Skysong Innovations
Advancing the Arizona State University Knowledge Enterprise

1475 N. Scottsdale Road, Suite 200
Scottsdale, AZ 85287-3538
Phone: 480 884 1996 Fax: 480 884 1984

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Inventors

Joshua LaBaer

Vel Murugan

Inam (Maryam) Ridha

Contact

Jovan Heusser
jovan.heusser@skysonginnovations.com

Multiplexed Methylated DNA Immunoprecipitation Sequencing (Mx-MeDIP-Seq)

DNA methylation is an epigenetic process that plays a critical role in gene expression modulation and has been implicated in many diseases, particularly cancer. One method to study the variability in methylation patterns is whole-genome bisulfite sequencing (WGBS), which analyzes single base methylation through immunoprecipitations using antibody or methyl binding domain proteins. While WGBS enables the analysis of DNA methylation with single base resolutions, it degrades DNA, requires microgram amounts of input DNA and purification. Further it is cost prohibitive and cannot distinguish between some distinct epigenetic modifications. Another method is Methylated DNA immunoprecipitation followed by sequencing (MeDIP-seq) which enriches methylated DNA fragments using monoclonal antibodies. This method has decent resolution and can detect differentially methylated regions, but it is incapable of multiplexed analyses.

Researchers at the Biodesign Institute of Arizona State University have developed a novel method to perform multiplexed methylated DNA immunoprecipitation sequencing (Mx-MeDIP-Seq). Because every run of the Mx-MeDIP-Seq can contain up to 15 different samples, this technique can analyze massive numbers of DNA in a parallel manner with low DNA input amounts. With as little as 10 ng of input DNA a greater than 95% specificity can be achieved and with as little as 1 ng input DNA, a greater than 75% specificity can be achieved. To demonstrate the reliability of the multiplexed protocol, MeDIP was performed, individually, on the same samples as those for Mx-MeDIP-Seq, and showed similar results.

This novel technique provides a simpler, faster and more cost-effect method for DNA methylation analyses in a multiplexed format.

Potential Applications

- Multiplexed methylated DNA sequencing
  - Early disease diagnoses
  - Forensic science studies
  - Research
  - Stem cell applications

Benefits and Advantages

- Can multiplex different prepared libraries prior to methylated DNA immunoprecipitation
- Can work on as little as 1ng of prepared library DNA
- Reduces the time, cost and amount of starting DNA/sample
- Reduced reagent needs
- Decreased complexity with minimal hands-on time and simplified labor-intensiveness

For more information about the inventor(s) and their research, please see

Dr. LaBaer's Biodesign Institute webpage

Dr. Murugan’s Biodesign Institute webpage