Centre for Addiction and Mental Health
Centre de toxicomanie et de santé mentale

Technology for large scale DNA Methylation Profiling

Description of the Technology:

Invention: The general principle of this technology consists of efficient enrichment of DNA fractions using methylation-sensitive restriction enzymes and subsequent amplification with DNA polymerase. The enriched fragments can be hybridized to microarrays containing thousand of genomic regions or may be used to perform deep-sequencing for genome-wide analysis. The statistical evaluation of signal intensity differences across different individuals enables the identification of the genomic regions bearing epigenetic differences, nominating candidates for biomarker validation.

Utility: This invention provides methods for detecting epigenetic changes throughout the genome that might be associated to 'dysfunctional' genes involved in complex diseases or traits. Such information will lead to the discovery of biomarkers for the development of tests for accurate and sensitive diagnosis, even at early stages. Furthermore, this technology identifies and categorizes the epigenetic factors that underlie differences among individuals in their response to drugs, with an application in patient stratification for the selection of the most appropriate therapeutic options.

Advantages: Among the advantages of the invention there are replicability, informativeness, works with limited DNA resources and has the flexibility to be effective with platforms for large-scale analysis, being microarray or deep-sequencing technologies. Sensitivity is significantly higher compared to other amplification-based technologies. In addition, clinical samples (tissue biopsies), animal models or cell line panels can be studied, for different research setups.

Publication:

Schumacher, A., et al., Microarray-based DNA methylation profiling: technology and applications. Nucleic Acids Res, 2006. 34(2): p. 528-42.

Patents:

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