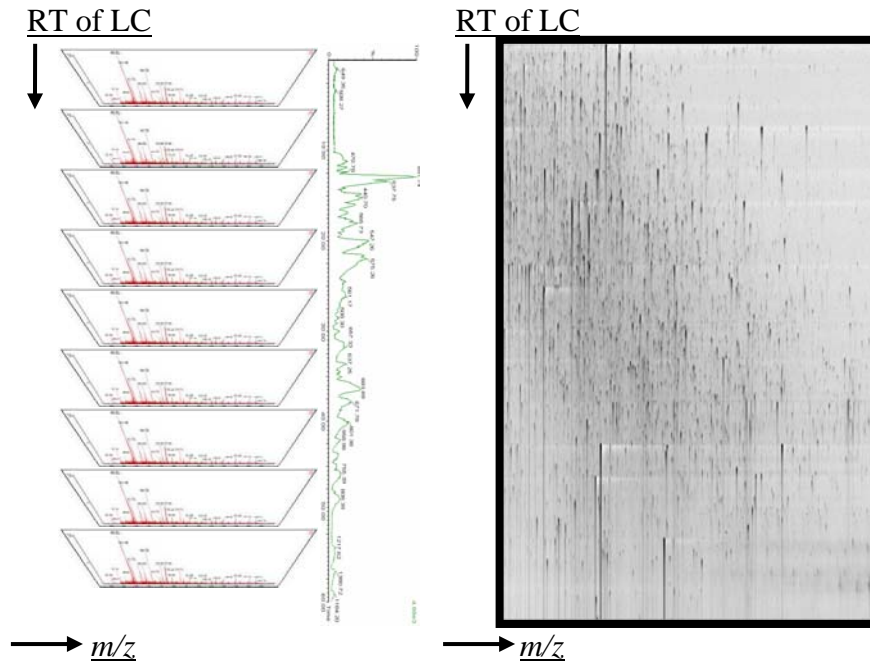


Principle of 2DICAL

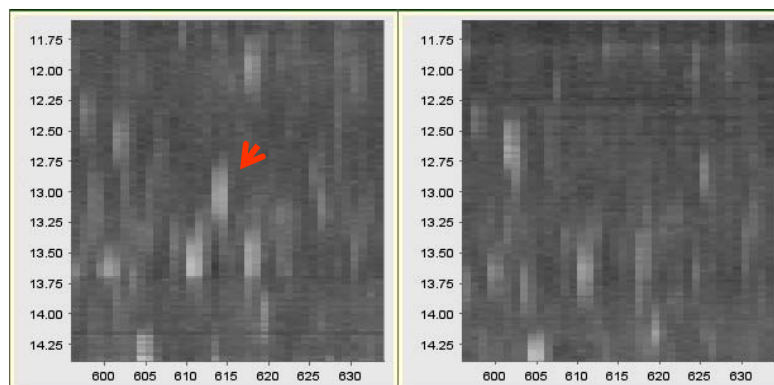
After obtaining 3600 MS spectra by using the MS mode of nano-ESI (electrospray ionization) hybrid quadrupole time-of-flight (Q-TOF) MS (left), and they were displayed in a two-dimensional plane, with mass-to-charge ratio (m/z) values along the X axis and retention time (RT) (right).



2DICAL makes it possible to detect more than 100,000 MS peaks in 1-hour LC run without isotope labeling the protein samples.

Detection of proteins differentially expressed in two samples

Proteins in concentrations as low as 100 fmol can be detected and quantified in a highly accurate manner.

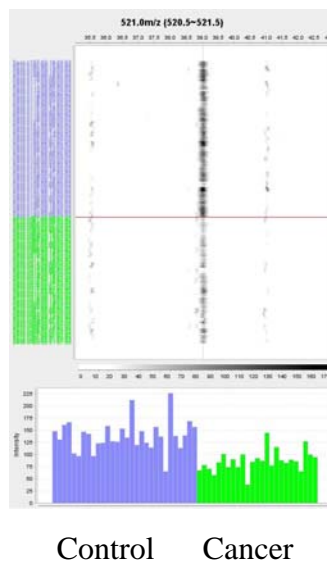


Comparison of a large number of protein samples by 2DICAL

In order to be able to apply 2DICAL to clinical studies that require comparison of samples from a large number of patients we recently refined the calculation algorithm of 2DICAL so that peptide peaks of the same m/z are aligned and displayed with axes of RT and samples.

Identification of a biomarker candidate

Gel-like view of an MS peak whose intensity was significantly different in 25 cancer patients (green) and 30 controls (blue).



Targeted protein identification by MS/MS

Proteins can be identified by MS/MS on peaks having the RT and m/z of interest in the preparatory LC-MS run.



2DICAL computer system

The amount of data reaches 2 gigabytes per LC-MS run. We use a high-performance computer cluster consisting of 10 processors with a clock speed of 3.6 GHz connected in parallel to increase calculation speed.

