

論文 / 著書情報
Article / Book Information

題目(和文)	
Title(English)	Development of practical proteomics through high-performance 2-DE and its implementation
著者(和文)	Sing Ying Wong
Author(English)	Sing Ying Wong
出典(和文)	学位:博士(理学), 学位授与機関:東京工業大学, 報告番号:甲第11579号, 授与年月日:2020年9月25日, 学位の種別:課程博士, 審査員:林 宣宏,一瀬 宏,相澤 康則,長田 俊哉,田川 陽一
Citation(English)	Degree:Doctor (Science), Conferring organization: Tokyo Institute of Technology, Report number:甲第11579号, Conferred date:2020/9/25, Degree Type:Course doctor, Examiner:,,,,
学位種別(和文)	博士論文
Category(English)	Doctoral Thesis
種別(和文)	要約
Type(English)	Outline

Thesis outline

Proteomics: A useful approach that has been extensively used over the last decade due to its ability to unveil the proteome of a cell, tissue, or organism and explicitly exhibit their dynamic states. Since genes are known as the life's blueprint, proteins would then be the "bricks and mortar" from which it is built. This is especially important because this means the study of proteins would later allow us to learn more about the functional molecules in cells, which reflect the actual conditions.

With the aid of gel-based method such as two-dimensional gel electrophoresis (2-DE), the study of post-translational modifications of a protein, which can profoundly affect its function becomes feasible. Two-dimensional gel electrophoresis (2-DE) is a key tool for comparative proteomics research. This technology first separates mixtures of proteins according to their isoelectric point during the first dimension and further separates in the second dimension according to the molecular weight on 2-DE gels. As a result, a 2-DE gel profile with hundreds to thousands of protein spots could be obtained.

The present study focuses on the development of high-performance 2-DE technique and its various practical implementations. Several modifications were made in the present technology to ameliorate the limitations commonly found in conventional techniques. This technique is highly reproducible and generates proteomic data of high quality, enabling reliable comparison between samples to be performed. With its implementation, several non-invasive biological specimens including human hair, serum, tear and zebrafish embryos were examined. The analysis of longitudinal serum proteome has successfully screened for multiple potential biomarkers and revealed the pathophysiology of sepsis progression and post-HSCT complications. Furthermore, ongoing efforts in establishing novel proteomic protocols for the application of human hair, tear and zebrafish embryos on various comparative studies were also described.