Real-time PCR array analysis of human histone-modifying enzyme mRNA levels in pediatric acute myeloid leukemia

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Histone modification is dysregulated in various cancers, including pediatric acute myeloid leukemia (AML). Currently, the expression profile of histone-modification enzymes in pediatric AML is unclear. A real-time PCR array was designed and tested, and then used to profile mRNA expression of 85 genes encoding histone-modification enzymes in 27 pediatric AML samples and 20 normal controls. The histone-modifying enzyme mRNA expression profile in pediatric AML is significantly different from that of normal controls. A total of 28 genes were successfully clustered, including 15 up-regulated genes and 13 down-regulated genes in pediatric AML. GCN5L2, SETD8, KDM5C, AURKA, and AURKB were up-regulated and putative tumor suppressor gene EP300, PRMT3, PRMT8, and NOTCH2 were down-regulated in AML. Ingenuity Pathway Analysis revealed that gene expression, cancer, and embryonic development were the highest rated networks with 31 focus molecules and a significance score of 68. In addition, Ingenuity Pathway Analysis indicated that Rb, CDKN2C, and E2F1 are upstream regulators of histone-modifying enzymes in pediatric AML. Future studies will seek to validate these results and examine the role of Rb, CDKN2C, and E2F1 in the molecular basis of leukemia. This work may provide novel clues for understanding the aberrant molecular alterations that occur in pediatric AML.

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