The MassARRAY technology is used by the leading genetics institutions worldwide. The bench top MassARRAY Analyzer 4 system is a multi-application platform that addresses the following applications:

- Quantitative Methylation Analysis
- SNP Genotyping
- Somatic Mutations
- Quantitative Gene Expression
- Comparative Sequence Analysis

MassARRAY® Genetic Analysis System

Flexibility of Scale with Versatility of Application

MassARRAY Advantage
MassARRAY® genotyping facilitates identification and prioritization of genetic targets and in each stage of biomedical research. From targeted discovery utilizing 10s to 100s of multiplexed assays to validation of select markers against 100s to 1000s of samples, the MassARRAY system powers a variety of genomic studies.

MassARRAY® Quantitative Methylation Analysis

For more information please contact your area Sequenom office.

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Publications


#sq189_methyl_v4(0113-2011)
Overview
Unprecedented Levels of Performance
The EpiTYPER Assay
The EpiTYPER quantifies DNA methylation status and identifies differentially methylated CpG sites in any genomic region or candidate gene.

Efficiency
• Selectively hydrolyzes DNA to detect and quantify all methylated CGs with equal sensitivity.
• Conveniently isolated CpGs in amplicons of all size (up to 600 bp).
• Consistently determines fixed CpG sites in every sample.

Precision & Accuracy
• High precision (CV) within and between runs.

Sensitivity
• Detects down to 2% change in methylation levels.

Cost Effective
• No need to design CpG-specific primers.
• Many Cs can be analyzed in one simple reaction.

Simple Workflow
• No need to design CpG-specific primers.
• No PCR post-priming purification required.

Superior Performance – MassARRAY® EpiTYPER allows you to cost-effectively and quantitatively assess the methylation status of multiple CpGs in one or more PCR amplicons. Combined with the data quality and reporting functions, EpiTYPER is an indispensable tool for large-scale methylation studies.

The EpiTYPER Software

Data Analyzer Mode
DATA SET SELECTION
• Quickly access or build data sets to determine which data set is included in tab pages and EpiGram.

SPECROGRAM PANE
• Automatically displays the mass spectrum for all analyzed amplicons and identifies the selected Cs Site (e.g., 5-methylcytosine).

METYHILATION TAB PANE
• Customizable visual presentation of amplicon data in the most useful format that best suits your needs.

AmpliCap Display Mode
HIGH DEGREE OF PROGRAM CUSTOMIZATION
• Accessing these menus allows fine-tuning of program parameters to display and methylation color coding of Cs Sites.

EpiPlot PANE
• This pane provides graphical representations of the Cs Site within the selected amplicon. Such a color-coded representation of the degree of methylation shown in the methylation comparison pane to provide reliable comparison between samples and Cs Sites.

How It Works

MassARRAY® EpiTYPER is the method of choice for the quantitative analysis of DNA methylation and identification of differentially methylated CpG sites in any genomic region or candidate gene.

The EpiTYPER Assay

- The starting point of the protocol is bisulfite treatment of genomic DNA. This treatment converts non-methylated cytosine into uracil, thereby generating methylation-dependent sequence changes in the genomic DNA.
- PCR, with T7 Promoter-tagged primers, is used to amplify the template while preserving the induced sequence changes. After SAP treatment in vitro transcription is performed on the generated transcript, which is subjected to a proprietary base-specific cleavage process.
- The resulting fragments differ in size and mass depending on the sequence changes generated through bisulfite treatment. The fragment mass is determined by MALDI-TOF MS.
- The EpiTYPER software generates a report that contains quantitative information for each analyzed fragment.

Software
- The EpiTYPER software provides an advanced and convenient solution for the quantitative analysis of CpG Methylation. Harmonized and graphical interpretation tools are available and the data are automatically matched to the provided sequence.
- Bias statistical analysis and confidence ratings are available for each sample, allowing you to cost-effectively and quantitatively assess the methylation status of multiple CpGs in one or more PCR amplicons.

Testimonial

"We are successfully using Sequenom’s EpiTYPER for quantitative DNA methylation analysis in our comprehensive cancer research programs. This product enables us to analyze multiple CpGs within a single reaction and to easily compare their methylation status between individual samples. It provides a superior method for assessing methylation events at individual sites in whole genome and in multiple samples simultaneously across multiple CpG sites over a wide sample set, thereby covering the scope and spectrum of analysis."

Norma J. Nowak, Ph.D.,
Associate Professor, Director, Scientific Planning and Support Services,
RPCI and University at Buffalo, NY
Overview

Unprecedented Levels of Performance

The EpiTYPER Assay is the method of choice for the quantitative analysis of DNA methylation and identification of differentially methylated CpG sites in any genomic region or candidate gene.

**Efficiency**
- Detects multiple CpGs in amplifications of up to 600 bp.
- Complementary to other methods to verify the presence of methylated cytosine.

**Sensitivity**
- Detects down to 5% change in methylation levels.

**Cost Effective**
- Detects down to 5% change in methylation levels.

**Precise & Accurate**
- Confirms the presence of methylated regions.

**Simple Workflow**
- No need to design CpG-specific primers.
- No PCR product purification required.

**Data Analyzer Mode**
- This pane provides an advanced and convenient solution for the quantitative analysis of DNA Methylation.

