Clin. Lab. 2022;68:1-2

SHORT COMMUNICATION

Methylation of DNA Repair Genes as a Prognostic Biomarker in AML of a TCGA-LAML Cohort

Sholhui Park, Min-Kyung So, Jungwon Huh

Department of Laboratory Medicine, College of Medicine, Ewha Womans University, Seoul, Republic of Korea

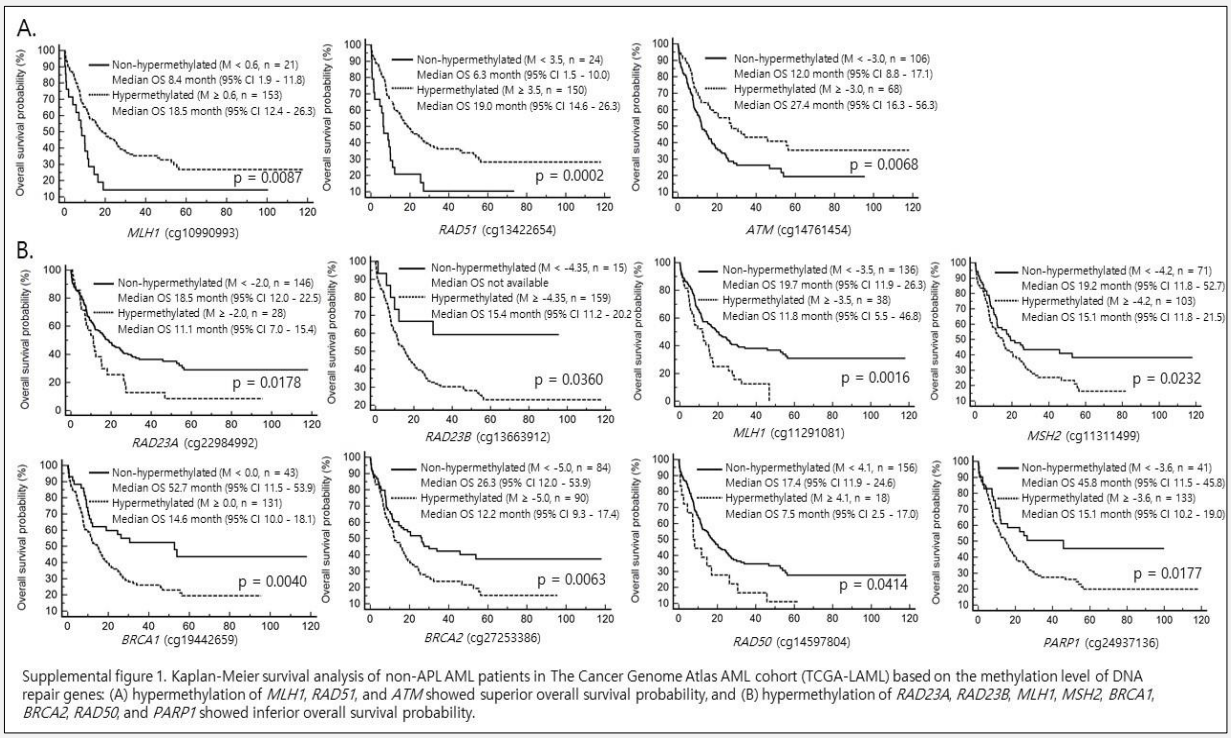
SUMMARY

Background: **Dysregulation of DNA damage response and altered DNA methylation in acute myeloid leukemia (AML) have been reported, but the impact of methylation of DNA repair genes has not yet been researched. We aimed to predict the prognosis of non-APL AML patients based on the known CpG site methylation levels of DNA repair genes through The Cancer Genome Atlas AML project (TCGA-LAML).**
Methods: **We utilized TCGA-LAML cohort (174 non-APL AML) for the methylation data of 22 DNA repair genes.**
Results: **In univariate analysis among 174 non-APL AML patients of the TCGA-LAML cohort, the hypermethylation of *MLH1*, *RAD51*, and *ATM* showed superior overall survival (OS) than non-hypermethylated groups, while hypermethylation of *RAD23A*, *RAD23B*, *MLH1*, *MSH2*, *BRCA1*, *BRCA2*, *RAD50*, and *PARP1* was associated with poor OS. We demonstrated that CpG hypermethylation levels of DNA repair genes differed according to the AML cytogenetic risk groups. In multivariate analysis, hypermethylation of *MLH1* and *RAD51* showed better OS than non-hypermethylated patients, but hypermethylation of *MSH2* and *RAD50* showed worse OS than non-hypermethylated patients.**
Conclusion: **Methylation of 4 DNA repair genes, such as *MLH1*, *RAD51*, *MSH2*, and *RAD50*, have the potential to be independent risk factors in non-APL AML patients.**
(Clin. Lab. 2022;68:1-2. DOI: 10.7754/Clin.Lab.2021.211025)

