# ROLE OF 3D GENOME ANALYSIS IN THE DIAGNOSIS AND THERAPY OF LEUKEMIA AND CANCER

In a recent paper in Nature[1] Xu *et al*. explore the relationship between three-dimensional (3D) chromatin structure and related methylation alterations in acute myeloid leukemia (AML). The authors conclude that changes in DNA methylation and 3D genome structure may provide subtype-specific clues for understanding and treating the disease.

The study was based on a variety of approaches through which profiles of chromatin organization compartments, topologically associating domains, and chromatin loop features in the context of other genomic alterations were analyzed in more than two dozen AML cases.

The analyses have highlighted that genetic subtypes of AML differ in chromatin organization features, with recurrent chromatin loops showing specific enhancer or silencer activity on promoters in the diverse myeloid tissue malignancies.

The AML-related genome organization and expression effects appear to be somewhat reversed in the presence of hypomethylating agents, such as 5-azacytidine or decitabine or in cells with lower-than-usual levels of genes coding for DNA methyltransferase enzymes. The results suggest that treatment with an HMA may achieve therapeutic efficacy, at least partly, through restoring normal chromatin architecture and opening new mechanism-based therapeutic approaches to improve treatment outcomes in AML and other cancers.

1. https://www.nature.com/articles/s41586-022-05365-x