Okinawa Analytical Instrument Network Meeting 2019

11/22/2019

Instrumental Analysis Section
Okinawa Institute of Science and Technology Graduate University

OIST

Okinawa Analytical Instrument Network Meeting 2019

沖縄分析機器ネットワーク研究会 2019

General Information

Meeting Name: Okinawa Analytical Instrument Network Meeting 2019
(沖縄分析機器ネットワーク研究会 2019)

Date: November 22nd, 2019

Organizer: Instrumental Analysis Section, Okinawa Institute of Science and Technology Graduate University
(沖縄科学技術大学院大学 機器分析セクション)

Location: Okinawa Institute of Science and Technology Graduate University
Tancha 1919-1 Onna-son Kunigami-gun Okinawa, Japan 904-0495
(〒904-0495 沖縄県国頭郡恩納村谷茶 1919-1 沖縄科学技術大学院大学)

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Preface

Okinawa is notably unique place compare to other part of Japan and this is not only the location of nature rich tropic islands away from center of Japan. If we think center of East Asia, Okinawa can be the key of the "network" for these cities and contribute the sustainable development for all countries. Nowadays, the science is the large investment for the sustainable development and the "high quality research instrument" is one of the major parts of it. The purpose of this meeting is, as the member of scientist of these area, establishment of the "network" of "high quality research instrument" and contribution to the advance science and technology in Okinawa and the rest of the world. Annual meeting of "Okinawa Analytical Instrument Network Meeting" is started from last year to support this idea.

This year, we target the Mass Spectrometry (MS) with OMICS application for this meeting. MS is widely installed and used in locally for the routine use but MS for OMICS research needs high-end instrument and extensive skill of specialist. Four researchers from Japan, Singapore, Taiwan, and U.S.A. are invited to give the lecturer using "state-of-the-art instrument" MS and discuss about the future of research include the collaboration/network of MS for OMICS.

Registration of Meeting, Optional Lab Tour, and Updated Information

Registration of this meeting and optional lab tour is free but required from the website.
Deadline of lab tour registration is November 5th, 2019.
研究会とオプションの施設見学会の参加費は無料ですが web サイトから登録が必要です。施設見学会の参加登録は 2019 年 11 月 5 日までに行ってください。

https://groups.oist.jp/ias/okinawa-analytical-instrument-network-discussion-group-meeting-2019

Scan QR code and go to Registration Website

Program

10:00-11:00	(option) Tour of OIST and Instrumental Analysis Section
12:00-	Open Door
12:25-12:30	Opening Remarks
12:30-13:00	Introduction Lecture – Dr. Andreas Huhmer (Thermo Fisher Scientific Inc.) *"High-Throughput Single Cell Proteomics Analysis with Nanodroplet Sample Processing, Multiplex TMT labeling, and Ultra-Sensitive LC-MS analysis in a New Orbitrap Tribrid Mass Spectrometer."*
13:00-13:50	Lecture – Professor Yet-Ran Chen (Academia Sinica, Taiwan) *"Development of MS-Based OMICs Approaches for the Study of Plant Immune Signaling"*
13:50-14:40	Lecture – Professor Newman Siu Kwan SZE (Nanyang Technological University, Singapore) *"emHILIC-MS/MS proteomics technology for profiling deamidatome to unravel proteinopathy in complex age-related diseases"*
15:00-15:50	Lecture – Dr. Benjamin C. Orsburn (University of Virginia Medical School, U.S.A.) *"Best Practices for Maximum Protein Coverage and Reproducible Measurements in Shotgun Proteomics"*
15:50-16:40	Lecture – Professor Takeshi Bamba (Kyushu University, Japan) *"Development of metabolic profiling methodologies by supercritical fluid technologies"*
16:40-16:45	Closing Remarks

Access Information

[Access to OIST] https://www.oist.jp/access-map

[Campus Map and Parking] https://www.oist.jp/parking

Onna-village is the top resort area of Okinawa and there are many luxury hotels to B&B. The center of hotel area is around "moon beach bus stop" and several restaurants are around there. You can reach OIST by car, taxi or local bus (bus stop "Daigakuin-Daigaku-Mae") from the center of Onna-village. If you come by a vehicle, please park at "Village Center Parking" or "Parking Building". If you reach by OIST Shuttle, the bus will stop in front of Conference Center. Please proceed to main reception, go up to Floor B by lift and reach to Venue B250, Center Bldg.