**Superior Performance**
- MassARRAY EpiTYPER allows you to cost-effectively and quantitatively assess the methylation status of multiple CpGs in one or more PCR amplicons. Combined with the data quality and reporting functions, EpiTYPER is an indispensable tool for medium to large scale methylation studies.

The EpiTYPER Software

**Data Analyst Mode**
- Click on one or both of these buttons to determine which data set is included in tab pane and EpiGram.

**SEQUENCE VIEW PANE**
- This display shows the entire forward and reverse nucleotide sequence for the selected amplicon.

**AmpliSeq Display Mode**
- A high degree of program customization.
- Accessing these menus allows fine-tuning of program parameters to suit display and methylation color coding of CpG Sites.

**EpiGram TAB PANE**
- This pane provides graphical representations of the CpG Sites within the selected amplicon. Each color-coded representing the degree of methylation shown in the methylation pattern pane to provide a reliable control between samples and CpG Sites.
Quantitative Methylation Analysis

Overview

Unprecedented Levels of Performance

The EpiTYPER assay is based on thermal bisulfite conversion biochemistry followed by PCR and a proprietary base-specific cleavage process. The resulting clavage products depend on the presence of methylated cytosine in the original genomic DNA. The clavage products are then quantitatively and qualitatively analyzed by MALDI-TOF mass spectrometry. This combination creates a highly accurate, sensitive, and high-throughput method for the quantitative analysis of DNA methylation.

MassARRAY EpiTYPER is scalable and allows you to analyze multiple samples without compromising sensitivity, selectivity, or reproducibility. The EpiTYPER software provides convenient solutions for data analysis and export.

The EpiTYPER Assay

MassARRAY EpiTYPER is the method of choice for the quantitative analysis of DNA methylation and identification of differentially methylated CpG sites in any genomic region or candidate gene.

Efficiency

- Directly treated DNA to as little as 48 hours.
- Covers multiple CpGs in amplification.
- Up to 600 bp.
- Compatible with formalin-fixed paraffin-embedded tissue samples.

Precise & Accurate

- High precision (3% CV).
- High-caliber operational reliability.

Sensitive

- Detects down to 0.1% change in methylation levels.

Cost Effective

- 96 and 384 well microplates formats available.
- Multiple CpGs analyzed in one simple reaction.
- 96 and 384 well microplates formats available.
- PCR, with T7-promotor tagged reverse primers, is used to amplify the template while preserving the induced sequence changes.
- After SAP treatment and in vitro transcription is performed, the generated transcript is subjected to exo III to further degrade base specific cleavage.
- The resulting fragments differ in size and mass depending on the sequence changes generated through bisulfite treatment. The fragment mass is determined by MALDI-TOF MS and the EpiTYPER software generates a report that contains quantitative information for each analyzed fragment.

How it Works

Base-specific cleavage with MassCLEAVE – The starting point of the protocol is bisulfite treatment of genomic DNA. This treatment converts non-methylated cytosine into uracil, thus generating methylation-dependent sequence changes in the genomic DNA templates. PCR with T7-promotor tagged reverse primers, is used to amplify the template while preserving the induced sequence changes. After SAP treatment and in vitro transcription is performed, the generated transcript is subjected to exo III to further degrade base specific cleavage.

Superior Performance – MassARRAY EpiTYPER allows you to cost-effectively and quantitatively assess the methylation status of multiple CpGs in one or more PCR amplicons. Combined with the data quality and reporting functions, EpiTYPER is an indispensable tool for researchers to large-scale methylation studies.

Testimonial

“We are successfully using Sequenom’s EpiTYPER for quantitative DNA methylation analysis in our comprehensive cancer research program. This product enables us to analyze multiple CpGs in one reaction and to reliably compare their methylation status between individual samples. The simple method for accessing methylation events at multiple sites in the genome makes MassARRAY EpiTYPER quantitative screening economical and substantially reduces multiple GBS sites over a single sample dramatically increasing the scope and throughput of analysis.”

—Norma J. Nowak, Ph.D., RPCI and University at Buffalo, NY

The EpiTYPER Software

Data Analyzer Mode

DATA SET SELECTION

- Click on one or both of these buttons to determine which data set is included in tab panels and EpiGram.

SPECTRUM PANE

- Automatically display the mass spectrum for all analyzed amplicons and identify the selected CpG Site (i.e., green arrow in spectrum).

METHYLATION TAB PANE

- Optional customized visual presentation of amplicon data in the most useful format that best suits your needs.

SEQUENCE VIEW PANE

- This display shows the entire forward and reverse nucleotide sequence for the selected amplicon.

AmpliCap Display Mode

HIGH DEGREE OF PROGRAM CUSTOMIZATION

- Accessing three menus allows fine-tuning of program parameters to display and methylation color coding of CpG Sites.

EpiMap Tab Pane

- This pane provides graphical representations of the CpG Sites with the selected amplicon. Each color-coded rectangle represents the degree of methylation shown in the methylation contour map to provide a reliable, relative comparison between samples and CpG Sites.
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