GS02-3 **Quantitative targeted proteomics of pancreatic cancer for clarifying mechanism of drug sensitivity**

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Multiple proteins involved in metabolism and transport of Gemcitabine (Gem), a first-line drug for pancreatic cancer, and it is necessary to analyze those “protein network” to clarify Gem sensitivity mechanism. The purpose of this study was to identify expression profile of 106 proteins in pancreatic cancers and clarify proteins responsible for Gem sensitivity by targeted absolute proteomics with LC-MS/MS. Crude membrane and cytosol fraction of cancer tissue was alkylated, trypsinized and, then, the digests mixed with isotope labeled peptide was quantified by LC-MS/MS MRM mode. Pancreatic cancers were classified into three groups based on CA19-9 values; Gem Responsive (RS, n=3), Gem Non-Responsive (NR, n=3), Surgery Effective (SE, n=3). Significant difference in the expression levels of dCK and cN-Ⅱ were observed between RS and NR group. However, prediction of Gem sensitivity based on these proteins was controversial in SE group. Gem sensitivity prediction formula was examined by calculating the expression ratio of transporters and enzymes. The expression ratios calculated by four formulas containing dCK, MRP1, MRP4, cN-Ⅱ and/or CTPS1 were significantly different between RS and NR group, and prediction of Gem sensitivity by each formulas were consistent in SE group. These proteins were suggested to contribute to Gem sensitivity in pancreatic cancer and the expression ratio of these proteins would be a good predictor for Gem sensitivity in pancreatic cancer.