恩納村は沖縄でも有数のリゾート地で高級ホテルから安宿まで多様な施設があります。ホテルエリアの中心地の「ムーンビーチ前バス停」付近では周辺にはいくつか飲食店あります。恩納村中心部から OIST へは車かタクシーか路線バス（バス停「大学院大学前」）で来ることができます。車でお越しの場合は「ヴィレッジセンター駐車場」か「立体駐車場」に車を止めてください。OIST シャトルバスでお越しの場合はカンファレンス・センター前にバスは止まります。受付を通って、エレベータで B 階まで上がり会場のセンター棟 B250 までお越しください。

Contact

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Affiliated Workshop in University of the Ryukyus - *only in Japanese Language* "Okinawa Open Facility Network Workshop" (おきなわオープンファシリティネットワークワークショップ)

Instrumental Research Facility of University of the Ryukyus assent the importance of the analytical instrument network in this region and hosts the affiliated workshop on November 28th, 2019.

The information will be published on their website (http://irc1.lab.u-ryukyu.ac.jp/) and please contact them for more details.

High-Throughput Single Cell Proteomics Analysis with Nanodroplet Sample Processing, Multiplex TMT labeling, and Ultra-Sensitive LC-MS analysis in a New Orbitrap Tribrid Mass Spectrometer.

Andreas Huhmer
Thermo Fisher Scientific

Abstract

Understanding heterogeneity at single cell level is of great interest for biomedical research. MS-based proteomics is a promising technique for single cell analysis by enabling identification and quantification of thousands of proteins in unbiased manner. However, due to inefficient single cell isolation, large sample losses during sample preparation and low throughput, the extension to single cell studies has been largely ineffective. To address these challenges, we combined nanoPOTS (Nanodroplet Processing in One-pot for Trace Samples) technology with Thermo Scientific™ Tandem Mass Tag™ (TMT™) isobaric labeling to efficiently process and analyze single mammalian cells containing <0.2 ng total proteins on new Thermo Scientific™ Orbitrap Eclipse™ Tribrid™ mass spectrometer with Real-Time Search to improve single cell proteome coverage and enhance quantification accuracy.

Discovery of Innate Peptide Elicitors for Regulating Plant Defense and Immune Responses

Yet-Ran Chen
Agricultural Biotechnology Research Center, Academia Sinica, Taipei, Taiwan

Abstract

Many important cell-cell communication events in animals are mediated by signaling peptides, but only few such events have been identified in plants. With the development of more sensitive and reliable technology platform for the detection and quantification of peptides using mass spectrometry, we are able to perform global quantification of signaling peptides in plants. With the use of this platform, a wound-induced peptide CAPE1 (CAP-derived peptide1) derived from PR-1 (pathogenesis-related protein 1) family was found and demonstrated to regulate plant antipathogen and antiherbivore responses in tomato. In addition, based on the discovery of CAPE1 functioning as a key systemic immune signal in tomato, a homolog CAPE1 peptide in Arabidopsis (AtCAPE1) was recently found to regulate not only on plant immunity but also on the salt-tolerance. Because the PR-1 and CAPE1 are highly conserved in different plant species, our discovery highlights a role for PR-1 in plant defense signaling and suggests the potential application of plant endogenous peptides in efforts to defeat different threats in crop production or induce the biosynthesis of key bioactive secondary metabolite in the herbal plants.

