

# Methylation status of SOCS1 and SOCS3 genes in patients with acute lymphoid leukemia: A case-control study

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## Abstract

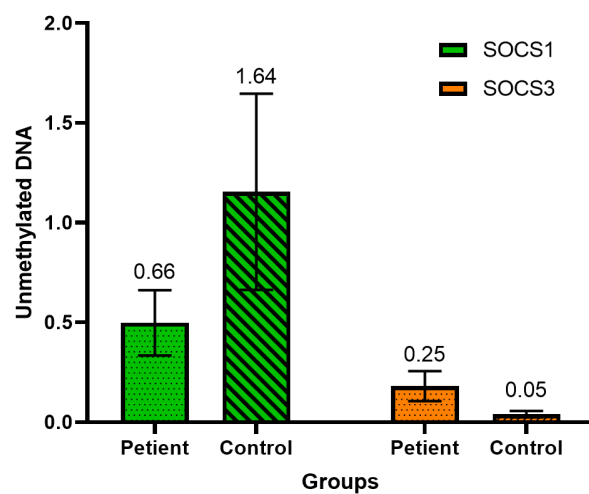
**Objective:** Acute Lymphoid Leukemia (ALL) is the leading childhood cancer with high mortality and morbidity. Studies have suggested an association of epigenetic transformations with prognosis, recurrence, and immunophenotypes of ALL. SOCS1 and SOCS3 are tumor suppressors inhibiting JAK/STAT signaling pathway and the resultant aberrant cell proliferation. We aimed to assess the methylated status of these genes in patients with ALL, using bone marrow and peripheral blood samples. **Materials and Methods:** 18 patients with ALL and 13 children with no malignancies were included. Using Bisulfite conversion, quantitative multiplex methylation-specific PCR and  $2^{-([?]/[?]\text{Ct})}$  formula, the methylated DNA in the promoters of SOCS1 and SOCS3 were measured. **Results:** ALL patients had higher mean methylation in SOCS1 promoter and lower mean methylation in SOCS3 promoter, compared to the control group. However, neither of these mean differences were statistically significant. **Conclusion:** This finding can set the foundation for further large-sample studies with the use of healthy children as the control group to strengthen the hypothetical association of the methylation status of SOCS1 and SOCS3 with ALL.

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**Figure 1:** Comparison of unmethylated DNA of SOCS1 and SOCS3 promoters in patients with ALL and healthy controls (Mean ± SEM).

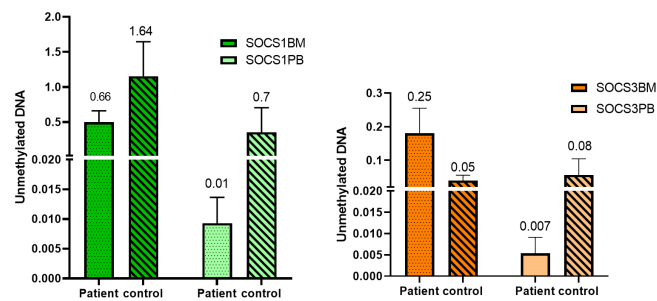


Figure 2: Comparison of unmethylated DNA of SOCS1 and SOCS3 promoters in patients with ALL and healthy controls in both sample groups Bone Marrow (BM) and Peripheral Blood (PB) (Mean  $\pm$  SEM).

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