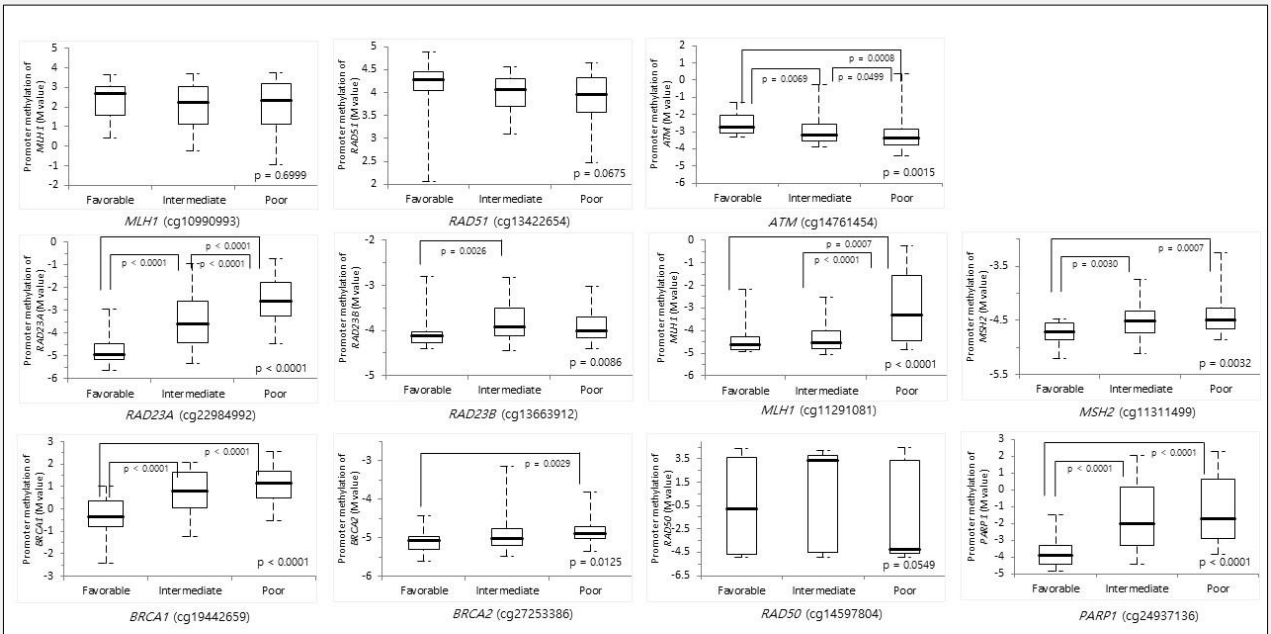
Correspondence:
Jungwon Huh, MD
Department of Laboratory Medicine
College of Medicine
Ewha Womans University
1071 Anyangcheon-ro, Yangcheon-gu
Seoul 07985
Republic of Korea
Phone: + 82 2-2650-5320
Fax: + 82 2-2650-5091
E-mail: JungWonH@ewha.ac.kr
ORCID: 0000-0001-8758-9847

Short Communication accepted October 25, 2021

Supplementary Tables and Figures



Supplemental figure 1. Kaplan-Meier survival analysis of non-APL AML patients in The Cancer Genome Atlas AML cohort (TCGA-LAML) based on the methylation level of DNA repair genes: (A) hypermethylation of *MLH1, RAD51,* and *ATM* showed superior overall survival probability, and (B) hypermethylation of *RAD23A, RAD23B, MLH1, MSH2, BRCA1, BRCA2, RAD50,* and *PARP1* showed inferior overall survival probability.



Supplemental figure 2. Relative methylation of DNA repair genes of non-APL AML cytogenetic risk groups in TCGA-LAML
The horizontal bars represent medians, boxes represent inter-quartile ranges, and dotted lines represent 5th and 95th percentiles.