References

1. Y. L. Chen, K. T. Fan, S. C. Hung and **Y. R. Chen*** (2019) “The Role of Protein-Derived Peptides in Eliciting Plant Stress Reactions” *New Phytologyst*, 2019 Oct 8. doi: 10.1111/nph.16241. (SCI Category: Plant Science, IF(5-year, 2018):8.344)
2. Y. L. Chen, W. H. Chang, C. Y. Lee, **Y. R. Chen*** (2019) “An Improved Scoring Method for the Identification of Endogenous Peptides based on Mascot MS/MS Ion Search” *Analyst*, 144, 3045. (SCI Category: Analytical Chemistry, IF(2018):4.019)
3. Y. L. Chen, C. Y. Lee, K. T. Cheng, W. H. Chang, R. N. Huang, H. G. Nam and **Y. R. Chen*** “Quantitative Peptidomics Study Reveals a Wound-Induced Peptide from PR-1 Regulates Immune Signaling in Tomato” *Plant Cell,* 2014, **26**, *4135*. (SCI Category: Plant Science, IF(5-year):10.125, Category Ranking (excluding review journals):**1/194**)
4. W. H. Chang, C. Y. Lee, C. Y. Lin; M. C. Chen, W. S. Tzou and **Y. R. Chen*** “UniQua: A Universal Signal Processor for MS-Based Qualitative and Quantitative Proteomics Applications” *Anal. Chem.*, 2013, **85**, *890.* (SCI Category: Chemistry, Analytical, IF(5-year):5.796, Category Ranking(exclude review journals):**1/73**)
5. C. J. Chen, W. Y. Chen, M. J. Tseng and **Y. R. Chen*** “Tunnel Frit: A Nonmetallic In-Capillary Frit for Nanoflow Ultra High-Performance Liquid Chromatography - Mass Spectrometry Applications” *Anal. Chem.*, 2012, **84**, *297*. (SCI Category: Chemistry, Analytical, IF(5-year):5.796, Category Ranking(exclude review journals):**1/73**)

emHILIC-MS/MS proteomics technology for profiling deamidatome to unravel proteinopathy in complex age-related diseases.

Newman Siu Kwan Sze
School of Biological Sciences, Nanyang Technological University, 60 Nanyang Drive, Singapore 637551.

Abstract
Protein deamidation is a spontaneous degenerative protein modification (DPM) that disrupts the structure and function of both endogenous and therapeutic proteins. It has long been recognized as mediators of various human degenerative diseases and natural aging, however, progress of research in this field is extremely slow because of the technical challenges associated with studying this DPM in complex biological sample. To better understand the role of deamidation in the pathology of biological aging and degenerative diseases, we recently developed mixed mode electrostatic-interaction modified hydrophilic interaction liquid chromatography (emHILIC-MS/MS) coupled to high resolution tandem mass spectrometry for proteome-wide studying endogenous deamidatome in complex clinical samples.

Deamidation products which predominantly accumulate in the long-lived extracellular matrix (ECM) proteins which may subsequently degraded, change function, or misfolded and aggregation, leading to the loss in protein functions have implications in the onset of age-related dysfunctions, including cataract, cancer and neurodegenerative diseases (Alzheimers, Huntington and Parkinsons). Interestingly, our recent research uncovered that 'protein aging' by deamidation can also confer paradoxical 'gain-of-function' changes that actively enhance cardiovascular diseases (CVD) development. Specifically, the age-related ECM protein damage in atheroclerotic plaque and vascular bed of CVD patients can generate integrin-binding (isoD)GR motifs that promote leukocyte recruitment to vascular beds. Moreover, the (iso)DGR-integrin binding induces an outside-in signalling cascade in leukocyte which stimulates expression of pro-inflammatory cytokines and chemokines in blood vessel walls and promote atherosclerotic plaque development and disease progression. Thus, the gain-of-function integrin binding ECM proteins are potential biomarkers and therapeutic targets for atheroclerotic CVD.

Best Practices for Maximum Coverage and Reproducibility in Proteomics

Benjamin Orsburn, Ph.D.

Senior Scientist UVA Medical School

Abstract

“Proteomics” is a word that was coined directly after “genomics” and implied similar power. The “protein-ome” suggests the analysis of all of the proteins in an organism. Despite the promise made by this word over 20 years ago, only very recent developments have allowed the routine analysis of the 10,000 or more proteins present in complex organisms. Even today, with the very instruments, achieving complete theoretical protein coverage is not always an easy task. In this talk I will review the common technical pitfalls of proteomics and describe some of the newest proteomic techniques, from single cell analysis through new strategies that allow unprecedented proteome coverage in more rapid time. Examples include the use of isobaric tags to amplify the signal from peptides, thereby permitting the identification of thousands of proteins from normal single human cells. I’ll also describe the creative new data acquisition techniques inspired by the BoxCar strategy that massively improve on weaknesses in mass spectrometry ion physics. Finally, I’ll describe evidence that proteomics can be reproducible and demonstrate that this perceived weakness of the field is largely a problem of informatics.

