“Calling Cards,” a Novel Approach for Identifying Transcription Factor-DNA Interactions, Uncovers AML-related HOXA9-NUP98 Fusion Product Targets

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UPDARTE ABSTRACT

INTRODUCTION

BACKGROUNDs

The NUP98-HOXA9 fusion transcript is recognized that has been described in acute myeloid leukemia (AML) as a hematopoietic cell marker and has been shown to induce cell cycle regulation and greater differentiation. However, its identification has been controversial, and the role of the fusion protein has not been well characterized. NUP98-HOXA9 fusion proteins have been associated with increased proliferation of hematopoietic cells and decreased differentiation. However, the function of the aberrant transcription factor has not been well characterized. This is in part because current methods of gene expression profiling do not provide sufficient information on the function of the aberrant transcription factor. Furthermore, these methods often have gaps in specific regions of the genome and can only identify a limited number of transcription factors. This study aimed to identify the transcription factors involved in AML and to confirm their involvement in AML using the NUP98-HOXA9 fusion transcript.

METHOD

BIOLOGY

The NUP98-HOXA9 fusion transcript is recognized that has been described in acute myeloid leukemia (AML) as a hematopoietic cell marker and has been shown to induce cell cycle regulation and greater differentiation. However, its identification has been controversial, and the role of the fusion protein has not been well characterized. NUP98-HOXA9 fusion proteins have been associated with increased proliferation of hematopoietic cells and decreased differentiation. However, the function of the aberrant transcription factor has not been well characterized. This is in part because current methods of gene expression profiling do not provide sufficient information on the function of the aberrant transcription factor. Furthermore, these methods often have gaps in specific regions of the genome and can only identify a limited number of transcription factors. This study aimed to identify the transcription factors involved in AML and to confirm their involvement in AML using the NUP98-HOXA9 fusion transcript.

RESULTS

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CONCLUSION

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