frontiers in Bioengineering and Biotechnology

PERSPECTIVE
published: 23 July 2021
doi: 10.3389/fbioe.2021.703268

SERS-Based Evaluation of the DNA Methylation Pattern Associated With Progression in Clonal Leukemogenesis of Down Syndrome

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Here we show that surface-enhanced Raman scattering (SERS) analysis captures the relative hypomethylation of DNA from patients with acute leukemia associated with Down syndrome (AL-DS) compared with patients diagnosed with transient leukemia associated with Down syndrome (TL-DS), an information inferred from the area under the SERS band at 1005 cm^{-1} attributed to 5-methycytosine. The receiver operating characteristic (ROC) analysis of the area under the SERS band at 1005 cm^{-1} yielded an area under the curve (AUC) of 0.77 in differentiating between the AL-DS and TL-DS groups. In addition, we showed that DNA from patients with non-DS myeloproliferative neoplasm (non-DS-MPN) is hypomethylated compared to non-DS-AL, the area under the SERS band at 1005 cm^{-1} yielding an AUC of 0.78 in separating between non-DS-MPN and non-DS-AL. Overall, in this study, the area of the 1005 cm^{-1} DNA SERS marker band shows a stepwise decrease in DNA global methylation as cells progress from a pre-leukemia to a full-blown acute leukemia, highlighting thus the potential of SERS as an emerging method of analyzing the methylation landscape of DNA in the context of leukemia genesis and progression.

Keywords: SERS, down syndrome, acute leukemia, transient leukemia associated with down syndrome, myeloproliferative neoplasm

Abbreviations: SERS, surface-enhanced Raman scattering; AL, acute leukemia; AL-DS, acute leukemia associated with down syndrome; TL-DS, transient leukemia associated with down syndrome; MPN, myeloproliferative neoplasm; Non-DS-MPN, non-down syndrome myeloproliferative neoplasm; Non-DS-AL, non-down syndrome acute leukemia.

OPEN ACCESS

Edited by:
Aidan D. Meade, Technological University Dublin, Ireland

Reviewed by:
Ravi Manjithaya, Jawaharlal Nehru Centre for Advanced Scientific Research, India
Long Ma, Tianjin University of Science and Technology, China

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Specialty section:
This article was submitted to Nanobiotechnology, a section of the journal Frontiers in Bioengineering and Biotechnology

Received: *30 April 2021*
Accepted: *30 June 2021*
Published: *23 July 2021*

Citation:
Moisoiu V, Sas V, Stefancu A, Iancu SD, Jurj A, Pasca S, Iluta S, Zimta A-A, Tigu AB, Teodorescu P, Turcas C, Blag C, Dima D, Popa G, Arghirescu S, Man S, Colita A, Leopold N and Tomuleasa C (2021) SERS-Based Evaluation of the DNA Methylation Pattern Associated With Progression in Clonal Leukemogenesis of Down Syndrome. Front. Bioeng. Biotechnol. 9:703268. doi: 10.3389/fbioe.2021.703268