Development of metabolic profiling methodologies by supercritical fluid technologies

Takeshi Bamba
Medical Institute of Bioregulation, Kyushu Univ., Fukuoka, Japan
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Supercritical fluids have desirable properties like high density, low viscosity, and high diffusivity, which make them suitable mobile phases for supercritical fluid chromatography (SFC), an analytical technique that is amenable to high-throughput, high-resolution analysis. Since supercritical carbon dioxide ($SCCO_2$), generally used as the mobile phase in SFC, is automatically emitted at room temperature, SFC is commonly used as a preparative method. However, SFC can also be used for high-precision biomolecular analysis, especially for hydrophobic metabolites, owing to the low polarity of $SCCO_2$. Combining mass spectrometry (MS) with SFC can widen the scope of applications of SFC to the analysis of biological components. Thus, we attempted to apply SFC/MS to metabolic profiling. Furthermore, we tried to expand the range of applications of SFC for diverse compounds, including polar compounds.

Additionally, we have developed supercritical fluid extraction (SFE) technologies for metabolic profiling. SFE can be used to extract labile compounds without degradation or loss. We applied SFE to the extraction of various metabolites and combined it with online SFC/MS for metabolic profiling. Furthermore, we developed a new online SFE-SFC-MS instrument.

In this presentation, I will discuss the possibility of using SFE and SFC technologies as analytical tools in the metabolic profiling of various compounds.

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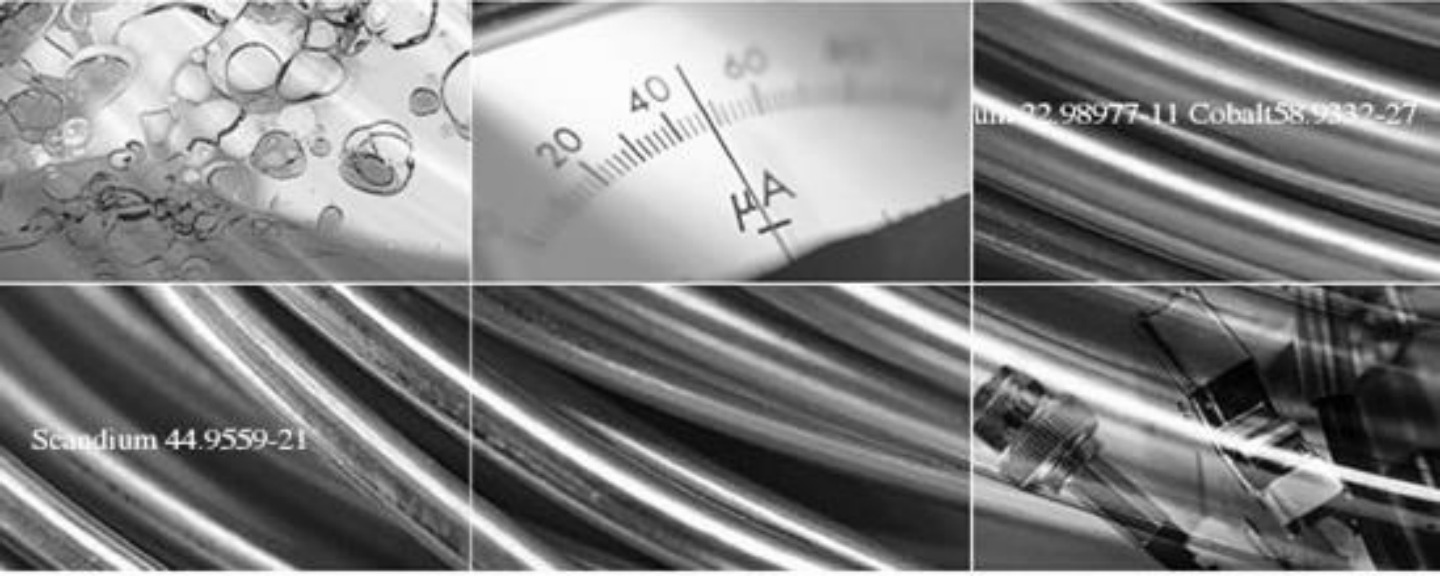

研　究　者　様　へ
徹底したサポートを追及

株式会社ウインクスは、2020年、東京五輪開催の年に、おかげさまで創立30周年を迎えます。

今後もバイオ・ライフサイエンス研究や科学技術研究のお客様に最先端の機器、ソフトウェア、消耗品、試薬、技術サポート等をご提供して参ります。

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