

シーケノム株式会社 技術セミナーのご案内

(筑波大学 形質転換植物デザイン研究拠点 テクニカルセミナー(3))

日時; 2010年9月9日(木) 13:30~14:30

場所; セミナー室

MassARRAY System (MALDI-TOF/MA) を用いた 高感度ゲノム解析アプリケーションのご紹介



●ゲノム研究における、定量と定性解析を実現!

- SNPタイピング...パイアレル、トリアレル、Mutationも解析
- 遺伝子発現定量解析...1aMの極微量遺伝子の定量も可能
- DNAメチル化定量解析...CpGユニットのメチル化比率を定量化
- 染色体コピー数解析...CNVの定量解析を実現
- リシーケンス解析...特定領域の多検体リシーケンス

ゲノムワイド解析以後、遺伝子やSNP、メチル化サイトなど、特定のゲノム・バイオマーカーを絞り込み、検証を重ねるステージに威力を発揮する、高感度ゲノム解析システムをご紹介します。

MassARRAY システムは、PCRの検出感度を活用したシンプルなサンプル調整プロトコルと、MALDI-TOF 質量分析計の検出精度を組み合わせることで、ハイスループットかつ高精度な定量解析ができるシステムです。SNPタイピング、メチル化定量解析、DNA/RNA定量解析といった複数のアプリケーションを組み合わせることで、バイオマーカー同定を効果的に行うことができます。また、各種アプリケーションでのPCR反応では、多重化反応(マルチプレックス)させることができ、SNPでは最大40アレル、遺伝子発現では、20遺伝子など、ハイスループット解析をサポートします。従来の、アレイ技術やリアルタイムPCRの原理である、蛍光色素による標識や、ハイブリダイゼーション反応などが不要のため、時間と費用コストを抑えることができます。

このようなSEQUENOMのMassARRAYシステムについて、基本的な機器とアプリケーションのご紹介と、植物ゲノミクスでの実用例について、ご紹介させていただきます。

センター内連絡先: 小口 (ext7726)

(Theme) SEQUENOM MassARRAY system for genomics research on Agricultural Bioscience.

(Presentator) Jenny Xiao , Sequenom, Inc.

(Over View SEQUENOM)

MassARRAY[®] technology is trusted by the leading genetics institutions worldwide. The new benchtop MassARRAY Analyzer 4 system makes this reference-standard DNA analysis technology accessible to more laboratories. The MassARRAY system addresses the many changing requirements for each stage of biomedical research. Its SNP Discovery and Genotyping capabilities help to identify and prioritize genetic targets. The Quantitative Gene Expression and Methylation applications are employed in the functional analysis and characterization of targets.

Applications: Multiple [applications](#) can be performed on one system that include:

- **SNP Genotyping:** iPLEX[®] Gold for SNP Genotyping will revolutionize your validation studies. Multiplex up to 36 SNPs in a single well and process up to 384 samples in parallel.
- **DNA Methylation:** EpiTYPER[®] for DNA Methylation analysis delivers individual methylation ratios for CpGs within a target sequence. It also is very accurate: relative methylation ratios can be assessed in a range between 10-90% with a standard deviation of 5%
- **Molecular Typing:** iSEQ[™] for Molecular Typing offers a combination of automation, versatility and discriminatory power that is superior to any other comparative sequence analysis system. The versatility of the iSEQ[™] software and open database access enables comparative sequencing with a wide range of global reference databases. Analysis results for 384 reactions are automatically achieved in less than an hour.
- **Somatic Mutation Profiling:** The Oncocarta[™] Panel v1.0 provides a comprehensive oncogene panel for profiling somatic mutations, enabling cancer researchers to profile genetic changes rapidly for basic research, clinical research, and/or drug development studies.
- **Quantitative Gene Expression:** QGE combines competitive PCR with MALDI-TOF mass spectrometry enabling a highly accurate, sensitive, and high-throughput method for the quantitative analysis of gene expression

Research Areas

MassARRAY technology and its applications have been used over the years in several Research Areas; to facilitate your understanding of the technology we have grouped some of the most important ones.

Translational Research: While whole genome studies have yielded large numbers of candidate biomarkers for disease diagnosis and predictive drug outcome, very few to date have been clinically validated. Closing the gap between discovery and clinical utilization requires high-throughput tools that enable efficient and cost-effective validation of panels of biomarkers in population-based studies.

Cancer Solutions: The utility of genetic profiles as biomarkers in the field of cancer biology is well accepted and widely documented. From gene polymorphisms in BRAF and EGFR, to methylation and expression profiles, genetic markers have been used for risk, progression, and prognosis.

Agricultural Genomics: MassARRAY technology is a powerful tool for downstream marker validation and large-scale screening. In addition to SNP genotyping, Sequenom offers a broad portfolio of solutions for agricultural genomics including copy number variation (CNV), methylation, and gene expression (QGE).

System

The new [MassARRAY Analyzer 4](#) system brings the power of mass spectrometry, robust molecular biology, and advanced data analysis software to meet the needs of high- and low-throughput laboratories. The system provides increased throughput, faster time-to-results, and the ability to cost effectively run from tens to thousands of samples - making the Analyzer 4 system an ideal genetic analysis system for use in basic and translational research laboratories.